

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 06:49:11 ; Search time 7466 Seconds  
(without alignments)  
10896.907 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679  
Sequence: 1 gttgtccttcagcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hg.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_atg.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1679	100.0	1679	6	CQ768055 Sequence
2	1679	100.0	1679	6	AR528639 Sequence
3	1679	100.0	1679	6	AX358872 Sequence
4	1679	100.0	1679	6	AX362365 Sequence
5	1679	100.0	1679	6	AX403748 Sequence
6	1679	100.0	1679	6	AX454470 Sequence
7	1679	100.0	1679	6	AX464242 Sequence
8	1679	100.0	1679	6	AX490948 Sequence
9	1679	100.0	1679	9	AX358331 Homo sapi
10	1661.4	99.0	1693	6	AX439649 Sequence
11	1432.8	85.3	1839	6	AX665342 Sequence
12	1432.8	85.3	1839	9	AF126426 Homo sapi
13	1032	61.5	1032	6	AX439648 Sequence
14	996.8	59.4	2040	10	RUU16845
15	976.4	58.2	1615	10	BC023307
16	939	55.9	939	6	AR439650
17	910.6	54.2	1410	10	AF282980
18	910.4	54.2	1068	6	AX665344 Sequence
19	874.4	52.1	1104	6	AX665346 Sequence

93	272.6	16.2	5582	9	HSM806161	BX538014 Homo sapi	166	108	6.4	172146	2	AC130272	AC130272 Papio anu
94	271	16.1	1119	6	AX675563	AX675563 Sequence	c 167	107.8	6.4	169206	10	AC123550	AC123550 Mus muscu
95	271	16.1	2383	6	AX747470	AX747470 Sequence	c 168	107.8	6.4	277603	2	AC179543	AC179543 Mus muscu
96	271	16.1	2383	9	AK092307	AK092307 Homo sapi	169	106.2	6.3	229330	2	AC137057	AC137057 Rattus no
97	269.4	16.0	2840	9	AX358132	AX358132 Homo sapi	c 170	106.2	6.3	238070	2	AC134313	AC134313 Rattus no
98	260.4	15.5	1017	6	AX644995	AX644995 Sequence	c 171	106.2	6.3	242260	2	AC094567	AC094567 Rattus no
99	258.8	15.4	1018	6	AX644993	AX644993 Sequence	c 172	106.2	6.3	225120	9	AC127219	AC127219 Rattus no
100	257.2	15.3	1136	6	AX644997	AX644997 Sequence	c 173	106	6.3	142000	9	AC078813	AC078813 Homo sapi
c 101	256	15.2	257	11	G07361	G07361 human STR	174	105.6	6.3	913	6	AR542162	AR542162 Sequence
102	254.2	15.1	5605	9	BC036771	BC036771 Homo sapi	175	104.4	6.2	237376	2	AC124949	AC124949 Rattus no
103	248.2	14.8	186110	2	AC103204	AC102204 Mus muscu	c 176	104.4	6.2	277228	2	AC106911	AC106911 Rattus no
104	246	14.7	1169	6	AX644999	AX644999 Sequence	177	102.2	6.1	131490	10	AC122207	AC122207 Mus muscu
105	238.4	14.2	20731	9	AP004721	AP004721 Homo sapi	178	102.2	6.1	177251	10	AC124565	AC124565 Mus muscu
106	238.4	14.2	43087	9	AP005155	AP005155 Homo sapi	179	100	6.0	219	6	AR030583	AR030583 Sequence
c 107	235.6	14.0	203572	9	AC016769	AC016769 Homo sapi	180	99	5.9	219713	2	AC112456	AC112456 Rattus no
c 108	229.2	13.7	251	11	BV199013	BV199013 sqm19956	181	99	5.9	234283	2	AC114113	AC114113 Rattus no
109	223.2	13.3	2070	5	BC080221	BC080221 Danio rer	c 182	99	5.9	250355	2	AC127766	AC127766 Rattus no
110	223.2	13.3	2455	5	AF241637	AF241637 Danio rer	183	99	5.9	263661	2	AC106603	AC106603 Rattus no
111	221.8	13.2	4323	10	AK122576	AK122576 Mus muscu	c 184	99	5.9	319104	2	AC106602	AC106602 Rattus no
c 112	220.4	13.1	197553	2	AC146103	AC146103 Pan trogl	185	98.4	5.9	411	6	CO731080	CO731080 Sequence
c 113	217.4	12.9	36000	9	AP003166	AP003166 Homo sapi	186	95.8	5.8	187746	2	CO87123	CO87123 Mus muscu
c 114	209.4	12.5	152686	2	AC018913	AC018913 Homo sapi	187	95.2	5.7	219	6	AR030584	AR030584 Sequence
115	207.6	12.4	786	5	GGA132998	AJ132998 Gallus ga	c 188	92.6	5.5	214942	10	AC125214	AC125214 Mus muscu
116	207.2	12.3	168745	2	AC119552	AC119552 Rattus no	189	89.8	5.3	114269	2	AP002341	AP002341 Homo sapi
c 117	207.2	12.3	248329	2	AC109989	AC109989 Rattus no	190	89.8	5.3	152797	2	AC012134	AC012134 Homo sapi
c 118	205.6	12.2	110000	2	AC102028	Continuation (2 of	c 191	89.8	5.3	159520	9	AC113009	AC113009 Homo sapi
c 119	203.8	12.1	189323	2	AC150620	AC150620 Callithri	192	89.8	5.3	172128	2	AP000762	AP000762 Homo sapi
120	203.8	12.1	193545	2	AC151029	AC151029 Callithri	193	89.8	5.3	150104	2	AP002831	AP002831 Homo sapi
121	197.4	11.8	189037	2	AC150026	AC150026 Papio anu	194	89.8	5.3	199079	9	AP000844	AP000844 Homo sapi
122	193.6	11.5	352	6	BD026522	BD026522 Sequence	c 195	89	5.3	987	6	CO734933	CO734933 Sequence
123	193.6	11.5	352	6	BD026522	BD026522 Sequence	c 196	89	5.3	170006	9	AP005122	AP005122 Homo sapi
124	180.4	10.7	5666	6	AX740565	AX740565 Sequence	197	88	5.2	882	2	CO732721	CO732721 Sequence
c 125	177.6	10.6	215743	2	AC148958	AC148958 Otlemur	c 198	87.2	5.2	163120	5	BR296535	BR296535 Zebrafish
c 126	176.6	10.5	540	6	AX665354	AX665354 Sequence	c 199	87.2	5.2	180842	2	CR536619	CR536619 Danio rer
127	176.6	10.5	116069	2	AP000784	AP000784 Homo sapi	c 200	87	5.2	438	6	AR416888	AR416888 Sequence
c 128	176.6	10.5	123320	9	AP000863	AP000863 Homo sapi	201	87	5.2	438	6	AX977582	AX977582 Sequence
129	176.6	10.5	176676	2	AC012234	AC012234 Homo sapi	202	87	5.2	438	6	BD112441	BD112441 EST and e
130	176.6	10.5	177102	2	AP002808	AP002808 Homo sapi	c 203	86.6	5.2	169582	2	AC102190	AC102190 Mus muscu
131	175	10.4	642	6	CO732119	CO732119 Sequence	c 204	86.2	5.1	74368	9	AL391239	AL391239 Human DNA
132	174.4	10.4	182	6	AR413330	AR413330 Sequence	c 205	86.2	5.1	131457	9	AL356600	AL356600 Human DNA
133	174.4	10.4	182	6	AX970164	AX970164 Sequence	c 206	86.2	5.1	153852	2	AC009694	AC009694 Homo sapi
134	174.4	10.4	182	6	BD108883	BD108883 EST and e	207	86.2	5.1	315761	2	AL158079	AL158079 Homo sapi
c 135	173.2	10.3	242565	2	AC094728	AC094728 Rattus no	208	85.8	5.1	162247	2	AC102328	AC102328 Mus muscu
136	173.2	10.3	251570	2	AC094463	AC094463 Rattus no	209	85.4	5.1	295	6	CO732164	CO732164 Sequence
137	172.2	10.3	133989	2	AC149777	AC149777 Bos tauru	c 210	84.2	5.0	246900	2	AC128465	AC128465 Rattus no
c 138	172.2	10.3	205738	4	AC150499	AC150499 Bos tauru	c 211	83.4	5.0	162717	10	AC127259	AC127259 Mus muscu
139	171.2	10.2	184012	10	AC116523	AC116523 Mus muscu	212	83.4	5.0	258847	2	AC112746	AC112746 Rattus no
140	166.8	9.9	504	6	CO715694	CO715694 Sequence	213	83.4	5.0	285603	2	AC104926	AC104926 Mus muscu
141	164.8	9.8	531	6	CO719449	CO719449 Sequence	214	81.8	4.9	110000	2	AC110642	Continuation (4 of
142	163.2	9.7	585	6	AX079674	AX079674 Sequence	215	78.6	4.7	420	6	AX665356	AX665356 Sequence
c 143	160	9.5	408	6	AX684132	AX684132 Sequence	c 216	78.6	4.7	113063	2	AC010946	AC010946 Homo sapi
144	156	9.3	371	6	CO731074	CO731074 Sequence	c 217	78.6	4.7	191204	9	AP000843	AP000843 Homo sapi
145	152.4	9.1	793	5	BX932289	BX932289 Gallus ga	218	78.6	4.7	202505	2	AP000912	AP000912 Homo sapi
c 146	152.2	9.1	168191	2	AC151813	AC151813 Dasyypu n	219	77.8	4.6	177	6	AR030585	AR030585 Sequence
147	147.6	8.8	259743	2	AC113965	AC113965 Mus muscu	220	77.8	4.6	177	6	AR030586	AR030586 Sequence
148	146	8.7	200	6	AX898567	AX898567 Sequence	221	76.8	4.6	479	6	AX665358	AX665358 Sequence
c 149	146	8.7	200	6	BD034100	BD034100 Sequence	222	71.4	4.3	480	6	AX665357	AX665357 Sequence
c 150	145	8.6	150308	10	AC098294	AC098294 Rattus no	223	69.2	4.1	62350	9	AC067725	AC067725 Homo sapi
151	145	8.6	225433	2	AC106484	AC106484 Rattus no	224	69	4.1	146352	2	CR548641	CR548641 Danio rer
152	145	8.6	237199	10	AC094830	AC094830 Rattus no	225	69	4.1	186279	5	BR950870	BR950870 Zebrafish
153	140.6	8.4	152686	2	AC018913	AC018913 Homo sapi	c 226	69	4.1	191779	2	CR376789	CR376789 Danio rer
154	135.2	8.1	268	4	AF271984	AF271984 Bos tauru	227	67	4.0	176744	2	AC027631	AC027631 Homo sapi
c 155	135.2	8.1	110000	2	AC102028	AC102028 Mus muscu	228	65.6	3.9	198	6	AR030587	AR030587 Sequence
c 156	135.2	8.1	186110	2	AC102204	AC102204 Mus muscu	c 229	65	3.9	195956	2	AC127626	AC127626 Rattus no
157	128	7.6	184716	2	AC018368	AC018368 Homo sapi	c 230	65	3.9	249701	2	AC108525	AC108525 Rattus no
158	113.6	6.8	195993	2	AC134953	AC134953 Pan trogl	231	63.4	3.8	198	6	AR030588	AR030588 Sequence
159	113.6	6.8	212752	9	AC063977	AC063977 Homo sapi	c 232	61.6	3.7	270	6	AX665353	AX665353 Sequence
c 160	112.8	6.7	157263	2	BX957285	BX957285 Danio rer	c 233	60.8	3.6	117951	9	AL359821	AL359821 Human DNA
161	110.6	6.6	292	6	CO716587	CO716587 Sequence	c 234	60.8	3.6	199301	2	AC119938	AC119938 Mus muscu
c 162	110.4	6.6	213331	2	AC125960	AC125960 Rattus no	235	60	3.6	60	6	CQ544101	CQ544101 Sequence
163	109.6	6.5	175963	2	AC148913	AC148913 Sus scrofa	236	58.6	3.5	2000	6	AX655393	AX655393 Sequence
164	109.4	6.5	134184	2	AC150028	AC150028 Canis fam	237	58.6	3.5	166417	10	AC127685	AC127685 Mus muscu
165	108	6.4	168861	2	AC130786	AC130786 Papio anu	c 238	58	3.5	143672	2	AP001806	AP001806 Homo sapi

c 239	57.6	3.4	420	6	AX665355	Sequence	AX665355	Sequence	c 312	51.6	3.1	8979	6	AX345686	Sequence	AX345686	Sequence
c 240	57.6	3.4	142882	9	AP003029	Homo sapi	AP003029	Homo sapi	c 313	51.6	3.1	8979	6	AX348663	Sequence	AX348663	Sequence
c 241	56	3.3	193180	2	AC112588	Rattus no	AC112588	Rattus no	c 314	51.6	3.1	68009	2	AC136304	Homo sapi	AC136304	Homo sapi
242	55.6	3.3	247	6	CQ524931	Sequence	CQ524931	Sequence	c 315	51.4	3.1	921	9	HTPSAPHI	Sequence	HTPSAPHI	Sequence
243	55.6	3.3	4459	9	HSB804634	Sequence	HSB804634	Sequence	316	51.4	3.1	1933	9	NSM806048	Homo sapi	NSM806048	Homo sapi
244	55.4	3.3	34930	2	AC099999	Mus muscu	AC099999	Mus muscu	317	51.4	3.1	77139	2	AC008466	Homo sapi	AC008466	Homo sapi
245	55	3.3	1598	9	BC013323	Homo sapi	BC013323	Homo sapi	c 318	51.4	3.1	86789	10	AL928642	Mouse DNA	AL928642	Mouse DNA
c 246	55	3.3	6359	6	AX348331	Sequence	AX348331	Sequence	c 319	51.4	3.1	179187	9	AC091549	Homo sapi	AC091549	Homo sapi
c 247	54.4	3.2	6171	6	AX345690	Sequence	AX345690	Sequence	320	51.2	3.0	392	6	CQ516508	Sequence	CQ516508	Sequence
248	54	3.2	1273	10	BC049640	Sequence	BC049640	Sequence	321	51.2	3.0	504	6	CQ526778	Sequence	CQ526778	Sequence
249	53.8	3.2	3294	10	BC053924	Mus muscu	BC053924	Mus muscu	322	51.2	3.0	1719	9	AK116650	Ciona int	AK116650	Ciona int
250	53.8	3.2	134609	2	AC021416	Homo sapi	AC021416	Homo sapi	323	51.2	3.0	2099	9	BC043572	Homo sapi	BC043572	Homo sapi
251	53.8	3.2	150407	2	AC093228	Homo sapi	AC093228	Homo sapi	324	51.2	3.0	2207	10	BC066857	Mus muscu	BC066857	Mus muscu
252	53.8	3.2	163538	9	AC012598	Homo sapi	AC012598	Homo sapi	325	51.2	3.0	2217	9	BC073932	Homo sapi	BC073932	Homo sapi
253	53.4	3.2	165291	2	AC114775	Homo sapi	AC114775	Homo sapi	326	51.2	3.0	2286	9	BC020211	Homo sapi	BC020211	Homo sapi
c 254	53.4	3.2	167449	2	AC025073	Homo sapi	AC025073	Homo sapi	327	51.2	3.0	2419	9	BC043583	Homo sapi	BC043583	Homo sapi
255	53.4	3.2	172538	2	AC041016	Homo sapi	AC041016	Homo sapi	328	51.2	3.0	2704	3	AB073429	Ciona sav	AB073429	Ciona sav
256	53	3.2	607	6	CQ526845	Sequence	CQ526845	Sequence	329	51.2	3.0	3305	10	BC040407	Mus muscu	BC040407	Mus muscu
257	53	3.2	3000	9	BC041174	Homo sapi	BC041174	Homo sapi	330	51.2	3.0	3383	9	HSB803701	Homo sapi	HSB803701	Homo sapi
258	52.8	3.1	514	10	BC061178	Mus muscu	BC061178	Mus muscu	331	51.2	3.0	3383	9	HSB803701	Homo sapi	HSB803701	Homo sapi
259	52.8	3.1	601	5	BC082926	Xenopus l	BC082926	Xenopus l	332	51.2	3.0	3626	9	BC012147	Homo sapi	BC012147	Homo sapi
260	52.8	3.1	645	3	AY168768	Branchios	AY168768	Branchios	333	51.2	3.0	5123	10	BC064466	Mus muscu	BC064466	Mus muscu
261	52.8	3.1	3351	3	AF031517	Drosophil	AF031517	Drosophil	334	51.2	3.0	202533	2	AC146464	Sequence	AC146464	Sequence
c 262	52.8	3.1	5567	6	AX346491	Sequence	AX346491	Sequence	335	51	3.0	1637	5	BC064270	Xenopus t	BC064270	Xenopus t
c 263	52.8	3.1	5567	6	AX356448	Sequence	AX356448	Sequence	336	51	3.0	1950	9	BC042196	Homo sapi	BC042196	Homo sapi
264	52.6	3.1	904	10	BC038167	Mus muscu	BC038167	Mus muscu	337	51	3.0	2730	9	BC053349	Homo sapi	BC053349	Homo sapi
c 265	52.6	3.1	2000	6	AX655393	Sequence	AX655393	Sequence	338	50.8	3.0	897	10	AC140335	Mus muscu	AC140335	Mus muscu
266	52.4	3.1	1793	10	BC062171	Mus muscu	BC062171	Mus muscu	339	50.8	3.0	1026	6	CQ708603	Sequence	CQ708603	Sequence
c 267	52.4	3.1	5586	6	AX348391	Sequence	AX348391	Sequence	340	50.8	3.0	1383	5	BC074687	Xenopus t	BC074687	Xenopus t
268	52.4	3.1	69696	2	AC137968	Mus muscu	AC137968	Mus muscu	341	50.8	3.0	1429	9	BC043584	Homo sapi	BC043584	Homo sapi
269	52.4	3.1	167660	9	AF000826	Homo sapi	AF000826	Homo sapi	342	50.8	3.0	1447	9	BC044232	Homo sapi	BC044232	Homo sapi
270	52.4	3.1	196461	10	AL627314	Mouse DNA	AL627314	Mouse DNA	343	50.8	3.0	1763	10	BC061098	Mus muscu	BC061098	Mus muscu
c 271	52.4	3.1	205825	2	AP000881	Homo sapi	AP000881	Homo sapi	344	50.8	3.0	1882	5	BC068036	Xenopus t	BC068036	Xenopus t
c 272	52.2	3.1	666	6	CQ418830	Sequence	CQ418830	Sequence	345	50.8	3.0	1959	10	BC060504	Mus muscu	BC060504	Mus muscu
273	52.2	3.1	766	8	AF531371	Gossypium	AF531371	Gossypium	346	50.8	3.0	2313	10	BC021410	Mus muscu	BC021410	Mus muscu
274	52.2	3.1	828	10	BC049756	Mus muscu	BC049756	Mus muscu	347	50.8	3.0	2643	9	BC032495	Homo sapi	BC032495	Homo sapi
275	52.2	3.1	2010	6	CQ586755	Sequence	CQ586755	Sequence	348	50.8	3.0	5966	9	HSB808184	Homo sapi	HSB808184	Homo sapi
276	52.2	3.1	3063	6	AX817158	Sequence	AX817158	Sequence	349	50.8	3.0	163311	2	AC102506	Mus muscu	AC102506	Mus muscu
277	52.2	3.1	3927	3	DMU78177	Drosophila	DMU78177	Drosophila	c 350	50.8	3.0	171550	2	AC117731	Mus muscu	AC117731	Mus muscu
278	52.2	3.1	4052	3	AY060363	Drosophil	AY060363	Drosophil	351	50.8	3.0	195601	2	AL807787	Mus muscu	AL807787	Mus muscu
279	52.2	3.1	5154	9	HSB805947	Homo sapi	HSB805947	Homo sapi	c 352	50.8	3.0	201821	10	AL671901	Mouse DNA	AL671901	Mouse DNA
c 280	52.2	3.1	18218	6	AX346850	Sequence	AX346850	Sequence	c 353	50.6	3.0	393	6	CQ408183	Sequence	CQ408183	Sequence
c 281	52.2	3.1	153869	10	AF532114	Mus muscu	AF532114	Mus muscu	354	50.6	3.0	909	10	BC035323	Mus muscu	BC035323	Mus muscu
c 282	52.2	3.1	177617	2	AC123634	Mus muscu	AC123634	Mus muscu	355	50.6	3.0	1930	5	BC066725	Danio rer	BC066725	Danio rer
c 283	52.2	3.1	189627	10	AC1122934	Mus muscu	AC1122934	Mus muscu	356	50.6	3.0	2356	10	BC061208	Mus muscu	BC061208	Mus muscu
284	52.2	3.1	199909	2	AC114668	Mus muscu	AC114668	Mus muscu	357	50.6	3.0	2924	6	AX683129	Sequence	AX683129	Sequence
285	52	3.1	484	6	CQ526860	Sequence	CQ526860	Sequence	358	50.6	3.0	2924	10	S68736	Rattus sp.	S68736	Rattus sp.
286	52	3.1	1732	9	HSB806991	Homo sapi	HSB806991	Homo sapi	359	50.6	3.0	3758	9	HSB801755	Homo sapi	HSB801755	Homo sapi
287	52	3.1	1788	9	HSB806673	Homo sapi	HSB806673	Homo sapi	c 360	50.6	3.0	4990	6	CQ493127	Sequence	CQ493127	Sequence
288	52	3.1	1877	5	BC077826	Xenopus l	BC077826	Xenopus l	c 361	50.6	3.0	4990	6	CQ493522	Sequence	CQ493522	Sequence
289	52	3.1	3720	9	BC028048	Homo sapi	BC028048	Homo sapi	c 362	50.6	3.0	6029	6	AX279994	Sequence	AX279994	Sequence
290	52	3.1	4807	9	HSB808173	Homo sapi	HSB808173	Homo sapi	c 363	50.6	3.0	6029	6	AX356432	Sequence	AX356432	Sequence
c 291	52	3.1	5739	6	AX345621	Sequence	AX345621	Sequence	c 364	50.6	3.0	170788	2	AC139387	Rattus no	AC139387	Rattus no
292	52	3.1	180842	2	CN536619	Danio rer	CN536619	Danio rer	c 365	50.6	3.0	186488	10	AC102668	Mus muscu	AC102668	Mus muscu
293	51.8	3.1	1590	9	HSB803698	Homo sapi	HSB803698	Homo sapi	366	50.6	3.0	221903	10	AC125223	Mus muscu	AC125223	Mus muscu
294	51.8	3.1	1657	10	BC057688	Mus muscu	BC057688	Mus muscu	367	50.6	3.0	224635	2	AC094848	Rattus no	AC094848	Rattus no
295	51.8	3.1	1885	10	BC051143	Mus muscu	BC051143	Mus muscu	c 368	50.6	3.0	263637	2	AC094254	Rattus no	AC094254	Rattus no
296	51.8	3.1	2910	9	BC042070	Homo sapi	BC042070	Homo sapi	c 369	50.6	3.0	349980	6	AX344556	Sequence	AX344556	Sequence
297	51.6	3.1	681	5	BC071507	Danio rer	BC071507	Danio rer	c 370	50.4	3.0	310	6	AX187085	Sequence	AX187085	Sequence
298	51.6	3.1	935	3	AX174210	Ciona int	AX174210	Ciona int	371	50.4	3.0	319	6	CQ670102	Sequence	CQ670102	Sequence
299	51.6	3.1	1604	9	BC044260	Homo sapi	BC044260	Homo sapi	372	50.4	3.0	655	3	AK174309	Ciona int	AK174309	Ciona int
300	51.6	3.1	1620	10	BC046622	Mus muscu	BC046622	Mus muscu	373	50.4	3.0	669	9	HSB800251	Homo sapi	HSB800251	Homo sapi
301	51.6	3.1	3508	6	BD227241	Secreted	BD227241	Secreted	374	50.4	3.0	931	10	BC049725	Mus muscu	BC049725	Mus muscu
c 302	51.6	3.1	5759	6	CQ807289	Sequence	CQ807289	Sequence	375	50.4	3.0	1027	9	BC035292	Homo sapi	BC035292	Homo sapi
c 303	51.6	3.1	8759	6	CQ807079	Sequence	CQ807079	Sequence	376	50.4	3.0	1044	10	BC049565	Mus muscu	BC049565	Mus muscu
c 304	51.6	3.1	8759	6	AX598909	Sequence	AX598909	Sequence	377	50.4	3.0	1245	10	BC049747	Mus muscu	BC049747	Mus muscu
c 305	51.6	3.1	8759	6	AX599037	Sequence	AX599037	Sequence	378	50.4	3.0	2677	9	BC050385	Homo sapi	BC050385	Homo sapi
c 306	51.6	3.1	8759	6	AX767495	Sequence	AX767495	Sequence	379	50.4	3.0	2815	9	BC038597	Homo sapi	BC038597	Homo sapi
c 307	51.6	3.1	8759	6	AX795857	Sequence	AX795857	Sequence	380	50.4	3.0	3183	9	BC044242	Homo sapi	BC044242	Homo sapi
c 308	51.6	3.1	8759	6	AX823377	Sequence	AX823377	Sequence	c 381	50.4	3.0	6668	6	AX346598	Sequence	AX346598	Sequence
c 309	51.6	3.1	8759	6	AX826017	Sequence	AX826017	Sequence	c 382	50.4	3.0	230193	10	AL929570	Mouse DNA	AL929570	Mouse DNA
c 310	51.6	3.1	8979	6	AX251876	Sequence	AX251876	Sequence	383	50.2	3.0	201	6	CQ487162	Sequence	CQ487162	Sequence
c 311	51.6	3.1	8979	6	AX344266	Sequence	AX344266	Sequence	384	50.2	3.0	240	6	I48979	Sequence	I48979	Sequence

C 385	50.2	3.0	383	6	CQ502211	Sequence	C 458	49.8	3.0	8712	6	AX344694	AX344694	Sequence
C 386	50.2	3.0	383	6	CQ511079	Sequence	C 459	49.8	3.0	13758	3	SST558163	AJ558163	Strongylo
C 387	50.2	3.0	384	6	CQ395463	Sequence	C 460	49.8	3.0	84299	5	BX469900	BX469900	Zebrafish
C 388	50.2	3.0	384	6	CQ401799	Sequence	C 461	49.8	3.0	132068	9	AC006965	AC006965	Homo sapi
C 389	50.2	3.0	384	6	CQ487104	Sequence	C 462	49.8	3.0	156254	10	AC129196	AC129196	Mus muscu
C 390	50.2	3.0	448	6	CQ516969	Sequence	C 463	49.8	3.0	183762	2	AC128232	AC128232	Rattus no
C 391	50.2	3.0	861	9	AK026600	Homo sapi	C 464	49.8	3.0	193796	2	AC123600	AC123600	Mus muscu
C 392	50.2	3.0	1090	10	BC049543	BC049543 Homo sapi	C 465	49.8	3.0	198615	10	AC123678	AC123678	Mus muscu
C 393	50.2	3.0	1418	10	BC052344	BC052344 Mus muscu	C 466	49.8	3.0	212604	5	AL805945	AL805945	Zebrafish
C 394	50.2	3.0	1619	9	BC032001	BC032001 Homo sapi	C 467	49.8	3.0	218319	2	AC107863	AC107863	Mus muscu
C 395	50.2	3.0	2078	9	BC042098	BC042098 Homo sapi	C 468	49.8	3.0	251721	2	AC136566	AC136566	Rattus no
C 396	50.2	3.0	2104	9	BC032371	BC032371 Homo sapi	C 469	49.8	3.0	263341	2	AC094581	AC094581	Rattus no
C 397	50.2	3.0	2641	10	BC044860	BC044860 Mus muscu	C 470	49.8	3.0	266869	2	AC123456	AC123456	Rattus no
C 398	50.2	3.0	4064	10	BC072632	BC072632 Mus muscu	C 471	49.8	3.0	289973	2	AC135678	AC135678	Rattus no
C 399	50.2	3.0	6476	6	AX345442	AX345442 Sequence	C 472	49.6	3.0	762	9	BC070287	BC070287	Homo sapi
C 400	50.2	3.0	150751	9	AC092609	AC092609 Homo sapi	C 473	49.6	3.0	793	9	BC018189	BC018189	Homo sapi
C 401	50.2	3.0	168136	2	AC138388	AC138388 Mus muscu	C 474	49.6	3.0	1003	5	BC067645	BC067645	Danio rer
C 402	50.2	3.0	182871	3	AC117176	AC117176 Dictyoste	C 475	49.6	3.0	1044	9	AB019565	AB019565	Homo sapi
C 403	50.2	3.0	189631	2	AC009920	AC009920 Homo sapi	C 476	49.6	3.0	1218	9	BC065742	BC065742	Homo sapi
C 404	50.2	3.0	203114	2	AC011818	AC011818 Homo sapi	C 477	49.6	3.0	1250	9	BC051908	BC051908	Homo sapi
C 405	50.2	3.0	349980	6	AX344553	AX344553 Sequence	C 478	49.6	3.0	1271	9	AF090934	AF090934	Homo sapi
C 406	50	3.0	325	6	CQ527169	Sequence	C 479	49.6	3.0	1340	9	BC073835	BC073835	Homo sapi
C 407	50	3.0	464	6	CQ519083	Sequence	C 480	49.6	3.0	1458	9	BC041443	BC041443	Homo sapi
C 408	50	3.0	471	6	CQ522475	Sequence	C 481	49.6	3.0	1530	9	BC036925	BC036925	Homo sapi
C 409	50	3.0	646	5	BC083988	BC083988 Xenopus 1	C 482	49.6	3.0	1606	10	BC051176	BC051176	Mus muscu
C 410	50	3.0	653	10	BC039566	BC039566 Mus muscu	C 483	49.6	3.0	1657	8	NTACS	X98492	Nicotiana t
C 411	50	3.0	842	9	BC051899	BC051899 Homo sapi	C 484	49.6	3.0	1787	9	BC046645	BC046645	Homo sapi
C 412	50	3.0	870	6	BD231669	BD231669 31 human	C 485	49.6	3.0	1993	3	AK112520	AK112520	Ciona int
C 413	50	3.0	2240	9	BC062587	BC062587 Homo sapi	C 486	49.6	3.0	2027	9	BC063512	BC063512	Homo sapi
C 414	50	3.0	2556	9	HSN805953	BX537854 Homo sapi	C 487	49.6	3.0	2081	9	HSN806272	HSN806272	Homo sapi
C 415	50	3.0	2936	5	BC077828	BC077828 Xenopus 1	C 488	49.6	3.0	2135	10	BC017640	BC017640	Mus muscu
C 416	50	3.0	3203	9	BC040941	BC040941 Homo sapi	C 489	49.6	3.0	2161	6	CQ414527	CQ414527	Sequence
C 417	50	3.0	3645	10	BC062916	BC062916 Mus muscu	C 490	49.6	3.0	2350	9	BC063427	BC063427	Homo sapi
C 418	50	3.0	3806	5	AJ720876	AJ720876 Gallus ga	C 491	49.6	3.0	2521	10	BC026021	BC026021	Mus muscu
C 419	50	3.0	4942	9	HSN808887	BX648736 Homo sapi	C 492	49.6	3.0	2870	9	HSN800882	HSN800882	Homo sapi
C 420	50	3.0	5387	6	AX344633	AX344633 Sequence	C 493	49.6	3.0	3141	10	BC017634	BC017634	Mus muscu
C 421	50	3.0	9747	9	HSN806689	BX640641 Homo sapi	C 494	49.6	3.0	3232	9	AF090901	AF090901	Homo sapi
C 422	50	3.0	21537	6	AX346901	AX346901 Sequence	C 495	49.6	3.0	3914	9	HSN803724	HSN803724	Homo sapi
C 423	50	3.0	110000	2	PFM413_07	Continuation (8 of	C 496	49.6	3.0	4385	9	HSN806219	HSN806219	Homo sapi
C 424	50	3.0	137697	2	AC126419	AC126419 Mus muscu	C 497	49.6	3.0	5134	9	BC032404	BC032404	Homo sapi
C 425	50	3.0	160706	2	AC137910	AC137910 Canis fam	C 498	49.6	3.0	5355	9	HSN806819	HSN806819	Homo sapi
C 426	50	3.0	173053	10	AL844145	AL844145 Mouse DNA	C 499	49.6	3.0	5520	6	AX345579	AX345579	Sequence
C 427	50	3.0	184057	10	AL928579	AL928579 Mouse DNA	C 500	49.6	3.0	6015	6	AX345579	AX345579	Sequence
C 428	50	3.0	184163	2	AC120245	AC120245 Rattus no	C 501	49.6	3.0	110000	2	AC102349	AC102349	Sequence
C 429	50	3.0	189649	2	AC139641	AC139641 Rattus no	C 502	49.6	3.0	142948	9	AC147025	AC147025	Pan trogl
C 430	50	3.0	212996	2	CR548633	CR548633 Danio rer	C 503	49.6	3.0	151802	3	AC114263	AC114263	Dictyoste
C 431	50	3.0	245677	10	AC129162	AC129162 Rattus no	C 504	49.6	3.0	173854	2	AC073047	AC073047	Homo sapi
C 432	50	3.0	249734	2	AC097362	AC097362 Rattus no	C 505	49.6	3.0	187418	10	AL672278	AL672278	Mouse DNA
C 433	49.8	3.0	263	6	CQ663258	CQ663258 Sequence	C 506	49.6	3.0	194398	10	AC135669	AC135669	Mus muscu
C 434	49.8	3.0	270	6	CQ655781	CQ655781 Sequence	C 507	49.6	3.0	214029	2	AC148335	AC148335	Mus muscu
C 435	49.8	3.0	311	6	CQ517391	CQ517391 Sequence	C 508	49.6	3.0	349980	6	AX344563	AX344563	Sequence
C 436	49.8	3.0	376	6	CQ526056	Sequence	C 509	49.4	2.9	408	6	CQ524818	CQ524818	Sequence
C 437	49.8	3.0	381	6	CQ522618	Sequence	C 510	49.4	2.9	438	6	CQ514042	CQ514042	Sequence
C 438	49.8	3.0	543	6	CQ524637	Sequence	C 511	49.4	2.9	481	9	BC070219	BC070219	Homo sapi
C 439	49.8	3.0	545	6	AX185705	AX185705 Sequence	C 512	49.4	2.9	579	6	CQ526842	CQ526842	Sequence
C 440	49.8	3.0	573	11	BV060605	BV060605 S209P6332	C 513	49.4	2.9	622	6	CQ427774	CQ427774	Sequence
C 441	49.8	3.0	726	9	HS4327951	AJ327951 Homo sapi	C 514	49.4	2.9	658	6	BD275413	BD275413	50 Human
C 442	49.8	3.0	815	9	BC070265	BC070265 Homo sapi	C 515	49.4	2.9	781	10	BC028530	BC028530	Mus muscu
C 443	49.8	3.0	854	3	AK174348	AK174348 Ciona int	C 516	49.4	2.9	1081	9	BC043527	BC043527	Homo sapi
C 444	49.8	3.0	894	9	BC044257	BC044257 Homo sapi	C 517	49.4	2.9	1310	9	HSN807559	HSN807559	Homo sapi
C 445	49.8	3.0	1048	6	BD223102	BD223102 98 human	C 518	49.4	2.9	1589	9	BC043543	BC043543	Homo sapi
C 446	49.8	3.0	1048	6	AR243800	AR243800 Sequence	C 519	49.4	2.9	1603	6	CQ490224	CQ490224	Sequence
C 447	49.8	3.0	1073	6	BD190930	BD190930 Secreted	C 520	49.4	2.9	1603	6	CQ491236	CQ491236	Sequence
C 448	49.8	3.0	1824	9	BC018641	BC018641 Homo sapi	C 521	49.4	2.9	1603	6	CQ496086	CQ496086	Sequence
C 449	49.8	3.0	1837	6	AX962574	AX962574 Sequence	C 522	49.4	2.9	1603	6	CQ497104	CQ497104	Sequence
C 450	49.8	3.0	2005	9	BC013372	BC013372 Homo sapi	C 523	49.4	2.9	1647	9	HSN806060	HSN806060	Homo sapi
C 451	49.8	3.0	2012	9	AY125488	AY125488 Homo sapi	C 524	49.4	2.9	2002	9	BC068030	BC068030	Homo sapi
C 452	49.8	3.0	2266	9	BC047898	BC047898 Homo sapi	C 525	49.4	2.9	2395	9	AF090903	AF090903	Homo sapi
C 453	49.8	3.0	2496	6	BD191411	BD191411 Secreted	C 526	49.4	2.9	3475	9	HSN808741	HSN808741	Homo sapi
C 454	49.8	3.0	2539	9	BC041100	BC041100 Homo sapi	C 527	49.4	2.9	4066	10	BC048824	BC048824	Mus muscu
C 455	49.8	3.0	2630	9	BC038222	BC038222 Homo sapi	C 528	49.4	2.9	4744	5	BC066770	BC066770	Xenopus 1
C 456	49.8	3.0	3230	9	BC063118	BC063118 Homo sapi	C 529	49.4	2.9	4782	14	AY744492	AY744492	Tomato sp
C 457	49.8	3.0	7346	6	AX345427	AX345427 Sequence	C 530	49.4	2.9	71532	2	AC023655	AC023655	Homo sapi



C 531	49.4	2.9	84821	10	BX276123	Mouse DNA	604	49	2.9	2700	9	BC064849	BC064849 Homo sapi
C 532	49.4	2.9	110000	3	AC116305	Dictyoste	605	49	2.9	2728	9	BC022218	BC022218 Homo sapi
C 533	49.4	2.9	138604	2	CR847865	Danio rer	606	49	2.9	3020	10	BC055068	BC055068 Mus muscu
C 534	49.4	2.9	169736	2	AC126225	Papio anu	607	49	2.9	3482	9	BSM000550	BSM000550 Homo sapi
C 535	49.4	2.9	187024	2	CR759947	Gorilla g	608	49	2.9	3499	10	BC007476	BC007476 Mus muscu
C 536	49.4	2.9	222723	2	AC141526	Rattus no	609	49	2.9	3856	9	BSM805531	BSM805531 Homo sapi
C 537	49.4	2.9	335050	3	FA929356	Alu29356	610	49	2.9	3870	9	BSM806049	BSM806049 Homo sapi
C 538	49.4	2.9	349980	6	AX344559	Sequence	611	49	2.9	3916	10	BC018439	BC018439 Mus muscu
C 539	49.4	2.9	349980	6	AX344566	Sequence	612	49	2.9	5703	10	BC054080	BC054080 Mus muscu
C 540	49.2	2.9	442	6	CQ526679	Sequence	613	49	2.9	5845	6	AX346564	AX346564 Sequence
C 541	49.2	2.9	539	6	CQ526992	Sequence	614	49	2.9	5930	6	CQ412529	CQ412529 Sequence
C 542	49.2	2.9	544	6	CQ524776	Sequence	615	49	2.9	6012	6	AX348960	AX348960 Sequence
C 543	49.2	2.9	554	6	CQ526772	Sequence	616	49	2.9	6161	6	AX345313	AX345313 Sequence
C 544	49.2	2.9	575	6	CQ526566	Sequence	617	49	2.9	6211	6	AX345708	AX345708 Sequence
C 545	49.2	2.9	621	6	AX187131	Sequence	618	49	2.9	6522	6	AX345952	AX345952 Sequence
C 546	49.2	2.9	650	9	BC034814	Homo sapi	619	49	2.9	6719	9	BSM801507	BSM801507 Homo sapi
C 547	49.2	2.9	758	9	BC062750	Homo sapi	620	49	2.9	11416	6	AX251758	AX251758 Sequence
C 548	49.2	2.9	1191	9	BC014547	Homo sapi	621	49	2.9	11416	6	AX345020	AX345020 Sequence
C 549	49.2	2.9	1381	5	BC063358	Xenopus t	622	49	2.9	40862	6	AX348567	AX348567 Sequence
C 550	49.2	2.9	1537	9	BSM803079	Sequence	623	49	2.9	125020	9	AF429315	AF429315 Homo sapi
C 551	49.2	2.9	1629	10	BC033451	Sequence	624	49	2.9	135050	2	AC118536	AC118536 Canis fam
C 552	49.2	2.9	1702	9	BC052993	Homo sapi	625	49	2.9	135050	2	AC118536	AC118536 Canis fam
C 553	49.2	2.9	2270	9	BSM806047	Sequence	626	49	2.9	160230	10	BSM806047	BSM806047 Sequence
C 554	49.2	2.9	2451	9	BC050636	Homo sapi	627	49	2.9	180352	2	AC120550	AC120550 Mus muscu
C 555	49.2	2.9	2501	6	AX599024	Sequence	628	49	2.9	198792	2	AC117825	AC117825 Mus muscu
C 556	49.2	2.9	2628	9	BC032691	Homo sapi	629	49	2.9	203422	2	AC107857	AC107857 Mus muscu
C 557	49.2	2.9	2661	10	BC026137	Sequence	630	49	2.9	248353	2	AC106139	AC106139 Rattus no
C 558	49.2	2.9	3030	3	AK116919	Ciona int	631	49	2.9	349980	6	AX344561	AX344561 Sequence
C 559	49.2	2.9	3300	9	BC011656	Homo sapi	632	49	2.9	349980	6	AX344561	AX344561 Sequence
C 560	49.2	2.9	3341	9	BC032308	Homo sapi	633	49	2.9	349980	6	AX344561	AX344561 Sequence
C 561	49.2	2.9	3392	3	AF300334	Dictyoste	634	49	2.9	349980	6	AX344561	AX344561 Sequence
C 562	49.2	2.9	3686	10	BC033773	Sequence	635	49	2.9	349980	6	AX344561	AX344561 Sequence
C 563	49.2	2.9	3836	9	BC063854	Homo sapi	636	49	2.9	349980	6	AX344561	AX344561 Sequence
C 564	49.2	2.9	4265	9	BSM807603	Sequence	637	49	2.9	349980	6	AX344561	AX344561 Sequence
C 565	49.2	2.9	6644	6	E23356	Virus vecto	638	49	2.9	349980	6	AX344561	AX344561 Sequence
C 566	49.2	2.9	7058	6	AX348438	Sequence	639	49	2.9	349980	6	AX344561	AX344561 Sequence
C 567	49.2	2.9	7372	6	E23357	Virus vecto	640	49	2.9	349980	6	AX344561	AX344561 Sequence
C 568	49.2	2.9	7797	6	E23355	Virus vecto	641	49	2.9	349980	6	AX344561	AX344561 Sequence
C 569	49.2	2.9	7996	6	E23359	Virus vecto	642	49	2.9	349980	6	AX344561	AX344561 Sequence
C 570	49.2	2.9	11394	6	AX323608	Sequence	643	49	2.9	349980	6	AX344561	AX344561 Sequence
C 571	49.2	2.9	35962	6	AX598904	Sequence	644	49	2.9	349980	6	AX344561	AX344561 Sequence
C 572	49.2	2.9	153064	9	AC011492	Homo sapi	645	49	2.9	349980	6	AX344561	AX344561 Sequence
C 573	49.2	2.9	162473	9	AC005803	Homo sapi	646	49	2.9	349980	6	AX344561	AX344561 Sequence
C 574	49.2	2.9	226142	2	AC126422	Sequence	647	49	2.9	349980	6	AX344561	AX344561 Sequence
C 575	49.2	2.9	245117	2	AC111284	Rattus no	648	49	2.9	349980	6	AX344561	AX344561 Sequence
C 576	49.2	2.9	302156	3	AC116977	Dictyoste	649	49	2.9	349980	6	AX344561	AX344561 Sequence
C 577	49.2	2.9	349980	6	AX344573	Sequence	650	49	2.9	349980	6	AX344561	AX344561 Sequence
C 578	49	2.9	256	6	AX182154	Sequence	651	49	2.9	349980	6	AX344561	AX344561 Sequence
C 579	49	2.9	347	6	CQ526680	Sequence	652	49	2.9	349980	6	AX344561	AX344561 Sequence
C 580	49	2.9	429	6	CQ525532	Sequence	653	49	2.9	349980	6	AX344561	AX344561 Sequence
C 581	49	2.9	469	6	CQ524790	Sequence	654	49	2.9	349980	6	AX344561	AX344561 Sequence
C 582	49	2.9	472	6	CQ525172	Sequence	655	49	2.9	349980	6	AX344561	AX344561 Sequence
C 583	49	2.9	541	6	CQ522598	Sequence	656	49	2.9	349980	6	AX344561	AX344561 Sequence
C 584	49	2.9	608	10	BC061544	Rattus no	657	49	2.9	349980	6	AX344561	AX344561 Sequence
C 585	49	2.9	757	9	BC051791	Homo sapi	658	49	2.9	349980	6	AX344561	AX344561 Sequence
C 586	49	2.9	967	9	BSM802777	Sequence	659	49	2.9	349980	6	AX344561	AX344561 Sequence
C 587	49	2.9	1232	10	BC060554	Rattus no	660	49	2.9	349980	6	AX344561	AX344561 Sequence
C 588	49	2.9	1414	3	AK112149	Ciona int	661	49	2.9	349980	6	AX344561	AX344561 Sequence
C 589	49	2.9	1755	9	BC031825	Homo sapi	662	49	2.9	349980	6	AX344561	AX344561 Sequence
C 590	49	2.9	1763	5	AY079192	Xenopus t	663	49	2.9	349980	6	AX344561	AX344561 Sequence
C 591	49	2.9	1850	9	BC040123	Homo sapi	664	49	2.9	349980	6	AX344561	AX344561 Sequence
C 592	49	2.9	1853	10	BC052346	Sequence	665	49	2.9	349980	6	AX344561	AX344561 Sequence
C 593	49	2.9	1869	5	BC076804	Sequence	666	49	2.9	349980	6	AX344561	AX344561 Sequence
C 594	49	2.9	1891	9	BSM807589	Sequence	667	49	2.9	349980	6	AX344561	AX344561 Sequence
C 595	49	2.9	1912	10	BC027060	Sequence	668	49	2.9	349980	6	AX344561	AX344561 Sequence
C 596	49	2.9	1935	5	BC065678	Danio rer	669	49	2.9	349980	6	AX344561	AX344561 Sequence
C 597	49	2.9	1954	6	BD270057	Secreted	670	49	2.9	349980	6	AX344561	AX344561 Sequence
C 598	49	2.9	1960	9	BC038806	Homo sapi	671	49	2.9	349980	6	AX344561	AX344561 Sequence
C 599	49	2.9	2045	9	BC047761	Homo sapi	672	49	2.9	349980	6	AX344561	AX344561 Sequence
C 600	49	2.9	2116	9	BC034379	Homo sapi	673	49	2.9	349980	6	AX344561	AX344561 Sequence
C 601	49	2.9	2197	9	BC045177	Homo sapi	674	49	2.9	349980	6	AX344561	AX344561 Sequence
C 602	49	2.9	2347	9	BC027875	Homo sapi	675	49	2.9	349980	6	AX344561	AX344561 Sequence
C 603	49	2.9	2553	10	BC061558	Rattus no	676	49	2.9	349980	6	AX344561	AX344561 Sequence

677	48.6	2.9	320	6	CQ517221	Sequence	750	48.4	2.9	3942	10	BC063741	Mus muscu
c 678	48.6	2.9	425	6	CQ506214	Sequence	751	48.4	2.9	4073	6	AX269342	Sequence
679	48.6	2.9	471	6	CQ515907	Sequence	c 752	48.4	2.9	4316	6	CQ806814	Sequence
680	48.6	2.9	547	9	BC070202	Homo sapi	c 753	48.4	2.9	4316	6	CQ807088	Sequence
681	48.6	2.9	816	6	CQ486089	Sequence	c 754	48.4	2.9	4316	6	AX795752	Sequence
682	48.6	2.9	835	9	HSM801514	Sequence	c 755	48.4	2.9	4316	6	AX795868	Sequence
683	48.6	2.9	843	10	BC026460	Homo sapi	c 756	48.4	2.9	4316	6	AX822260	Sequence
684	48.6	2.9	932	9	BC043537	Homo sapi	c 757	48.4	2.9	4316	6	AX822388	Sequence
685	48.6	2.9	1486	9	BC042084	Homo sapi	c 758	48.4	2.9	4316	6	AX825900	Sequence
686	48.6	2.9	1569	10	BC083659	Rattus no	c 759	48.4	2.9	4316	6	AX826028	Sequence
687	48.6	2.9	1642	5	BC064224	Xenopus t	c 760	48.4	2.9	5195	6	AX345823	Sequence
688	48.6	2.9	1781	9	BC043529	Homo sapi	c 761	48.4	2.9	6070	6	AX281468	Sequence
689	48.6	2.9	1808	6	AX535019	Sequence	c 762	48.4	2.9	6070	6	AX346581	Sequence
690	48.6	2.9	1959	9	BC043548	Homo sapi	c 763	48.4	2.9	6070	6	AX348804	Sequence
691	48.6	2.9	1994	3	AK116078	Ciona int	c 764	48.4	2.9	6070	6	AX458614	Sequence
692	48.6	2.9	2009	9	BC050391	Homo sapi	c 765	48.4	2.9	6577	6	AX251920	Sequence
693	48.6	2.9	2034	6	AX127529	Sequence	c 766	48.4	2.9	6577	6	AX346258	Sequence
694	48.6	2.9	2034	6	AX675184	Sequence	c 767	48.4	2.9	6577	6	AX348993	Sequence
695	48.6	2.9	2390	9	AF090900	Homo sapi	c 768	48.4	2.9	6690	9	HSM803755	Sequence
696	48.6	2.9	3000	9	BC036812	Homo sapi	c 769	48.4	2.9	6849	10	BS324169	Mouse DNA
c 697	48.6	2.9	5532	6	AX345680	Sequence	c 770	48.4	2.9	6944	6	AX347467	Sequence
c 698	48.6	2.9	8946	6	AX345813	Sequence	c 771	48.4	2.9	6944	6	AX349188	Sequence
c 699	48.6	2.9	14615	6	AX251461	Sequence	c 772	48.4	2.9	6944	6	AX657867	Sequence
700	48.6	2.9	68222	9	AL391904	Human DNA	c 773	48.4	2.9	7467	6	CQ807272	Sequence
c 701	48.6	2.9	111865	2	AL355883	Homo sapi	c 774	48.4	2.9	7467	6	CQ807272	Sequence
c 702	48.6	2.9	139772	2	AC068270	Homo sapi	c 775	48.4	2.9	8546	6	AX828406	Sequence
c 703	48.6	2.9	151736	2	AC068270	Homo sapi	c 776	48.4	2.9	8546	6	AX828406	Sequence
c 704	48.6	2.9	157311	10	AC132236	Mus muscu	c 777	48.4	2.9	9117	6	AX345970	Sequence
705	48.6	2.9	167489	5	BM664600	Zebrafish	c 778	48.4	2.9	11097	6	AX828972	Sequence
706	48.6	2.9	167728	2	AC115889	Mus muscu	c 779	48.4	2.9	11097	6	AX828974	Sequence
707	48.6	2.9	177083	10	AC126805	Mus muscu	780	48.4	2.9	18207	9	AX828384	Sequence
708	48.6	2.9	181226	10	AC147111	Mus muscu	781	48.4	2.9	18207	9	AF156100	Homo sapi
709	48.6	2.9	182229	2	AC138596	Mus muscu	782	48.4	2.9	26459	9	AL390854	Human DNA
c 710	48.6	2.9	184736	10	AL808128	Mouse DNA	783	48.4	2.9	42839	2	AC027282	Sequence
c 711	48.6	2.9	185291	2	AC1233147	Rattus no	c 784	48.4	2.9	73778	6	AX344575	Sequence
c 712	48.6	2.9	206324	10	AL807786	Mouse DNA	c 785	48.4	2.9	145275	9	AF189745	Homo sapi
713	48.6	2.9	210232	2	AC0733684	Sequence	c 786	48.4	2.9	149813	2	AX942840	Danio rer
714	48.6	2.9	210269	2	AX927280	Danio rer	c 787	48.4	2.9	165146	2	AP002415	Homo sapi
c 715	48.6	2.9	212557	2	AC120134	Mus muscu	c 788	48.4	2.9	167671	2	AC142166	Mus muscu
c 716	48.6	2.9	212908	2	CR847533	Danio rer	c 789	48.4	2.9	176929	9	AC004887	Homo sapi
c 717	48.6	2.9	221023	10	AL8444487	Mouse DNA	c 790	48.4	2.9	182871	3	AC117176	Dicystoste
c 718	48.6	2.9	231447	2	AC121422	Rattus no	c 791	48.4	2.9	183648	3	AC117081	Dicystoste
c 719	48.6	2.9	269576	2	AC0733684	Sequence	c 792	48.4	2.9	188555	10	AC122417	Mus muscu
720	48.4	2.9	147	6	AR418886	Sequence	793	48.4	2.9	198377	2	CR792437	Danio rer
721	48.4	2.9	147	6	AX979580	Sequence	c 794	48.4	2.9	199472	9	AC022267	Homo sapi
722	48.4	2.9	147	6	BD114439	EST and e	c 795	48.4	2.9	204278	10	AC124507	Mus muscu
723	48.4	2.9	186	6	CQ677473	Sequence	c 796	48.4	2.9	208921	2	AP001911	Homo sapi
c 724	48.4	2.9	388	6	CQ410454	Sequence	c 797	48.4	2.9	215676	2	AC131299	Mus muscu
725	48.4	2.9	432	6	CQ524989	Sequence	798	48.4	2.9	221944	2	AC119914	Mus muscu
726	48.4	2.9	451	6	CQ524930	Sequence	799	48.4	2.9	228178	2	AC101866	Mus muscu
727	48.4	2.9	661	10	BC051629	Mus muscu	c 800	48.4	2.9	232304	2	AC103201	Rattus no
728	48.4	2.9	1078	9	BC035314	Homo sapi	c 801	48.4	2.9	258658	3	AE014832	Plasmodiu
729	48.4	2.9	1117	6	AR123345	Sequence	c 802	48.4	2.9	349980	6	AX344558	Sequence
730	48.4	2.9	1175	5	BC063345	Homo sapi	c 803	48.4	2.9	349980	6	AX344570	Sequence
731	48.4	2.9	1445	9	BC063345	Homo sapi	c 804	48.2	2.9	153	6	AX340795	Sequence
732	48.4	2.9	1550	9	BC063432	Homo sapi	c 805	48.2	2.9	268	6	AX185659	Sequence
733	48.4	2.9	1586	9	BC027882	Homo sapi	c 806	48.2	2.9	317	6	CQ526915	Sequence
734	48.4	2.9	1727	10	BC050800	Mus muscu	c 807	48.2	2.9	359	6	CQ431130	Sequence
735	48.4	2.9	1872	9	BC038952	Homo sapi	c 808	48.2	2.9	385	6	CQ398297	Sequence
736	48.4	2.9	1978	9	BC012750	Homo sapi	c 809	48.2	2.9	430	6	CQ404584	Sequence
737	48.4	2.9	2065	5	BC066376	Danio rer	c 810	48.2	2.9	430	6	BC062435	Homo sapi
738	48.4	2.9	2184	9	AB060903	Macaca fa	c 811	48.2	2.9	453	6	CQ517526	Sequence
739	48.4	2.9	2238	5	BC063364	Danio rer	c 812	48.2	2.9	504	6	CQ525672	Sequence
740	48.4	2.9	2265	9	BC063477	Homo sapi	c 813	48.2	2.9	527	10	BC049658	Mus muscu
741	48.4	2.9	2402	5	BC077592	Xenopus l	c 814	48.2	2.9	633	10	BC059147	Rattus no
742	48.4	2.9	2652	3	AK174388	Ciona int	c 815	48.2	2.9	724	10	BC049721	Mus muscu
743	48.4	2.9	2679	10	BC006021	Mus muscu	c 816	48.2	2.9	745	10	BC049606	Mus muscu
744	48.4	2.9	3270	9	BC050552	Homo sapi	c 817	48.2	2.9	1119	10	BC021629	Mus muscu
745	48.4	2.9	3422	9	HSM805920	Homo sapi	c 818	48.2	2.9	1561	9	BC040443	Homo sapi
746	48.4	2.9	3454	9	HSM802993	Homo sapi	c 819	48.2	2.9	1608	10	BC057455	Mus muscu
747	48.4	2.9	3498	5	BC065888	Danio rer	c 820	48.2	2.9	1725	5	BC080409	Xenopus l
748	48.4	2.9	3521	9	BC027712	Homo sapi	c 821	48.2	2.9	1770	10	BC060519	Rattus no
749	48.4	2.9	3810	9	HSM803390	Homo sapi	c 822	48.2	2.9	1942	10	BC062081	Rattus no

823	48.2	2.9	2038	6	AX573129	Sequence	896	48	2.9	1985	9	AY358500	AY358500 Homo sapi
824	48.2	2.9	2096	10	BC034131	Mus muscu	897	48	2.9	2003	9	BC051760	BC051760 Homo sapi
825	48.2	2.9	2137	9	AB062938	Macaca fa	898	48	2.9	2081	10	BC043712	BC043712 Mus muscu
826	48.2	2.9	2406	9	BC017107	Homo sapi	899	48	2.9	2155	9	BC075814	BC075814 Homo sapi
827	48.2	2.9	4765	5	BC068982	Danio rer	900	48	2.9	2202	10	BC052362	BC052362 Mus muscu
828	48.2	2.9	7037	6	AX346553	Sequence	901	48	2.9	2209	9	BC063878	BC063878 Homo sapi
829	48.2	2.9	7238	6	AX345350	Sequence	902	48	2.9	2248	5	BC068963	BC068963 Xenopus l
830	48.2	2.9	8895	6	AX345234	Sequence	903	48	2.9	2590	9	BC064421	BC064421 Homo sapi
831	48.2	2.9	11996	6	AX281381	Sequence	904	48	2.9	2632	9	BC030698	BC030698 Homo sapi
832	48.2	2.9	110000	2	AL954350	Continuation (5 of	905	48	2.9	2777	5	BC063344	BC063344 Xenopus t
833	48.2	2.9	157996	10	AL772203	Mouse DNA	906	48	2.9	2905	3	AK174395	AK174395 Ciona int
834	48.2	2.9	161297	10	AC139135	Mus muscu	907	48	2.9	2915	10	BC061479	BC061479 Mus muscu
835	48.2	2.9	167418	10	AC133944	Mus muscu	908	48	2.9	3223	6	CQ806938	CQ806938 Sequence
836	48.2	2.9	171298	10	AC123735	Mus muscu	909	48	2.9	3223	6	CQ807212	CQ807212 Sequence
837	48.2	2.9	179206	2	AC113199	Sequence	910	48	2.9	3723	9	BSM80835	BSM80835 Homo sapi
838	48.2	2.9	185634	2	AC119930	Mus muscu	911	48	2.9	3880	10	BC048229	BC048229 Mus muscu
839	48.2	2.9	195888	10	AC114604	Sequence	912	48	2.9	3973	6	AX345073	AX345073 Sequence
840	48.2	2.9	218297	2	AC126035	Mus muscu	913	48	2.9	3983	9	BSM803572	BSM803572 Homo sapi
841	48.2	2.9	219106	10	AC123640	Mus muscu	914	48	2.9	4306	10	BC059824	BC059824 Mus muscu
842	48.2	2.9	22725	2	AC110732	Mus muscu	915	48	2.9	4389	10	BC058345	BC058345 Mus muscu
843	48.2	2.9	257700	2	AC147391	Pan trogl	916	48	2.9	5070	6	AX345703	AX345703 Sequence
844	48	2.9	312	6	CQ699683	Sequence	917	48	2.9	5338	9	BSM808825	BSM808825 Homo sapi
845	48	2.9	323	6	CQ524910	Sequence	918	48	2.9	5774	10	BC060122	BC060122 Mus muscu
846	48	2.9	452	6	CQ527434	Sequence	919	48	2.9	6145	6	AX345875	AX345875 Sequence
847	48	2.9	515	6	CQ526571	Sequence	920	48	2.9	6192	6	AX251440	AX251440 Sequence
848	48	2.9	533	6	CQ525634	Sequence	921	48	2.9	12669	6	AX252150	AX252150 Sequence
849	48	2.9	540	6	CQ526524	Sequence	922	48	2.9	12669	6	AX344518	AX344518 Sequence
850	48	2.9	580	10	BC006049	Mus muscu	923	48	2.9	12669	6	AX348921	AX348921 Sequence
851	48	2.9	583	11	HUMUT5097	Human SPS U	924	48	2.9	18281	6	AX345864	AX345864 Sequence
852	48	2.9	585	6	CQ526237	Sequence	925	48	2.9	193342	5	BX465846	BX465846 Zebrafish
853	48	2.9	602	9	BC008488	Homo sapi	926	48	2.9	170496	2	AC140472	AC140472 Mus muscu
854	48	2.9	606	6	CQ503221	Sequence	927	48	2.9	184039	10	AC139376	AC139376 Mus muscu
855	48	2.9	606	6	CQ512068	Sequence	928	48	2.9	184365	2	AC079639	AC079639 Mus muscu
856	48	2.9	721	9	AK026526	Sequence	929	48	2.9	187028	10	BX119956	BX119956 Mouse DNA
857	48	2.9	760	9	BC032326	Homo sapi	930	48	2.9	194180	2	AC069140	AC069140 Homo sapi
858	48	2.9	836	10	BC049716	Mus muscu	931	48	2.9	200510	2	AC097048	AC097048 Rattus no
859	48	2.9	869	10	BC054421	Mus muscu	932	48	2.9	213401	2	AC124940	AC124940 Rattus no
860	48	2.9	927	10	BC047927	Mus muscu	933	48	2.9	224630	2	AC101853	AC101853 Mus muscu
861	48	2.9	988	5	BC055636	Sequence	934	48	2.9	232080	2	AC145374	AC145374 Mus muscu
862	48	2.9	1248	5	BC071085	Xenopus l	935	48	2.9	232234	2	AC108634	AC108634 Rattus no
863	48	2.9	1277	5	BC084489	Xenopus t	936	48	2.9	239189	10	AC133208	AC133208 Mus muscu
864	48	2.9	1352	3	AX115954	Ciona int	937	48	2.9	247650	2	AC094213	AC094213 Rattus no
865	48	2.9	1391	5	BC074604	Sequence	938	48	2.9	257109	3	AC116963	AC116963 Dictyoste
866	48	2.9	1409	5	BC064261	Xenopus t	939	48	2.9	309805	2	AC026340	AC026340 Homo sapi
867	48	2.9	1409	10	BC040071	Mus muscu	940	48	2.9	321708	2	AC087142	AC087142 Mus muscu
868	48	2.9	1415	10	BC020016	Mus muscu	941	48	2.9	349980	6	AX344554	AX344554 Sequence
869	48	2.9	1426	5	BC054250	Xenopus l	942	48	2.9	349980	6	AX344555	AX344555 Sequence
870	48	2.9	1483	9	AK026528	Homo sapi	943	48	2.9	349980	6	AX344571	AX344571 Sequence
871	48	2.9	1526	5	BC084459	Xenopus t	944	47.8	2.8	212	6	CQ677317	CQ677317 Sequence
872	48	2.9	1608	9	AX358187	Homo sapi	945	47.8	2.8	233	6	CQ516563	CQ516563 Sequence
873	48	2.9	1622	9	BC043524	Homo sapi	946	47.8	2.8	309	6	CQ513146	CQ513146 Sequence
874	48	2.9	1632	5	BC068370	Danio rer	947	47.8	2.8	327	6	CQ408014	CQ408014 Sequence
875	48	2.9	1637	6	AX460089	Sequence	948	47.8	2.8	441	6	AR344256	AR344256 Sequence
876	48	2.9	1643	10	BC024405	Mus muscu	949	47.8	2.8	441	6	AX019230	AX019230 Sequence
877	48	2.9	1646	9	BC051812	Homo sapi	950	47.8	2.8	441	6	BD130456	BD130456 Expressio
878	48	2.9	1690	6	E32442	Mammal-deri	951	47.8	2.8	497	6	CQ526425	CQ526425 Sequence
879	48	2.9	1720	10	BC046603	Mus muscu	952	47.8	2.8	498	6	CQ481059	CQ481059 Sequence
880	48	2.9	1727	5	BC071446	Danio rer	953	47.8	2.8	503	6	CQ524887	CQ524887 Sequence
881	48	2.9	1860	9	BC058897	Homo sapi	954	47.8	2.8	503	10	BC054554	BC054554 Mus muscu
882	48	2.9	1985	6	BD172402	Secreted	955	47.8	2.8	515	6	CQ522671	CQ522671 Sequence
883	48	2.9	1985	6	BD172721	Secreted	956	47.8	2.8	535	6	CQ471891	CQ471891 Sequence
884	48	2.9	1985	6	BD173040	Secreted	957	47.8	2.8	543	11	BV064080	BV064080 S208P6631
885	48	2.9	1985	6	BD173359	Secreted	958	47.8	2.8	548	6	CQ516864	CQ516864 Sequence
886	48	2.9	1985	6	BD175393	Secretary	959	47.8	2.8	574	6	CQ525654	CQ525654 Sequence
887	48	2.9	1985	6	CQ881212	Sequence	960	47.8	2.8	639	6	CQ393100	CQ393100 Sequence
888	48	2.9	1985	6	AR410771	Sequence	961	47.8	2.8	639	6	CQ405378	CQ405378 Sequence
889	48	2.9	1985	6	AR439135	Sequence	962	47.8	2.8	711	6	CQ422915	CQ422915 Sequence
890	48	2.9	1985	6	AR473155	Sequence	963	47.8	2.8	756	3	AK174008	AK174008 Ciona int
891	48	2.9	1985	6	AR527141	Sequence	964	47.8	2.8	791	9	BC038970	BC038970 Homo sapi
892	48	2.9	1985	6	AR566174	Sequence	965	47.8	2.8	798	10	BC005501	BC005501 Mus muscu
893	48	2.9	1985	6	AX375960	Sequence	966	47.8	2.8	872	6	AX068322	AX068322 Sequence
894	48	2.9	1985	6	AX697621	Sequence	967	47.8	2.8	885	3	AK174656	AK174656 Ciona int
895	48	2.9	1985	6	BD075542	Secretary	968	47.8	2.8	980	10	BC063173	BC063173 Rattus no

969	47.8	2.8	990	9	BC070127	BC070127 Homo sapi	c1042	47.8	2.8	113515	6	AX347077	AX347077 Sequence
970	47.8	2.8	995	9	BC043534	BC043534 Homo sapi	1043	47.8	2.8	114897	2	AP003624	AP003624 Oryza sat
971	47.8	2.8	1004	9	BC043536	BC043536 Homo sapi	1044	47.8	2.8	124048	10	AC134526	AC134526 Mus muscu
972	47.8	2.8	1035	10	BC055104	BC055104 Mus muscu	1045	47.8	2.8	133276	2	AC087147	AC087147 Mus muscu
c 973	47.8	2.8	1052	8	AB840524	AB840524 Arabidops	1046	47.8	2.8	143226	9	ALJ353802	ALJ353802 Human DNA
974	47.8	2.8	1080	9	HS0805509	AL834421 Homo sapi	c1047	47.8	2.8	167181	2	AC1331701	AC1331701 Mus muscu
975	47.8	2.8	1110	9	BC040953	BC040953 Homo sapi	c1048	47.8	2.8	168025	10	AC117778	AC117778 Mus muscu
976	47.8	2.8	1115	10	BC0409575	BC0409575 Mus muscu	c1049	47.8	2.8	175107	10	AC119911	AC119911 Mus muscu
977	47.8	2.8	1264	6	BD227246	BD227246 Secreted	c1050	47.8	2.8	198965	10	AC145606	AC145606 Mus muscu
978	47.8	2.8	1279	9	BC062634	BC062634 Homo sapi	1051	47.8	2.8	199101	10	MMAE000665	AE000665 Mus muscu
979	47.8	2.8	1345	9	BC073861	BC073861 Homo sapi	c1052	47.8	2.8	201293	2	AC118780	AC118780 Rattus no
980	47.8	2.8	1368	10	BC083654	BC083654 Rattus no	1053	47.8	2.8	204437	10	AC117678	AC117678 Mus muscu
981	47.8	2.8	1375	9	BC043554	BC043554 Homo sapi	c1054	47.8	2.8	205939	10	AC145469	AC145469 Mus muscu
982	47.8	2.8	1488	10	BC055456	BC055456 Mus muscu	c1055	47.8	2.8	209947	2	AC121454	AC121454 Rattus no
983	47.8	2.8	1500	5	BC065586	BC065586 Danio rer	1056	47.8	2.8	214331	2	AC141645	AC141645 Mus muscu
984	47.8	2.8	1580	5	BC067146	BC067146 Danio rer	c1057	47.8	2.8	216799	10	AC125382	AC125382 Mus muscu
985	47.8	2.8	1728	9	AB070110	AB070110 Macaca fa	1058	47.8	2.8	225000	2	AC129674	AC129674 Rattus no
986	47.8	2.8	1743	10	BC051150	BC051150 Mus muscu	1059	47.8	2.8	228302	2	AC109973	AC109973 Rattus no
987	47.8	2.8	1767	9	HS0800099	AL049314 Homo sapi	c1060	47.8	2.8	233887	2	AC133687	AC133687 Rattus no
988	47.8	2.8	1788	5	BC084147	BC084147 Xenopus t	1061	47.8	2.8	247796	2	AC094539	AC094539 Rattus no
989	47.8	2.8	1819	9	BC073865	BC073865 Homo sapi	c1062	47.8	2.8	252504	2	AC073815	AC073815 Mus muscu
990	47.8	2.8	1863	10	BC083817	BC083817 Rattus no	1063	47.8	2.8	255408	2	AC129658	AC129658 Rattus no
991	47.8	2.8	2076	5	BC053185	BC053185 Danio rer	c1064	47.8	2.8	256391	2	AC107557	AC107557 Rattus no
992	47.8	2.8	2158	9	AB070046	AB070046 Macaca fa	c1065	47.8	2.8	257501	2	AC097734	AC097734 Rattus no
993	47.8	2.8	2172	9	AB096991	AB096991 Macaca fa	1066	47.8	2.8	258819	2	AC118292	AC118292 Rattus no
994	47.8	2.8	2173	10	BC048927	BC048927 Mus muscu	1067	47.8	2.8	333321	3	AC116986	AC116986 Dictyooste
995	47.8	2.8	2208	10	BC052921	BC052921 Mus muscu	1068	47.6	2.8	147	6	AR418757	AR418757 Sequence
996	47.8	2.8	2407	10	BC058192	BC058192 Mus muscu	1069	47.6	2.8	147	6	AX979451	AX979451 Sequence
997	47.8	2.8	2556	9	AF125948	AF125948 Homo sapi	1070	47.6	2.8	BD114310	6	BD114310 EST and e	BD114310 EST and e
998	47.8	2.8	3020	6	CQ491158	CQ491158 Sequence	1071	47.6	2.8	291	6	CQ517629	CQ517629 Sequence
999	47.8	2.8	3020	6	CQ497023	CQ497023 Sequence	c1072	47.6	2.8	345	6	CQ475827	CQ475827 Sequence
1000	47.8	2.8	3178	9	HS0803719	AL832411 Homo sapi	1073	47.6	2.8	358	6	CQ671266	CQ671266 Sequence
1001	47.8	2.8	3310	9	BC054816	BC054816 Homo sapi	1074	47.6	2.8	368	10	BC049735	BC049735 Mus muscu
1002	47.8	2.8	3430	9	BC065520	BC065520 Homo sapi	1075	47.6	2.8	376	6	CQ521729	CQ521729 Sequence
1003	47.8	2.8	3574	6	CQ412010	CQ412010 Sequence	1076	47.6	2.8	391	6	CQ524976	CQ524976 Sequence
1004	47.8	2.8	4057	10	BC067005	BC067005 Mus muscu	1077	47.6	2.8	394	6	CQ527287	CQ527287 Sequence
1005	47.8	2.8	4121	6	AR344255	AR344255 Sequence	1078	47.6	2.8	410	6	CQ522484	CQ522484 Sequence
1006	47.8	2.8	4121	6	AX019229	AX019229 Expressio	c1079	47.6	2.8	465	11	BV155767	BV155767 RPAMSEQ0
1007	47.8	2.8	4121	6	BD130455	BD130455 Sequence	1080	47.6	2.8	470	6	CQ516232	CQ516232 Sequence
1008	47.8	2.8	4213	5	BC084298	BC084298 Xenopus l	1081	47.6	2.8	479	6	CQ522457	CQ522457 Sequence
1009	47.8	2.8	4298	6	AX780085	AX780085 Sequence	1082	47.6	2.8	480	10	BC028543	BC028543 Mus muscu
1010	47.8	2.8	4562	9	HS0805779	BS537704 Homo sapi	1083	47.6	2.8	514	6	CQ522634	CQ522634 Sequence
1011	47.8	2.8	4636	10	BC057352	BC057352 Mus muscu	1084	47.6	2.8	520	6	CQ523964	CQ523964 Sequence
1012	47.8	2.8	4818	9	HS0807492	BX647348 Homo sapi	1085	47.6	2.8	529	5	BC053827	BC053827 Xenopus l
c1013	47.8	2.8	6486	6	AX458534	AX458534 Sequence	1086	47.6	2.8	631	10	MMU296942	AJ296942 Mus muscu
c1014	47.8	2.8	8079	6	AX356488	AX356488 Sequence	1087	47.6	2.8	732	5	AY522586	AY522586 Oreochrom
c1015	47.8	2.8	8298	6	AX344783	AX344783 Sequence	1088	47.6	2.8	873	6	AX780227	AX780227 Sequence
c1016	47.8	2.8	8913	6	AX599017	AX599017 Sequence	1089	47.6	2.8	889	10	BC049685	BC049685 Mus muscu
c1017	47.8	2.8	9021	6	AX347134	AX347134 Sequence	1090	47.6	2.8	959	9	BC031674	BC031674 Homo sapi
c1018	47.8	2.8	9021	6	AX347426	AX347426 Sequence	1091	47.6	2.8	1000	9	HS0806624	BX571748 Homo sapi
c1019	47.8	2.8	9021	6	AX348462	AX348462 Sequence	1092	47.6	2.8	1001	10	BC049605	BC049605 Mus muscu
c1020	47.8	2.8	9021	6	AX349147	AX349147 Sequence	1093	47.6	2.8	1130	10	BC043698	BC043698 Mus muscu
c1021	47.8	2.8	9021	6	AX657808	AX657808 Sequence	1094	47.6	2.8	1157	9	BC013883	BC013883 Homo sapi
c1022	47.8	2.8	9021	6	AX659082	AX659082 Sequence	1095	47.6	2.8	1314	5	BC054577	BC054577 Danio rer
c1023	47.8	2.8	11913	6	CQ0787442	CQ0787442 Sequence	1096	47.6	2.8	1343	10	BC061103	BC061103 Mus muscu
c1024	47.8	2.8	11913	6	CQ087085	CQ087085 Sequence	1097	47.6	2.8	1383	9	BC032432	BC032432 Homo sapi
c1025	47.8	2.8	11913	6	AX795865	AX795865 Sequence	1098	47.6	2.8	1408	10	BC048693	BC048693 Mus muscu
c1026	47.8	2.8	11913	6	AX822385	AX822385 Sequence	1099	47.6	2.8	1411	10	BC049571	BC049571 Mus muscu
c1027	47.8	2.8	11913	6	AX826025	AX826025 Sequence	1100	47.6	2.8	1412	3	AF083228	AF083228 Caenorhab
c1028	47.8	2.8	13606	6	AX251315	AX251315 Sequence	1101	47.6	2.8	1457	6	BD231695	BD231695 31 human
c1029	47.8	2.8	13606	6	AX278002	AX278002 Sequence	1102	47.6	2.8	1694	9	BC012597	BC012597 Homo sapi
c1030	47.8	2.8	13606	6	AX323699	AX323699 Sequence	1103	47.6	2.8	1744	8	BF009253	BT009253 Triticum
c1031	47.8	2.8	13606	6	AX346712	AX346712 Sequence	1104	47.6	2.8	1805	9	AB070053	AB070053 Macaca fa
c1032	47.8	2.8	15832	6	AX277943	AX277943 Sequence	1105	47.6	2.8	1820	5	BC066434	BC066434 Danio rer
c1033	47.8	2.8	15832	6	AX323630	AX323630 Sequence	1106	47.6	2.8	1836	10	BC034256	BC034256 Mus muscu
c1034	47.8	2.8	15832	6	AX346245	AX346245 Sequence	1107	47.6	2.8	1880	9	AB060863	AB060863 Macaca fa
1035	47.8	2.8	31656	2	AC149363	AC149363 Phakopsor	1108	47.6	2.8	2019	10	BC063758	BC063758 Mus muscu
c1036	47.8	2.8	56153	3	AC115682	AC115682 Dictyooste	1109	47.6	2.8	2085	5	BC077186	BC077186 Xenopus l
c1037	47.8	2.8	57538	3	AC101648	AC101648 Homo sapi	1110	47.6	2.8	2165	5	BC054602	BC054602 Danio rer
c1038	47.8	2.8	99930	9	AC068840	AC068840 Homo sapi	1111	47.6	2.8	2198	6	BD270040	BD270040 Secreted
1040	47.8	2.8	104992	2	AC005504	AC005504 Plasmodiu	1112	47.6	2.8	2284	6	AB055303	AB055303 Macaca fa
c1041	47.8	2.8	110000	3	PFMAL1P2_0	AL0311745 Plasmodiu	1113	47.6	2.8	2369	9	AK074384	AK074384 Homo sapi
							1114	47.6	2.8	2420	5	BC066695	BC066695 Danio rer

c1042	47.8	2.8	113515	6	AX347077	AX347077 Sequence
1043	47.8	2.8	114897	2	AP003624	AP003624 Oryza sat
1044	47.8	2.8	124048	10	AC134526	AC134526 Mus muscu
1045	47.8	2.8	133276	2	AC087147	AC087147 Mus muscu
1046	47.8	2.8	143226	9	ALJ353802	ALJ353802 Human DNA
c1047	47.8	2.8	167181	2	AC131701	AC131701 Mus muscu
c1048	47.8	2.8	168025	10	AC117778	AC117778 Mus muscu
c1049	47.8	2.8	175107	10	AC119911	AC119911 Mus muscu
c1050	47.8	2.8	198965	10	AC145606	AC145606 Mus muscu
1051	47.8	2.8	199101	10	MMAE000665	AE000665 Mus muscu
c1052	47.8	2.8	201293	2	AC118780	AC118780 Rattus no
1053	47.8	2.8	204437	10	AC117678	AC117678 Mus muscu
c1054	47.8	2.8	205939	10	AC145469	AC145469 Mus muscu
c1055	47.8	2.8	209947	2	AC121454	AC121454 Rattus no
1056	47.8	2.8	214331	2	AC141645	AC141645 Mus muscu
c1057	47.8	2.8	216799	10	AC125382	AC125382 Mus muscu
1058	47.8	2.8	225000	2	AC129674	AC129674 Rattus no
1059	47.8	2.8	228302	2	AC109973	AC109973 Rattus no
c1060	47.8	2.8	233887	2	AC133687	AC133687 Rattus no
1061	47.8	2.8	247796	2	AC094539	AC094539 Rattus no
c1062	47.8	2.8	252504	2	AC073815	AC073815 Mus muscu
1063	47.8	2.8	255408	2	AC129658	AC129658 Rattus no
c1064	47.8	2.8	256391	2	AC107557	AC107557 Rattus no
c1065	47.8	2.8	257501	2	AC097734	AC097734 Rattus no
1066	47.8	2.8	258819	2	AC118292	AC118292 Rattus no
1067	47.8	2.8	333321	3	AC116986	AC116986 Dictyoste
1068	47.6	2.8	147	6	AR418757	AR418757 Sequence
1069	47.6	2.8	147	6	AX979451	AX979451 Sequence
1070	47.6	2.8	147	6	BD114310	BD114310 EST and e
1071	47.6	2.8	291	6	CQ517629	CQ517629 Sequence
c1072	47.6	2.8	345	6	CQ475827	CQ475827 Sequence
1073	47.6	2.8	358	6	CQ671266	CQ671266 Sequence
1074	47.6	2.8	368	10	BC049735	BC049735 Mus muscu
1075	47.6	2.8	376	6	CQ521729	CQ521729 Sequence
1076	47.6	2.8	391	6	CQ524976	CQ524976 Sequence
1077	47.6	2.8	394	6	CQ527287	CQ527287 Sequence
1078	47.6	2.8	410	6	CQ522484	CQ522484 Sequence
c1079	47.6	2.8	465	11	BV155767	BV155767 RPAMSEQO
1080	47.6	2.8	470	6	CQ516232	CQ516232 Sequence
1081	47.6	2.8	479	6	CQ523457	CQ523457 Sequence
1082	47.6	2.8	480	10	BC028543	BC028543 Mus muscu
1083	47.6	2.8	514	6	CQ522634	CQ522634 Sequence
1084	47.6	2.8	520	6	CQ523964	CQ523964 Sequence
1085	47.6	2.8	529	5	BC053827	BC053827 Xenopus l
1086	47.6	2.8	631	10	MUJ296942	AJ296942 Mus muscu
1087	47.6	2.8	732	5	AY522586	AY522586 Oreochrom
1088	47.6	2.8	873	6	AX780227	AX780227 Sequence
1089	47.6	2.8	889	10	BC049685	BC049685 Mus muscu
1090	47.6	2.8	959	9	BC031674	BC031674 Homo sapi
1091	47.6	2.8	1000	9	HSMB06624	BX571748 Homo sapi
1092	47.6	2.8	1001	10	BC049605	BC049605 Mus muscu
1093	47.6	2.8	1130	10	BC043698	BC043698 Mus muscu
1094	47.6	2.8	1157	9	BC013883	BC013883 Homo sapi
1095	47.6	2.8	1314	5	BC054577	BC054577 Danio rer
1096	47.6	2.8	1343	9	BC061103	BC061103 Mus muscu
1097	47.6	2.8	1383	9	BC032432	BC032432 Homo sapi
1098	47.6	2.8	1408	10	BC048693	BC048693 Mus muscu
1099	47.6	2.8	1411	10	BC049571	BC049571 Mus muscu
1100	47.6	2.8	1412	3	AF083228	AF083228 Caenorhab
1101	47.6	2.8	1457	6	BD231695	BD231695 31 human
1102	47.6	2.8	1694	9	BC012597	BC012597 Homo sapi
1103	47.6	2.8	1744	8	BT009253	BT009253 Triticum
1104	47.6	2.8	1805	9	AB070053	AB070053 Macaca fa
1105	47.6	2.8	1820	5	BC066434	BC066434 Danio rer
1106	47.6	2.8	1836	10	BC034256	BC034256 Mus muscu
1107	47.6	2.8	1880	9	AB060863	AB060863 Macaca fa
1108	47.6	2.8	2019	10	BC063758	BC063758 Mus muscu
1109	47.6	2.8	2085	5	BC077186	BC077186 Xenopus l
1110	47.6	2.8	2165	5	BC054602	BC054602 Danio rer
1111	47.6	2.8	2198	6	BD270040	BD270040 Secretd
1112	47.6	2.8	2284	9	AB055303	AB055303 Macaca fa
1113	47.6	2.8	2369	9	AK074384	AK074384 Homo sapi
1114	47.6	2.8	2420	5	BC066695	BC066695 Danio rer

1115	47.6	2.8	2447	6	AR079032	Sequence
1116	47.6	2.8	2447	6	BD190886	Secreted
1117	47.6	2.8	2447	9	BC027927	Homo sapi
1118	47.6	2.8	2501	6	AX598878	Sequence
1119	47.6	2.8	2607	5	BC054610	Danio rer
1120	47.6	2.8	2610	10	BC063267	Mus muscu
1121	47.6	2.8	2621	10	MUS8RED	Mus muscu
1122	47.6	2.8	2674	6	AR183261	Sequence
1123	47.6	2.8	2674	6	AR456323	Sequence
1124	47.6	2.8	2752	9	HSMB06735	Homo sapi
1125	47.6	2.8	2770	9	HSMB07752	Homo sapi
1126	47.6	2.8	2782	9	HSMB03706	Homo sapi
1127	47.6	2.8	2804	9	HSMB07489	Homo sapi
1128	47.6	2.8	2840	10	BC052769	Mus muscu
1129	47.6	2.8	3448	10	BC034679	Mus muscu
1130	47.6	2.8	3582	10	BC053927	Mus muscu
1131	47.6	2.8	3924	10	MUS8REDA	Mus muscu
1132	47.6	2.8	4001	6	AX347363	Sequence
1133	47.6	2.8	4001	6	AX349084	Sequence
1134	47.6	2.8	4001	6	AX657851	Sequence
1135	47.6	2.8	4001	6	AX659125	Sequence
1136	47.6	2.8	4004	9	BC041086	Homo sapi
1137	47.6	2.8	4418	9	BC006195	Homo sapi
1138	47.6	2.8	4421	10	BC042512	Mus muscu
1139	47.6	2.8	4447	9	HSMB08517	Homo sapi
1140	47.6	2.8	4675	9	HSMB03445	Homo sapi
1141	47.6	2.8	5306	6	AX345413	Sequence
1142	47.6	2.8	6134	6	AX458624	Sequence
1143	47.6	2.8	6436	6	AX345583	Sequence
1144	47.6	2.8	6436	6	AX345583	Sequence
1145	47.6	2.8	6775	6	AX458643	Sequence
1146	47.6	2.8	6802	6	AX346133	Sequence
1147	47.6	2.8	7416	6	CQ574115	Sequence
1148	47.6	2.8	7967	3	AF222717	Plasmodiu
1149	47.6	2.8	8900	6	CQ806977	Sequence
1150	47.6	2.8	8900	6	CQ807251	Sequence
1151	47.6	2.8	8910	6	AX344725	Sequence
1152	47.6	2.8	9483	6	AX251786	Sequence
1153	47.6	2.8	9483	6	AX345278	Sequence
1154	47.6	2.8	9483	6	AX348947	Sequence
1155	47.6	2.8	9666	6	AX281420	Sequence
1156	47.6	2.8	9666	6	AX345987	Sequence
1157	47.6	2.8	9666	6	AX348688	Sequence
1158	47.6	2.8	11700	2	AC013911	Drosophil
1159	47.6	2.8	17848	6	AX277865	Sequence
1160	47.6	2.8	17848	6	AX323550	Sequence
1161	47.6	2.8	17848	6	AX348363	Sequence
1162	47.6	2.8	35962	6	AX598758	Sequence
1163	47.6	2.8	63585	2	AC026983	Homo sapi
1164	47.6	2.8	77322	2	AC021334	Homo sapi
1165	47.6	2.8	84492	2	AC021676	Homo sapi
1166	47.6	2.8	95026	3	AC125292	Drosophil
1167	47.6	2.8	110000	2	AC110244	Mus muscu
1168	47.6	2.8	110000	2	PFMAL13_11	Continuation (12 o
1169	47.6	2.8	110000	3	PFMAL13P2_2	Continuation (3 of
1170	47.6	2.8	110000	3	PFMAL1P2_0	Continuation (3 of
1171	47.6	2.8	113027	9	AC090669	Plasmodiu
1172	47.6	2.8	120211	10	AL0773515	Homo sapi
1173	47.6	2.8	127580	9	HSBJ74J1	Human DNA
1174	47.6	2.8	151501	9	BS000215	Human DNA
1175	47.6	2.8	155320	2	AC135762	Pan trogl
1176	47.6	2.8	155646	9	AC146044	Rattus no
1177	47.6	2.8	156459	10	AC147155	Pan trogl
1178	47.6	2.8	158803	2	AC117771	Mus muscu
1179	47.6	2.8	16025	10	AL844493	Mouse DNA
1180	47.6	2.8	166292	10	AC123049	Mus muscu
1181	47.6	2.8	168439	10	AC131803	Mus muscu
1182	47.6	2.8	173585	2	AC021113	Homo sapi
1183	47.6	2.8	174893	5	BX004876	Zebrafish
1184	47.6	2.8	175106	2	AC148984	Mus muscu
1185	47.6	2.8	176261	5	BX927252	Zebrafish
1186	47.6	2.8	179312	3	AC023745	Drosophil
1187	47.6	2.8	185195	10	AC134565	Mus muscu

1188	47.6	2.8	187545	10	AC127550	Mus muscu
1189	47.6	2.8	188823	2	AC016990	Homo sapi
1190	47.6	2.8	194760	9	CNS01RG7	Human chr
1191	47.6	2.8	199537	10	AL837510	Mouse DNA
1192	47.6	2.8	202640	2	AL113851	Rattus no
1193	47.6	2.8	211371	2	CR450764	Danio rer
1194	47.6	2.8	213397	2	AC125027	Mus muscu
1195	47.6	2.8	213558	2	AC149587	Mus muscu
1196	47.6	2.8	217740	2	AC139949	Rattus no
1197	47.6	2.8	226256	2	AC130087	Rattus no
1198	47.6	2.8	226734	2	AC103431	Rattus no
1199	47.6	2.8	233219	2	AC113253	Rattus no
1200	47.6	2.8	235660	2	AC128377	Rattus no
1201	47.6	2.8	241394	2	AC131549	Rattus no
1202	47.6	2.8	248214	2	AL138811	Homo sapi
1203	47.6	2.8	257700	2	AC147391	Pan trogl
1204	47.6	2.8	258818	2	AC135265	Rattus no
1205	47.6	2.8	264350	2	AC127094	Rattus no
1206	47.6	2.8	301536	2	AC134158	Rattus no
1207	47.6	2.8	315790	3	AE003484	Drosophil
1208	47.6	2.8	334028	2	AC116537	Drosophil
1209	47.6	2.8	349980	6	AX344552	Sequence
1210	47.6	2.8	349980	6	AX344572	Sequence
1211	47.4	2.8	267	6	CQ525163	Sequence
1212	47.4	2.8	268	6	CQ526263	Sequence
1213	47.4	2.8	291	6	CQ399019	Sequence
1214	47.4	2.8	291	6	CQ405298	Sequence
1215	47.4	2.8	301	6	CQ516510	Sequence
1216	47.4	2.8	376	6	CQ517117	Sequence
1217	47.4	2.8	406	6	CQ517355	Sequence
1218	47.4	2.8	407	6	CQ522526	Sequence
1219	47.4	2.8	439	6	CQ518358	Sequence
1220	47.4	2.8	453	6	CQ477688	Sequence
1221	47.4	2.8	467	3	AF156168	Butus ma
1222	47.4	2.8	472	6	CQ518059	Sequence
1223	47.4	2.8	484	6	CQ526160	Sequence
1224	47.4	2.8	506	6	CQ5218031	Sequence
1225	47.4	2.8	516	6	CQ524041	Sequence
1226	47.4	2.8	546	6	AX186746	Sequence
1227	47.4	2.8	589	10	BC049706	Mus muscu
1228	47.4	2.8	631	10	BC049570	Mus muscu
1229	47.4	2.8	643	6	CQ423476	Sequence
1230	47.4	2.8	671	5	BC082915	Xenopus l
1231	47.4	2.8	682	10	BC049545	Mus muscu
1232	47.4	2.8	685	10	BC049720	Mus muscu
1233	47.4	2.8	685	11	CNS06EJ4	T3 end of
1234	47.4	2.8	686	10	BC060302	Mus muscu
1235	47.4	2.8	688	6	CQ422987	Sequence
1236	47.4	2.8	690	9	BC040927	Homo sapi
1237	47.4	2.8	705	9	HSMB00237	Homo sapi
1238	47.4	2.8	805	10	BC063183	Rattus no
1239	47.4	2.8	811	11	BV073335	S212P6813
1240	47.4	2.8	824	9	BC070291	Homo sapi
1241	47.4	2.8	843	10	BC038641	Mus muscu
1242	47.4	2.8	883	10	BC049726	Mus muscu
1243	47.4	2.8	887	9	AB125184	Macaca fa
1244	47.4	2.8	902	10	BC048724	Mus muscu
1245	47.4	2.8	935	10	BC049693	Mus muscu
1246	47.4	2.8	942	5	BC049498	Danio rer
1247	47.4	2.8	971	10	BC030946	Mus muscu
1248	47.4	2.8	989	10	BC051033	Mus muscu
1249	47.4	2.8	997	9	BC047943	Homo sapi
1250	47.4	2.8	1068	9	BC071641	Homo sapi
1251	47.4	2.8	1071	9	BC073941	Homo sapi
1252	47.4	2.8	1107	3	AK173973	Ciona int
1253	47.4	2.8	1113	9	BC030277	Homo sapi
1254	47.4	2.8	1222	9	BC035237	Homo sapi
1255	47.4	2.8	1240	9	BC055418	Homo sapi
1256	47.4	2.8	1281	5	BC083538	Danio rer
1257	47.4	2.8	1299	10	BC021404	Mus muscu
1258	47.4	2.8	1332	10	BC060992	Mus muscu
1259	47.4	2.8	1348	9	BC070164	Homo sapi
1260	47.4	2.8	1425	9	BC036851	Homo sapi

1261	47.4	2.8	1433	5	BC082836	BC082836 Xenopus l	c1334	47.4	2.8	14006	6	AX346860	AX346860 Sequence
1262	47.4	2.8	1445	10	BC071177	BC071177 Rattus no	c1335	47.4	2.8	14798	6	AX345934	AX345934 Sequence
1263	47.4	2.8	1463	6	C0491467	C0491467 Sequence	c1336	47.4	2.8	17721	6	AX346631	AX346631 Sequence
1264	47.4	2.8	1463	6	CQ497350	CQ497350 Sequence	c1337	47.4	2.8	19289	2	AC090926	AC090926 Homo sapi
1265	47.4	2.8	1493	9	HS0805897	BS538346 Homo sapi	c1338	47.4	2.8	40324	6	AX458633	AX458633 Sequence
1266	47.4	2.8	1500	3	AK174058	AK174058 Ciona int	1339	47.4	2.8	57538	3	AC115682	AC115682 Dictyosce
1267	47.4	2.8	1591	9	HS0807298	BX647154 Homo sapi	c1340	47.4	2.8	67374	2	AC118933	AC118933 Mus muscu
1268	47.4	2.8	1653	10	BC083548	BC083548 Rattus no	c1341	47.4	2.8	72981	10	BX511117	BX511117 Mouse DNA
1269	47.4	2.8	1661	6	BC025753	BC025753 Homo sapi	c1342	47.4	2.8	73778	6	AX344562	AX344562 Sequence
1270	47.4	2.8	1696	6	AR256293	AR256293 Sequence	c1343	47.4	2.8	82771	2	AC011953	AC011953 Homo sapi
1271	47.4	2.8	1719	10	BC045148	BC045148 Mus muscu	1344	47.4	2.8	85916	3	AC117080	AC117080 Dictyosce
1272	47.4	2.8	1738	6	AR560934	AR560934 Sequence	c1345	47.4	2.8	110000	2	AC113129_2	Continuation (3 of
1273	47.4	2.8	1738	8	BT009079	BT009079 Triticum	c1346	47.4	2.8	110000	2	AC114623_1	Continuation (2 of
1274	47.4	2.8	1744	6	BC019265	BC019265 Homo sapi	c1347	47.4	2.8	110000	10	AE014180_1	Continuation (2 of
1275	47.4	2.8	1750	9	BC048294	BC048294 Homo sapi	1348	47.4	2.8	120653	5	BX649590	BX649590 Zebrafish
1276	47.4	2.8	1825	9	BC050524	BC050524 Homo sapi	1349	47.4	2.8	121554	2	AC142244	AC142244 Mus muscu
1277	47.4	2.8	1939	5	BC079974	BC079974 Xenopus l	c1350	47.4	2.8	142324	5	EX005420	EX005420 Zebrafish
1278	47.4	2.8	1980	10	BC027199	BC027199 Mus muscu	c1351	47.4	2.8	148053	2	CR352222	CR352222 Danio rer
1279	47.4	2.8	1999	9	BC020684	BC020684 Homo sapi	c1352	47.4	2.8	152506	10	AC145589	AC145589 Mus muscu
1280	47.4	2.8	2161	9	AB063084	AB063084 Macaca fa	1353	47.4	2.8	156060	2	AC004153	AC004153 Plasmodi
1281	47.4	2.8	2224	6	BD189940	BD189940 Tumor ant	c1354	47.4	2.8	162646	2	AC112977	AC112977 Mus muscu
1282	47.4	2.8	2224	9	AB062292	AB062292 Homo sapi	1355	47.4	2.8	163035	2	AC142822	AC142822 Macaca mu
1283	47.4	2.8	2237	3	AK112710	AK112710 Ciona int	1356	47.4	2.8	164520	2	AC020738	AC020738 Homo sapi
1284	47.4	2.8	2245	9	BC037547	BC037547 Homo sapi	c1357	47.4	2.8	166529	10	AC147621	AC147621 Mus muscu
1285	47.4	2.8	2307	5	BC081197	BC081197 Xenopus l	1358	47.4	2.8	179253	5	AL928870	AL928870 Zebrafish
1286	47.4	2.8	2320	10	BC046962	BC046962 Mus muscu	1359	47.4	2.8	181571	10	AC108949	AC108949 Mus muscu
1287	47.4	2.8	2335	5	BC068409	BC068409 Danio rer	c1360	47.4	2.8	191119	2	CR749163	CR749163 Danio rer
1288	47.4	2.8	2372	9	BC042652	BC042652 Homo sapi	c1361	47.4	2.8	194362	10	AC124716	AC124716 Mus muscu
1289	47.4	2.8	2403	9	HS0808752	BX648601 Homo sapi	1362	47.4	2.8	195972	10	AC117567	AC117567 Mus muscu
1290	47.4	2.8	2477	9	BC034692	BC034692 Homo sapi	1363	47.4	2.8	198590	10	AC113983	AC113983 Mus muscu
1291	47.4	2.8	2539	10	BC046284	BC046284 Mus muscu	1364	47.4	2.8	199274	2	AC123626	AC123626 Mus muscu
1292	47.4	2.8	2593	9	HS0807470	BX647326 Homo sapi	1365	47.4	2.8	200934	10	AC123850	AC123850 Mus muscu
1293	47.4	2.8	2601	5	BC072034	BC072034 Xenopus l	c1366	47.4	2.8	205878	2	CR392366	CR392366 Danio rer
1294	47.4	2.8	2765	3	AK115430	AK115430 Ciona int	1367	47.4	2.8	212144	2	AC140356	AC140356 Mus muscu
1295	47.4	2.8	2783	10	BC058527	BC058527 Mus muscu	1368	47.4	2.8	215427	2	AC130980	AC130980 Rattus no
1296	47.4	2.8	2789	3	AK114441	AK114441 Ciona int	1369	47.4	2.8	219491	2	AC092256	AC092256 Mus muscu
1297	47.4	2.8	2824	5	BC042665	BC042665 Homo sapi	1370	47.4	2.8	221068	2	AC102378	AC102378 Mus muscu
1298	47.4	2.8	2980	6	BD270060	BD270060 Secreted	c1371	47.4	2.8	229332	2	AC137869	AC137869 Mus muscu
1299	47.4	2.8	3149	10	BC040763	BC040763 Mus muscu	c1372	47.4	2.8	223869	2	AC119834	AC119834 Mus muscu
1300	47.4	2.8	3186	5	BC068331	BC068331 Danio rer	1373	47.4	2.8	227395	10	AL512346	AL512346 Mouse DNA
1301	47.4	2.8	3446	9	HS0803955	AL713742 Homo sapi	1374	47.4	2.8	230184	10	AC138679	AC138679 Mus muscu
1302	47.4	2.8	3492	5	BC078645	BC078645 Danio rer	1375	47.4	2.8	235664	2	AC126522	AC126522 Rattus no
1303	47.4	2.8	3502	9	HS0807726	BX647580 Homo sapi	1376	47.4	2.8	238781	10	AC127351	AC127351 Mus muscu
c1304	47.4	2.8	3664	6	AX598782	AX598782 Sequence	c1377	47.4	2.8	240185	2	AC115132	AC115132 Rattus no
c1305	47.4	2.8	3664	6	AX598928	AX598928 Sequence	1378	47.4	2.8	240931	2	AC107097	AC107097 Rattus no
c1306	47.4	2.8	3664	6	AX705378	AX705378 Sequence	c1379	47.4	2.8	240931	2	AC107097	AC107097 Rattus no
c1307	47.4	2.8	3664	6	AX705400	AX705400 Sequence	c1380	47.4	2.8	244656	10	AC031278	AC031278 Mus muscu
1308	47.4	2.8	3930	9	BC027963	BC027963 Homo sapi	c1381	47.4	2.8	245859	2	AC099418	AC099418 Rattus no
1309	47.4	2.8	3964	5	BC077739	BC077739 Xenopus l	c1382	47.4	2.8	252632	3	AE014818	AE014818 Plasmodi
1310	47.4	2.8	3997	6	AX086658	AX086658 Sequence	c1383	47.4	2.8	253441	2	AC135668	AC135668 Mus muscu
1311	47.4	2.8	4154	9	HS0803629	AL832322 Homo sapi	c1384	47.4	2.8	255189	2	AC106391	AC106391 Rattus no
1312	47.4	2.8	4180	10	BC042645	BC042645 Mus muscu	1385	47.4	2.8	258938	2	AC099416	AC099416 Mus muscu
1313	47.4	2.8	4237	6	BD057918	BD057918 Secreted	c1386	47.4	2.8	262640	2	AC139057	AC139057 Mus muscu
1314	47.4	2.8	4550	10	AB015672	AB015672 Mus muscu	c1387	47.4	2.8	267140	2	AC097568	AC097568 Rattus no
1315	47.4	2.8	4679	9	HS0808418	BX648270 Homo sapi	1388	47.4	2.8	275156	2	AC105868	AC105868 Rattus no
c1316	47.4	2.8	5182	6	AX252007	AX252007 Sequence	c1389	47.4	2.8	302489	2	AC100742	AC100742 Mus muscu
c1317	47.4	2.8	5182	6	AX348780	AX348780 Sequence	1390	47.2	2.8	203	6	CQ524826	CQ524826 Sequence
c1318	47.4	2.8	5349	6	AX345242	AX345242 Sequence	1391	47.2	2.8	240	6	CQ663206	CQ663206 Sequence
c1319	47.4	2.8	5437	6	AX346644	AX346644 Sequence	c1392	47.2	2.8	281	6	CQ410312	CQ410312 Sequence
c1320	47.4	2.8	5893	6	AX345761	AX345761 Sequence	1393	47.2	2.8	348	6	CQ524785	CQ524785 Sequence
c1321	47.4	2.8	6664	6	AX252071	AX252071 Sequence	1394	47.2	2.8	396	6	CQ525748	CQ525748 Sequence
c1322	47.4	2.8	6664	6	AX822358	AX822358 Sequence	1395	47.2	2.8	504	6	CQ526419	CQ526419 Sequence
c1323	47.4	2.8	6664	6	AX822486	AX822486 Sequence	1396	47.2	2.8	539	10	BC031454	BC031454 Mus muscu
c1324	47.4	2.8	6664	6	AX825998	AX825998 Sequence	1397	47.2	2.8	623	9	BC043516	BC043516 Homo sapi
c1325	47.4	2.8	6664	6	AX826126	AX826126 Sequence	1398	47.2	2.8	625	10	BC059134	BC059134 Rattus no
c1326	47.4	2.8	6898	6	AX344814	AX344814 Sequence	1399	47.2	2.8	656	6	CQ487057	CQ487057 Sequence
1327	47.4	2.8	8305	5	BC076779	BC076779 Xenopus l	1400	47.2	2.8	675	10	BC059112	BC059112 Rattus no
c1328	47.4	2.8	8305	6	AX346470	AX346470 Sequence	1401	47.2	2.8	720	3	AK174023	AK174023 Ciona int
c1329	47.4	2.8	8607	6	AR453095	AR453095 Sequence	1402	47.2	2.8	749	9	BC008417	BC008417 Homo sapi
c1330	47.4	2.8	8607	6	AX281207	AX281207 Sequence	c1403	47.2	2.8	756	6	CQ399155	CQ399155 Sequence
c1331	47.4	2.8	8607	6	AX356478	AX356478 Sequence	c1404	47.2	2.8	756	6	CQ405433	CQ405433 Sequence
c1332	47.4	2.8	12138	6	AX346530	AX346530 Sequence	1405	47.2	2.8	760	9	BC040885	BC040885 Homo sapi
c1333	47.4	2.8	12138	6	AX348420	AX348420 Sequence	c1406	47.2	2.8	780	8	CNS019TW	AL112092 Botrytis

1407	47.2	2.8	859	9	AK026608	Homo sapi	AK026608 Homo sapi
1408	47.2	2.8	891	14	TMO308687	Tobacco m	AJ308687 Tobacco m
1409	47.2	2.8	1087	5	BC083541	Danio rer	BC083541 Danio rer
1410	47.2	2.8	1097	6	AX082180	Sequence	AX082180 Sequence
1411	47.2	2.8	1117	8	AF243375	Glycine m	AF243375 Glycine m
1412	47.2	2.8	1155	9	BC036792	Homo sapi	BC036792 Homo sapi
1413	47.2	2.8	1285	9	BSM801947	Homo sapi	BSM801947 Homo sapi
1414	47.2	2.8	1316	9	BC073942	Homo sapi	BC073942 Homo sapi
1415	47.2	2.8	1352	9	BC043573	Homo sapi	BC043573 Homo sapi
1416	47.2	2.8	1368	5	BC064278	Xenopus t	BC064278 Xenopus t
1417	47.2	2.8	1464	9	IR2005397	Homo sapi	AL389978 Homo sapi
1418	47.2	2.8	1490	5	BC074522	Xenopus t	BC074522 Xenopus t
1419	47.2	2.8	1556	5	BC063349	Xenopus t	BC063349 Xenopus t
1420	47.2	2.8	1563	9	BC071790	Homo sapi	BC071790 Homo sapi
1421	47.2	2.8	1568	5	BC050177	Danio rer	BC050177 Danio rer
1422	47.2	2.8	1738	3	AK112524	Ciona int	AK112524 Ciona int
1423	47.2	2.8	1742	9	HSM806670	Homo sapi	BX640624 Homo sapi
1424	47.2	2.8	1756	9	BC069223	Homo sapi	BC069223 Homo sapi
1425	47.2	2.8	1812	10	BC055113	Mus muscu	BC055113 Mus muscu
1426	47.2	2.8	1816	9	BC050396	Homo sapi	BC050396 Homo sapi
1427	47.2	2.8	1820	9	BC053581	Homo sapi	BC053581 Homo sapi
1428	47.2	2.8	1877	5	BC066464	Danio rer	BC066464 Danio rer
1429	47.2	2.8	1885	9	HSM807866	Homo sapi	BX647720 Homo sapi
1430	47.2	2.8	1889	9	HSM805887	Homo sapi	BX537794 Homo sapi
1431	47.2	2.8	1913	9	BC030546	Homo sapi	BC030546 Homo sapi
1432	47.2	2.8	1944	9	BC025786	Homo sapi	BC025786 Homo sapi
1433	47.2	2.8	1985	6	BD275145	48 Human	BD275145 48 Human
1434	47.2	2.8	2000	9	BC063423	Homo sapi	BC063423 Homo sapi
1435	47.2	2.8	2036	9	BC030243	Homo sapi	BC030243 Homo sapi
1436	47.2	2.8	2057	9	HSM808552	Homo sapi	BX648404 Homo sapi
1437	47.2	2.8	2060	10	BC038004	Mus muscu	BC038004 Mus muscu
1438	47.2	2.8	2196	9	HSM805743	Homo sapi	BX537439 Homo sapi
1439	47.2	2.8	2244	9	HSM807352	Homo sapi	BX647208 Homo sapi
1440	47.2	2.8	2287	9	BC044220	Homo sapi	BC044220 Homo sapi
1441	47.2	2.8	2393	5	BC070538	Xenopus l	BC070538 Xenopus l
1442	47.2	2.8	2499	9	HSM801350	Homo sapi	AL133016 Homo sapi
1443	47.2	2.8	2517	5	BC075907	Danio rer	BC075907 Danio rer
1444	47.2	2.8	2660	10	BC046318	Mus muscu	BC046318 Mus muscu
1445	47.2	2.8	2729	5	XJ068387	Xenopus lae	U68387 Xenopus lae
1446	47.2	2.8	2846	9	HSM802834	Homo sapi	AL442082 Homo sapi
1447	47.2	2.8	2868	10	BC006583	Mus muscu	BC006583 Mus muscu
1448	47.2	2.8	2991	9	BC030556	Homo sapi	BC030556 Homo sapi
1449	47.2	2.8	3141	10	BC066161	Mus muscu	BC066161 Mus muscu
1450	47.2	2.8	3307	9	BC025714	Homo sapi	BC025714 Homo sapi
1451	47.2	2.8	3525	10	BC034207	Mus muscu	BC034207 Mus muscu
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AUTHORS	Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, J.		
TITLE	Human neurotrophin homologue		
JOURNAL	Patent: EP 1386931-A 522 04-FEB-2004;		
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ACCESSION AR528639  
VERSION AR528639.1 GI:53916717  
KEYWORDS Unknown.  
SOURCE ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1679)  
AUTHORS Bollinger, C.L. Jr.  
TITLE Crane test weight assembly and method  
JOURNAL Patent: US 6725730-A 375 27-APR-2004;  
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VERSION AX358872.1 GI:18675337  
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REFERENCE 1  
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;  
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LOCUS  
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ACCESSION AX403748  
VERSION AX403748.1 GI:21437184  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
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AUTHORS Ashkenazi, A., Baker, K., Botstein, D., Deenoyers, L., Eaton, D.L.,  
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, W.E.,  
Goddard, A., Godowski, P., Gurney, A., Kijavini, I.J., Mather, J.,  
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,  
Williams, P.M., Wood, W.I. and Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;  
Genentech Inc. (US)  
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DEFINITION AX454470  
ACCESSION AX454470  
VERSION AX454470.1 GI:21713859  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.  
TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 55 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)  
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LOCUS Sequence 375 from Patent WO0140466.
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ACCESSION AX464242
VERSION AX464242.1 GI:21899137
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REFERENCE
1 Baker,K.P., Bersini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
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Secreted and transmembrane polypeptides and nucleic acids encoding
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Patent: WO 0140466-A 375 07-JUN-2001;
Genentech Inc. (US)
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LOCUS Sequence 55 from Patent WO0200690.

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ACCESSION AX490948

VERSION AX490948.1 GI:22323811

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

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AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 020690-A 55 03-JAN-2002;

Genentech, Inc. (US)

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ACCESSION AY358331  
VERSION AY358331.1 GI:37181786  
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SOURCE Homo sapiens (human)  
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REFERENCE 1 (bases 1 to 1679)  
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,  
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,  
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,  
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Xie, M.H., Yansura, B., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
Goddard, A., Wood, W.I. and Godowski, P.  
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 1679)  
AUTHORS Clark, H.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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DEFINITION Sequence 2 from patent US 6664383.  
ACCESSION AR439649  
VERSION AR439649.1 GI:42665573  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1693)  
AUTHORS Fukushima,D., Shibayama,S. and Tada,H.  
TITLE Polypeptides, cDNA encoding the same and utilization thereof  
JOURNAL Patent: US 6664383-A 2 16-DEC-2003;  
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ACCESSION AX665342
VERSION AX665342.1 GI:29290464
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REFERENCE 1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 100 09-JAN-2003;
Cancer Research Technology Limited (GB)
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ACCESSION  
AF126426.1 GI:7158997  
KEYWORDS  
SOURCE Homo sapiens (human)  
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AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.  
TITLE Cloning and identification of human neurotrophin full length cDNA  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1839)  
AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.  
TITLE Direct Submission  
JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical  
Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China  
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Matches 1464; Conservative 0; Mismatches 2; Indels 20; Gaps 1;  
Qy 214 AGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAAGCTATGGACAACGTCACCGT 273  
Db 345 AGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAAGCTATGGACAACGTCACCGT 404  
Qy 274 CCGCAGCGGGAGAGCGCCACCTCAGGTGCATATTGACAACCGGGTCACCCGGGTGGC 333  
Db 405 CCGCAGCGGGAGAGCGCCACCTCAGGTGCATATTGACAACCGGGTCACCCGGGTGGC 464  
Qy 334 CTGGTAAACCGCAGACCATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCTCTCG 393  
Db 465 CTGGTAAACCGCAGACCATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCTCTCG 524  
Qy 394 CGTGGTCTCTGAGCAACACCCAAACGACGTACAGCATCGAGATCCAGAACGTCGATGT 453  
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Qy 454 GTATGACGAGGCGCCTTACACCTGCTGGTGCAGACAGAACCAACCAAGACCTCTAG 513  
Db 585 GTATGACGAGGCGCCTTACACCTGCTGGTGCAGACAGAACCAACCAAGACCTCTAG 644  
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Qy 754 GGCCTGCGCTGTGTGACGAGAGTAAGGTCACTGTAACCTATCCACATCATTTTCAGA 813  
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Qy 874 AGTCCCTTCAGCAGAAATTCAGTGTGTACAGGATGACAAAGACTGATTGAAGGAAGAA 933  
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Qy 1634 CCACGGCGTGTGTTGTGAAACGTGAAATATAAAGAGCAAAAAA 1679  
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RESULT 13  
AR439648 LOCUS 1032 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 1 from patent US 6664383.  
AR439648  
ACCESSION AR439648  
VERSION AR439648.1 GI:42665572  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1032)  
AUTHORS Fukushima, D., Shibayama, S. and Tada, H.  
TITLE Polypeptides, cDNA encoding the same and utilization thereof  
JOURNAL Patent: US 6664383-A 1 16-DEC-2003;  
FEATURES Location/Qualifiers  
source 1..1032  
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/mol\_type="genomic DNA"  
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Query Match 61.5%; Score 1032; DB 6; Length 1032;  
Best Local Similarity 100.0%; Pred. No. 1.6e-262;  
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 134 ATGAAACCATCCAGCCCAAAATTCACAAATCTCTTGGGCAATCTTCAACGGGCTG 193  
Db 1 ATGAAACCATCCAGCCCAAAATTCACAAATCTCTTGGGCAATCTTCAACGGGCTG 60  
Qy 194 GCTGCTCTGTGCTCTTCCAGGAGTGCCTGCGGAGAGATGCCACCTTCCCCAAA 253  
Db 61 GCTGCTCTGTGCTCTTCCAGGAGTGCCTGCGGAGAGATGCCACCTTCCCCAAA 120  
Qy 254 GCTATGACAAACGTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313  
Db 121 GCTATGACAAACGTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180  
Qy 314 AACCGGCTCACCGGGTGGCTGTGTAATGACGAGGAGCCATCTCTATGCTGGGNAATGAC 373  
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Qy 374 AAGTGTGCTGTGATCTCTGCGTGGTCTCTGAGAACACCCAAACGACGTACAGCATC 433  
Db 241 AAGTGTGCTGTGATCTCTGCGTGGTCTCTGAGAACACCCAAACGACGTACAGCATC 300  
Qy 434 GAGATCCAGAAACGTGGATGTGTATGACGAGGCGCTTTACACCTGCTGGTGCAGACAGAC 493  
Db 301 GAGATCCAGAAACGTGGATGTGTATGACGAGGCGCTTTACACCTGCTGGTGCAGACAGAC 360  
Qy 494 AACCAACCAAGACCTCTAGGTCACCTGATGTCGAGAGTATCTCCCAAAATTTGTAGAG 553  
Db 361 AACCAACCAAGACCTCTAGGTCACCTGATGTCGAGAGTATCTCCCAAAATTTGTAGAG 420  
Qy 554 ATTTCTTTCAGATATCTCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613  
Db 421 ATTTCTTTCAGATATCTCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480  
Qy 614 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673  
Db 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540  
Qy 674 AGTGAAGCAATATCTTGGAAATTCAGGGCATCCCGGGAGGAGCTCAGGGGACTACGAG 733  
Db 541 AGTGAAGCAATATCTTGGAAATTCAGGGCATCCCGGGAGGAGCTCAGGGGACTACGAG 600  
Qy 734 TGCACTGCTCCAATGAGTGGCGCGCGCTGGTACGAGAGTAAAGGTCAACGCTGAAC 793  
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JOURNAL	Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
Series: IRAC Plate: 41 Row: h Column: 10				
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26986610.				
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QY	214	AGGAGTGCCCGTGGCGAGAGATGCCACCTTCCCAAGCTATGGACAACGTCACGGT	273	

124	AGGAGTCCCGGTGCGTATAGCGGAGNATGCCACTTTTCCAAAGCTATATGCAACCGTGACGGT	183
274	CCGGCAGCGGGAGAGCCGCCCTTCAGGTGCATCTATTTGACAAACCGGTGCACCCGGGTGGC	333
184	CAGCAGCGGGGANGCGCCACCTTCAGGTGCACNATTTGACNACCGAGTCAACCGGGTGGC	243
334	CTGGCTAAACCGCAGCAGCAACATCTCTATATGTGGGAATGACAAGTGTGTCTTGATCTCTCG	393
244	CTGGCTAAACCGCAGTACCATCTCTATGTGTGGAAATGACAAGTGTGTCTTAGATCTCTCG	303
394	CGTGGTCTCTTGAGCAACACCCNAAACGCGAGTACAGCATCGAGATCAGAACTGGATGT	453
304	TGTGGTCTCTTGAGTAACACCCAGACCCAGTACAGCATTTGAGATTCAGAAATGTGGATGT	363
454	GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCAACCAAGACCTCTAG	513
364	GTACGATGAGGGCCCTTATACCTGCTCGGTACAGACAGACNACCAACCTTAAGACCTCCAG	423
514	GGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCAT	573
424	GGTCCACCTCATTTGTACAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCAT	483
574	TAATGAAGGNAACAATATTAGCTCACTCGATAGCAACTGTGTAGACCAAGCCTACCGT	633
484	TAATGAAGGNAACAATCAAGCTCACTTCATATGATACGCCACAGGTAGACCGGAGCCTACAGT	543
634	TACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGACGAATCTTTGGA	693
544	AACCTGGAGACATATTTCTCCAAAGCGTTGGCTTTGTGAGTGAAGATGAGTACCTTGA	603
694	AAATTCAAGGCATCAACCGGGAGCAGTCAAGGGGACTACGAGTGCAGTGCCCTCCAATGACGT	753
604	GATCCAGGGCATCACTCGGGAACAGTCAAGCGAGTACGAGTGCAGCGCCTCCAACGACGT	663
754	GGCCGCGCCGTGTGTACGAGAGTAAAGTCAACCGTGAACTATCCACCATACATTTTCAGA	813
664	GGCGCACCAAGTGTGTACGAAGTGAAGGTCAACCGTGAACATATCCACATACATCTCAGA	723
814	AGCCAAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC	873
724	AGCTAAGGGCACAGGTGTCCCGTGGGGGAGAGGGGACTCTGCAGTGTGAAGCTTCCGC	783
874	AGTCCCTCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAAAGACTGATTGAAGGAAGAA	933
784	AGTCCCTCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAAAGACTGTCGAGGAAGAA	843
934	AGGGGTGAAGTGAAGAAACAGACCTTCTCTCTCAAAACTCATCTTCTTCAATGTCTCTGA	993
844	GGGAGTCAAAAGTGAAGAAACAGACCTTCTCTTCAAAACTCACCTTTTTCACCGTCTCTGA	903
994	ACATGACTATGGGAACATACACTTCGCTGGCTCCCAACAGCTGGGCCACACCACTGACG	1053
904	ACATGACTATGGGAACATACACTGTGTGGCTCTCAACAAAGCTGGGTCAACCAACGCGCAG	963
1054	CATCATGTCTATTTGGTCCAGCGCGCGTCAAGCGAGGTGAGCAACCGCACGTCGAGGAGGGC	1113
964	CATCATGTCTATTTGGTCCCGGTGTGTCTCAGTGAAGTCAACATGGGACATCAGGAGGGC	1023
1114	AGGCTGCGTCTGGTCTGTGCTCTTCTTGGTCTTGCACTGTCTTCTCAAAATTTTGATGTGA	1173
1024	AGGCTGCATTTGGCTCTCTCTCTCTCTTCTTGGTCTTACACTGTCTCTCAAAATTTTGATGTGA	1083
1174	GTGCCACTTCCCACCCGGGNAAGCTTCGCCGACCAACCACCACCAACACACAGCAATG	1233
1084	GTGCCCTTCCCTGCTGGGGAGA-GCTGCTGCCACCGCATC--TCAATACAACAGCACTG	1140
1234	GCAACACCGACGCAACCAATCAGATATATACAAATGAAATTTAGAAGAAACACAGCCCTCA	1293
1141	-----CAAAATGAAGCACAAGTCAGATCAATGAAATTCGAGAAATCACAGCC-AA	1192
1294	TGGACACGAAATTTGAGGAGGGGAAACAAAGAATATCTTTG-----GGGGGAAAAAGTTT	1348
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Query Match	100.0%;	Score 1679;	DB 6;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 6				
ID ABL88099 standard; cDNA; 1679 BP.				
DE Human PRO337 cDNA sequence SEQ ID NO:55.				
PN W0200200690-A2.				
PD 03-JAN-2002.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1679;	DB 6;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 7				
ID ABL95588 standard; cDNA; 1679 BP.				
DE Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.				
PN W0200208284-A2.				
PD 31-JAN-2002.				
PA (GETH ) GENENTECH INC.				
PA (BAKE ) BAKER K P.				
PA (FERR ) FERRARA N.				
PA (GERB ) GERBER H.				
PA (GERE ) GERRITSEN M E.				
PA (GODD ) GODDARD A.				
PA (GODO ) GODOWSKI P J.				
PA (GURN ) GURNEY A L.				
PA (HILL ) HILLAN K J.				
PA (MARS ) MARSTERS S A.				
PA (PANJ ) PAN J.				
PA (PAON ) PAONI N F.				
PA (STEP ) STEPHAN J F.				
PA (WATA ) WATANABE C K.				
PA (WILL ) WILLIAMS P M.				
PA (WOOD ) WOOD W I.				
Query Match	100.0%;	Score 1679;	DB 6;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 8				
ID ACA63892 standard; cDNA; 1679 BP.				
DE Novel human secreted and transmembrane protein PRO337 cDNA.				
PN US2002192706-A1.				
PD 19-DEC-2002.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1679;	DB 8;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 9				
ID ACA03790 standard; cDNA; 1679 BP.				
DE cDNA encoding human PRO polypeptide #188.				
PN US2003036180-A1.				
PD 20-FEB-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1679;	DB 8;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 10				
ID ACA04996 standard; cDNA; 1679 BP.				
DE Novel human secreted and transmembrane protein PRO337 cDNA.				
PN US2003032063-A1.				
PD 13-FEB-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1679;	DB 8;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 11				
ID ACA72056 standard; cDNA; 1679 BP.				
DE Human secreted and transmembrane PRO polypeptide #37 cDNA.				
PN US2002177553-A1.				
PD 28-NOV-2002.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1679;	DB 8;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 12				
ID ABX89328 standard; cDNA; 1679 BP.				
DE cDNA encoding novel secreted and transmembrane protein PRO337.				
PN US2003017563-A1.				
PD 23-JAN-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1679;	DB 8;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		

RESULT 13  
ID ABX92696 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO337 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 8; Length 1679;  
Pred. No. 0;  
RESULT 14  
ID ACD41982 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #188.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 8; Length 1679;  
Pred. No. 0;  
RESULT 15  
ID ACA60526 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 8; Length 1679;  
Pred. No. 0;  
RESULT 16  
ID ACA04516 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 DNA.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 8; Length 1679;  
Pred. No. 0;  
RESULT 17  
ID ACA66437 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO337.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 8; Length 1679;  
Pred. No. 0;  
RESULT 18  
ID ACA68559 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 8; Length 1679;  
Pred. No. 0;  
RESULT 19  
ID ACA04211 standard; cDNA; 1679 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 8; Length 1679;  
Pred. No. 0;  
RESULT 20  
ID ACA65657 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO337.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 21  
ID ADA45894 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US200302328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 22

ID ADA76325 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
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Pred. No. 0;  
RESULT 23  
ID ABT44288 standard; cDNA; 1679 BP.  
DE Human PRO337 cDNA.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 24  
ID ADA18975 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 25  
ID ADA61598 standard; cDNA; 1679 BP.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 26  
ID ADB19383 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 27  
ID ADB27924 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 28  
ID ADA86403 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 29  
ID ADB15967 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 30  
ID ADA47753 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;  
Pred. No. 0;  
RESULT 31  
ID ADA67548 standard; cDNA; 1679 BP.



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DE Human PRO polynucleotide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 32
  ID ADB30555 standard; cDNA; 1679 BP.
  DE cDNA encoding human PRO polypeptide #188.
  PN US2003068794-A1.
  PD 10-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 33
  ID ADA85851 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003082693-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 34
  ID ADA97063 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003082705-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 35
  ID ADA79367 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003082763-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 36
  ID ADA87506 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003087345-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 37
  ID ADB16708 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003087349-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 38
  ID ADA91800 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003082694-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 39
  ID ADB14863 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003087351-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 40
  ID ADA25061 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003068798-A1.
  PD 13-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 41
  ID ADA47275 standard; cDNA; 1679 BP.
  DE Human secreted/transmembrane polypeptide PRO337 cDNA.
  PN US2003044844-A1.
  PD 06-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 42
  ID ADB18824 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003073211-A1.
  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 43
  ID ADA94039 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003077722-A1.
  PD 24-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 44
  ID ADB19935 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003082691-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 45
  ID ADB13247 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003082710-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 46
  ID ACD98611 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003044945-A1.
  PD 06-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 47
  ID ACD30038 standard; cDNA; 1679 BP.
  DE Novel human secreted and transmembrane protein PRO337 cDNA.
  PN US2003050240-A1.
  PD 13-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 48
  ID ADA12722 standard; cDNA; 1679 BP.
  DE Human cDNA encoding secreted/transmembrane polypeptide PRO337.
  PN US2003055216-A1.
  PD 20-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1679; DB 9; Length 1679;
  RESULT 49
  ID ADA74501 standard; cDNA; 1679 BP.
  DE Human PRO polynucleotide #188.
  PN US2003068798-A1.
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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADB24734 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SRQ ID NO 375.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ADA82258 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADA75221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADA85229 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADA84747 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADB30003 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADA80531 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ADA75773 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ADA46998 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADB25294 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ADA93470 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADB26820 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ADB31107 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ABT44571 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADA61035 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADB24182 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADA96511 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADA81083 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADA95959 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADB26268 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADB21753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ACD82238 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ACD29453 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #133.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADA77532 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADB18272 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADA86955 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADA88058 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADB28476 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADB29028 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADA88610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADB27372 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADB22305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ACD30273 standard; cDNA; 1679 BP.
DE Human cDNA encoding Pro337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ABT43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.
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PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 87  
ID ADA66996 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 88  
ID ADB22857 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 89  
ID ADB23630 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 90  
ID ADA92352 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 91  
ID ADB15415 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 92  
ID ADB83615 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 93  
ID ADB80721 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US200308068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 94  
ID ADB73262 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 95  
ID ADB38667 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082766-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 96  
ID ADB78344 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 97  
ID ADB38115 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 98  
ID ADB66587 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 9; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 99  
ID ADB84992 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 100  
ID ADB89667 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 101  
ID ADB90399 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 102  
ID ADB39500 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 103  
ID ADB78098 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 104  
ID ADB74028 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide sequence #133.  
PN US2003045462-A1.  
PD 06-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 105  
ID ADB87164 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
FN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 106  
ID ADB84746 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
FN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 107  
ID ADB47123 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 108  
ID ADB83861 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 109  
ID ADB86730 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
FN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 110  
ID ADB73016 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 111  
ID ADB76744 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide sequence #133.  
FN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 112  
ID ADB77335 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 113  
ID ADB34492 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
FN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 114  
ID ADB35596 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
FN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 115  
ID ADB33940 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
FN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 116  
ID ADB35044 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
FN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 117  
ID ADB36148 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
FN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 118  
ID ADB46543 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 119  
ID ADC44170 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
FN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 120  
ID ADC61930 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
FN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 121  
ID ADC63894 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
FN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 122  
ID ADC66994 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
FN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 123  
ID ADC69118 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 124  
ID ADC63178 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 125  
ID ADC68243 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 126  
ID ADC41563 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 127  
ID ADC67618 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 128  
ID ADC62554 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 129  
ID ADC36854 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 130  
ID ADC42187 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 131  
ID ADC21844 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 132  
ID ADC50416 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO3337 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 133  
ID ADC71963 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO3337 cDNA.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 134  
ID ADC59942 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO3337 cDNA.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 135  
ID ADC49875 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO3337 cDNA.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 136  
ID ADC49074 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO3337 cDNA.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 137  
ID ADC49591 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO3337 cDNA.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 138  
ID ADC47452 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO3337 cDNA.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 139  
ID ADC52949 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID375.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 140  
ID ADC57303 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID375.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 141

ID ADC60494 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 142  
ID ADC50969 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 143  
ID ADC65496 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
FN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 144  
ID ADC54594 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID375.  
FN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 145  
ID ADC53555 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID375.  
FN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 146  
ID ADC59078 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID375.  
FN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 147  
ID ADC55956 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID375.  
FN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 148  
ID ADC58526 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID375.  
FN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 149  
ID ADC47197 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 150  
ID ADD03200 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.

DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 151  
ID ADC90192 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 152  
ID ADC69611 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
FN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 153  
ID ADC48500 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
FN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 154  
ID ADD10029 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
FN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 155  
ID ADC78072 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 156  
ID ADD04604 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 157  
ID ADD06307 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 158  
ID ADC80560 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 159  
ID ADD11067 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.

PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 160  
ID ADD10344 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #28.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 161  
ID ADC47948 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 162  
ID ADC77826 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US200308066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 163  
ID ADC80008 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 164  
ID ADD11304 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #28.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 165  
ID ADD09477 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 166  
ID ADD50789 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 167  
ID ADD41190 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 168  
ID ADD52329 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003194769-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 169  
ID ADD51035 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 170  
ID ADD53069 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 171  
ID ADD53621 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 172  
ID ADD37097 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #28.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 173  
ID ADD51777 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 174  
ID ADD02576 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 175  
ID ADD50516 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 176  
ID ADD02010 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 177  
ID ADD54192 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003203432-A1.  
PD 30-OCT-2003.



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 178  
ID ADE35610 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 179  
ID ADE51281 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 180  
ID ADE49556 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 181  
ID ADE92509 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 182  
ID ADE91405 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 183  
ID ADE804019 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 184  
ID ADE32316 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 185  
ID ADE22248 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 186  
ID ADE79472 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 187  
ID ADE35610 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 188  
ID ADE16724 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 189  
ID ADE73339 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 190  
ID ADE42008 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 191  
ID ADE17825 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 192  
ID ADE91957 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 193  
ID ADE33420 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 194  
ID ADE33972 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 195  
ID ADE80024 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;

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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADD93061 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ADD72697 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ADE19481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ADE18929 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ADE43125 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ADP95914 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ADE22800 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ADD78918 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ADE32868 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ADE42560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ADE17348 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ADD80576 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ADD89604 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ADE40888 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ADE04687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ADF47362 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ADG21525 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
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ID ADG23166 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 215  
ID ADF97501 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
FN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 216  
ID ADG80565 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
FN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 217  
ID ADG53119 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
FN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 218  
ID ADG60439 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
FN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 219  
ID ADG80013 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
FN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 220  
ID ADG63784 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane polypeptide PRO337 cDNA.  
FN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 221  
ID ADH55305 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 222  
ID ADH55857 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 223  
ID ADI61199 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
FN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 224  
ID ADI64076 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 225  
ID ADI65025 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 226  
ID ADI63524 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 227  
ID ADH81938 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 228  
ID ADH81386 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 229  
ID ACD24040 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 230  
ID ACA6903 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #63.  
FN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 231  
ID ACD42387 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
FN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 232  
ID ACD42857 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.

PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 233  
ID ACB68655 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 234  
ID ACA67181 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 10; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 235  
ID ADM82555 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 11; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 236  
ID ADNI15954 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 11; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 237  
ID ADNI16583 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 11; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 238  
ID ADNI15402 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 11; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 239  
ID ADNI14850 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 11; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 240  
ID ADC48828 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 241  
ID ADC81112 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003092115-A1.

PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 242  
ID ADE20999 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 243  
ID ADE05843 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 244  
ID ADD76560 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 245  
ID ADD75072 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 246  
ID ADD75818 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 247  
ID ADD85050 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 248  
ID ADD86876 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 249  
ID ADE20753 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 250  
ID ADE39050 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US200309362-A1.  
PD 22-MAY-2003.



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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ADE24547 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 270
ID ADD87372 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 271
ID ADE05105 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 272
ID ADD75318 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 273
ID ADD76862 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 274
ID ADD86630 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 275
ID ADE89238 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 276
ID ADE41198 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 277
ID ADD78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 278
ID ADE18377 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 279
ID ADE88686 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 280
ID ADE89957 standard; cDNA; 1679 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 281
ID ADD77606 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 282
ID ADD77852 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 283
ID ADB85310 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
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ID ADF27307 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 303  
ID ADF27943 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 304  
ID ADF2264 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 305  
ID ADF90565 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 306  
ID ADF41537 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 307  
ID ADF33216 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 308  
ID ADF25582 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 309  
ID ADF26683 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 310  
ID ADF34472 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 311  
ID ADF46709 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 312  
ID ADF91712 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 313  
ID ADF05638 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 314  
ID ADF27192 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 315  
ID ADF02291 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 316  
ID ADF22077 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 317  
ID ADF20147 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 318  
ID ADF98053 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 319  
ID ADF24270 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 320  
ID ADF98624 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.



PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 321  
ID ADG03455 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 322  
ID ADF991176 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 323  
ID ADG16761 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 324  
ID ADG05220 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 325  
ID ADG19487 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 326  
ID ADG11255 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 327  
ID ADG13324 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 328  
ID ADG08381 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 329  
ID ADG15551 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003219885-A1.

PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 330  
ID ADG12034 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 331  
ID ADF96949 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 332  
ID ADG06134 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 333  
ID ADG23718 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 334  
ID ADG04007 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 335  
ID ADG24908 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 336  
ID ADF94591 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 337  
ID ADG07205 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;  
RESULT 338  
ID ADG07757 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207356-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 339  
ID ADG6687 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 340  
ID ADG55252 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 341  
ID ADG60916 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 342  
ID ADG62020 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 343  
ID ADG82221 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 344  
ID ADG57460 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 345  
ID ADG56908 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 346  
ID ADG55804 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 347  
ID ADG58564 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 348  
ID ADG70930 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 349  
ID ADH39031 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 350  
ID ADG58012 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 351  
ID ADG53596 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 352  
ID ADG71482 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 353  
ID ADG50695 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 354  
ID ADG81669 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 355  
ID ADH30631 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 356  
ID ADG63633 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane polypeptide PRO337 cDNA.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 357  
ID ADH1198 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 358  
ID ADG50071 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 359  
ID ADG51943 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 360  
ID ADG52420 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 361  
ID ADG54148 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 362  
ID ADG49447 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 363  
ID ADG81117 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 364  
ID ADG56356 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 365  
ID ADH12622 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 366

ID ADG48823 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 367  
ID ADG61468 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 368  
ID ADH28555 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 369  
ID ADG54700 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 370  
ID ADG59740 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 371  
ID ADG51319 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 372  
ID ADH43488 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #28.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 373  
ID ADG59263 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 374  
ID ADG34121 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 375  
ID ADG62719 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 376  
ID ADI181164 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 377  
ID ADI33591 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 378  
ID ADH69685 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 379  
ID ADH25744 standard; cDNA; 1679 BP.  
DE Human PRO337 encoding cDNA SEQ ID NO:522.  
PN EPI386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 380  
ID ADG09907 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 381  
ID ADI15378 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 382  
ID ADG09255 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 383  
ID ADI14710 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 384  
ID ADI29846 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.

PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 385  
ID ADI18305 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 386  
ID ADM27243 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 387  
ID ADJ63586 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 388  
ID ADJ77481 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 389  
ID ADK82833 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #28.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 390  
ID ADK66601 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 391  
ID ADJ65603 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 392  
ID ADM27739 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 393  
ID ADM17521 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2004048332-A1.

PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 394  
ID ADL07355 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 395  
ID ADM42463 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 396  
ID ADM28325 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 12; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 397  
ID AD195807 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 13; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 398  
ID AD196359 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1679; DB 13; Length 1679;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 399  
ID AA247893 standard; cDNA; 1693 BP.  
DE Human protein encoding cDNA SEQ ID NO:3.  
PN WO9958668-A1.  
PD 18-NOV-1999.  
PA (ONOY ) ONO PHARM CO LTD.  
Query Match 99.0%; Score 1661.4; DB 3; Length 1693;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 400  
ID AAA88791 standard; cDNA; 2012 BP.  
DE Human SECX cDNA Clone 11753149.0.37.  
PN WO200061754-A2.  
PD 19-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 97.9%; Score 1643.4; DB 3; Length 2012;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 401  
ID ADD18290 standard; DNA; 2012 BP.  
DE Human molecule (MOL) protein MOL11 DNA sequence.  
PN WO2003003984-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 97.9%; Score 1643.4; DB 10; Length 2012;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 402  
ID AA88790 standard; cDNA; 1603 BP.  
DE Human SECX cDNA Clone 11753149.0.6.  
PN WO200061754-A2.  
PD 19-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 95.4%; Score 1601.4; DB 3; Length 1603;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 403  
ID ADD18288 standard; DNA; 1603 BP.  
DE Human molecule (MOL) protein MOL10 DNA sequence.  
PN WO2003003984-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 95.4%; Score 1601.4; DB 10; Length 1603;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 404  
ID ABK49272 standard; cDNA; 1873 BP.  
DE Human Kruppel associated DNA binding protein 42 cDNA.  
PN WO200183541-A1.  
PD 08-NOV-2001.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
Query Match 89.9%; Score 1509.8; DB 6; Length 1873;  
Best Local Similarity 93.1%; Pred. No. 0;  
RESULT 405  
ID AAI57869 standard; cDNA; 1678 BP.  
DE Human polynucleotide SEQ ID NO 72.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 86.8%; Score 1457; DB 4; Length 1678;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 406  
ID ADQ22984 standard; DNA; 3987 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 85.7%; Score 1438.4; DB 12; Length 3987;  
Best Local Similarity 98.9%; Pred. No. 0;  
RESULT 407  
ID ADQ24601 standard; DNA; 3987 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 85.7%; Score 1438.4; DB 12; Length 3987;  
Best Local Similarity 98.9%; Pred. No. 0;  
RESULT 408  
ID ABT17390 standard; DNA; 1839 BP.  
DE Human IG gene related nucleic acid SEQ ID No 16.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 85.3%; Score 1432.8; DB 8; Length 1839;  
Best Local Similarity 98.5%; Pred. No. 0;  
RESULT 409  
ID ABX76448 standard; DNA; 1839 BP.  
DE Lung cancer-associated polynucleotide #312.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 85.3%; Score 1432.8; DB 8; Length 1839;  
Best Local Similarity 98.5%; Pred. No. 0;  
RESULT 410  
ID ADG63208 standard; DNA; 1839 BP.  
DE Human neurotiximin DNA.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 85.3%; Score 1432.8; DB 10; Length 1839;  
Best Local Similarity 98.5%; Pred. No. 0;  
RESULT 411  
ID ADN39137 standard; cDNA; 1839 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match  
Best Local Similarity 85.3%; Score 1432.8; DB 11; Length 1839;  
RESULT 412  
ID ADI21817 standard; cDNA; 2884 BP.  
DE Novel human protein cDNA #76.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 85.3%; Score 1432.8; DB 10; Length 2884;  
RESULT 413  
ID ADI35771 standard; DNA; 2129 BP.  
DE Human neurotrophin DNA.  
PN US2003100485-A1.  
PD 29-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 84.5%; Score 1418.2; DB 10; Length 2129;  
RESULT 414  
ID AA159655 standard; cDNA; 1690 BP.  
DE Human polynucleotide SEQ ID NO 3644.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 78.3%; Score 1315; DB 4; Length 1690;  
RESULT 415  
ID ADI21360 standard; cDNA; 1690 BP.  
DE Novel human expressed sequence tag, EST #59.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 78.3%; Score 1315; DB 10; Length 1690;  
RESULT 416  
ID AA247892 standard; cDNA; 1032 BP.  
DE Human protein encoding cDNA SEQ ID NO:2.  
PN WO958668-A1.  
PD 18-NOV-1999.  
PA (ONOF) ONO PHARM CO LTD.  
Query Match  
Best Local Similarity 61.5%; Score 1032; DB 3; Length 1032;  
RESULT 417  
ID ABT17393 standard; DNA; 1061 BP.  
DE Human IG gene related nucleic acid SEQ ID No 19.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 58.0%; Score 974; DB 8; Length 1061;  
RESULT 418  
ID AA247894 standard; cDNA; 939 BP.  
DE Human protein encoding cDNA SEQ ID NO:5.  
PN WO958668-A1.  
PD 18-NOV-1999.  
PA (ONOF) ONO PHARM CO LTD.  
Query Match  
Best Local Similarity 55.9%; Score 939; DB 3; Length 939;  
RESULT 419  
ID ABT17391 standard; DNA; 1094 BP.  
DE Human IG gene related nucleic acid SEQ ID No 17.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 55.4%; Score 931; DB 8; Length 1094;  
RESULT 420  
ID ADG63210 standard; DNA; 1068 BP.  
DE Human neurotrophin DNA +33bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match  
Best Local Similarity 54.2%; Score 910.4; DB 10; Length 1068;  
RESULT 421  
ID ABT17392 standard; DNA; 1130 BP.  
DE Human IG gene related nucleic acid SEQ ID No 18.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 53.1%; Score 891.8; DB 8; Length 1130;  
RESULT 422  
ID ADG63212 standard; DNA; 1104 BP.  
DE Human neurotrophin DNA +69bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match  
Best Local Similarity 52.1%; Score 874.4; DB 10; Length 1104;  
RESULT 423  
ID ADG63214 standard; DNA; 1140 BP.  
DE Human neurotrophin DNA +108bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match  
Best Local Similarity 50.7%; Score 851.8; DB 10; Length 1140;  
RESULT 424  
ID AA44536 standard; cDNA; 832 BP.  
DE Human secreted expressed sequence tag SEQ ID NO:1111.  
PN WO200021991-A1.  
PD 20-APR-2000.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 47.9%; Score 803.8; DB 3; Length 832;  
RESULT 425  
ID ADE07017 standard; DNA; 3298 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #83.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 33.6%; Score 564.2; DB 10; Length 3298;  
RESULT 426  
ID AAQ51015 standard; cDNA; 3069 BP.  
DE Rat opioid receptor gene.  
PN WO9321309-A1.  
PD 28-OCT-1993.  
PA (LEEN) LEE N M.  
PA (LOHH) LOH H H.  
PA (LIPP) LIPPMAN D.  
Query Match  
Best Local Similarity 32.2%; Score 540.8; DB 2; Length 3069;  
RESULT 427  
ID ABT17409 standard; DNA; 1478 BP.  
DE Human IG gene related nucleic acid SEQ ID No 35.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 32.1%; Score 539.2; DB 8; Length 1478;  
RESULT 428  
ID ABT17406 standard; DNA; 3110 BP.  
DE Human IG gene related nucleic acid SEQ ID No 32.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 32.1%; Score 539.2; DB 8; Length 3110;  
RESULT 429  
ID ADG63206 standard; DNA; 3110 BP.  
DE Opioid-binding protein/cell adhesion molecule-like DNA.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

Query Match 32.1%; Score 539.2; DB 10; Length 3110;  
Best Local Similarity 73.0%; Pred. No. 1.1e-131;  
RESULT 430  
ID ABT17408 standard; DNA; 1071 BP.  
DE Human IG gene related nucleic acid SEQ ID No 34.  
FN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 32.0%; Score 537.6; DB 8; Length 1071;  
Best Local Similarity 72.9%; Pred. No. 1.7e-131;  
RESULT 431  
ID ABT17407 standard; DNA; 1080 BP.  
DE Human IG gene related nucleic acid SEQ ID No 33.  
FN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 32.0%; Score 537.6; DB 8; Length 1080;  
Best Local Similarity 72.9%; Pred. No. 1.7e-131;  
RESULT 432  
ID AAQ51017 standard; cDNA; 2179 BP.  
DE Rat opioid receptor gene.  
FN WO9321309-A1.  
PD 28-OCT-1993.  
PA (LEEN/) LEE N M.  
PA (LOHH/) LOH H H.  
PA (LIPP/) LIPPMAN D.  
Query Match 31.1%; Score 523; DB 2; Length 2179;  
Best Local Similarity 72.2%; Pred. No. 1.7e-127;  
RESULT 433  
ID AAQ51016 standard; cDNA; 2337 BP.  
DE Rat opioid receptor gene.  
FN WO9321309-A1.  
PD 28-OCT-1993.  
PA (LEEN/) LEE N M.  
PA (LOHH/) LOH H H.  
PA (LIPP/) LIPPMAN D.  
Query Match 31.1%; Score 523; DB 2; Length 2337;  
Best Local Similarity 72.2%; Pred. No. 1.8e-127;  
RESULT 434  
ID AAQ51016 standard; cDNA; 2337 BP.  
DE Human EST DNA42301.  
FN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 2; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 435  
ID AAC78591 standard; cDNA; 503 BP.  
DE Human EST DNA42301 nucleotide sequence SEQ ID NO:524.  
FN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 3; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 436  
ID ACA63893 standard; cDNA; 503 BP.  
DE Novel human secreted and transmembrane protein DNA42301.  
FN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 8; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 437  
ID ACA72057 standard; DNA; 503 BP.  
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.  
FN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 8; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 438  
ID ABX92697 standard; cDNA; 503 BP.  
DE Human PRO337 EST polynucleotide sequence.

PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 8; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 439  
ID ACA66438 standard; cDNA; 503 BP.  
DE Human secreted/transmembrane protein EST DNA42301.  
FN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 8; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 440  
ID ADA25063 standard; cDNA; 503 BP.  
DE Novel human secreted and transmembrane protein EST DNA42301.  
FN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 9; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 441  
ID ACD30039 standard; cDNA; 503 BP.  
DE Novel human secreted and transmembrane protein EST DNA42301.  
FN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 9; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 442  
ID ADA12724 standard; cDNA; 503 BP.  
DE Human secreted/transmembrane polypeptide PRO337 EST.  
FN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 9; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 443  
ID ACD29454 standard; cDNA; 503 BP.  
DE Novel human secreted and transmembrane polypeptide cDNA #134.  
FN US2003049633-A1.  
PD 13-MAR-2003.  
Query Match 30.0%; Score 503; DB 9; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 444  
ID ADB74030 standard; cDNA; 503 BP.  
DE Human PRO polynucleotide sequence #134.  
FN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 445  
ID ADB76746 standard; cDNA; 503 BP.  
DE Human PRO polynucleotide sequence #134.  
FN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 446  
ID ADC44172 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
FN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 447  
ID ADC61932 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
FN US2003049684-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 448  
ID ADE63896 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 449  
ID ADE66996 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 450  
ID ADE69120 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 451  
ID ADE63180 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 452  
ID ADE68245 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 453  
ID ADC41565 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 454  
ID ADC67620 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 455  
ID ADC62556 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 456  
ID ADC42189 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 457  
ID ADE49558 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 458  
ID ADE35612 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 459  
ID ADE16726 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 460  
ID ADD73341 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 461  
ID ADD72699 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 462  
ID ADE17350 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 463  
ID ADF47364 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 464  
ID ADG53121 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 465  
ID ADG60441 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO3337.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;



Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 466  
ID AD161201 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 467  
ID ACD42858 standard; cDNA; 503 BP.  
DE Novel human secreted and transmembrane protein EST DNA42301.  
PN US2003050339-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 10; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 468  
ID ADE48858 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 469  
ID ADE89959 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUNA/) TUNAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 470  
ID ADF61599 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 471  
ID ADF40291 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 472  
ID ADF46087 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 473  
ID ADF24483 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 474  
ID ADF40915 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 475  
ID ADF23859 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 476  
ID ADF33842 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 477  
ID ADF27309 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 478  
ID ADF27945 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 479  
ID ADF41539 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 480  
ID ADF33218 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;

Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 481  
ID ADP25584 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 482  
ID ADP26685 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 483  
ID ADP34474 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 484  
ID ADP46711 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 485  
ID ADG50697 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 486  
ID ADG50073 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 487  
ID ADG51945 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 488  
ID ADG49449 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 489  
ID ADG48825 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;

RESULT 490  
ID ADG51321 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 491  
ID ADG59265 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 492  
ID ADG62721 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 493  
ID ADH25746 standard; cDNA; 503 BP.  
DE Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.  
PN EPI386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 494  
ID ADMI7523 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 495  
ID ADL07357 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 30.0%; Score 503; DB 12; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.6e-122;  
RESULT 496  
ID AAC91321 standard; cDNA; 537 BP.  
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.  
PN WO200073509-A2.  
PD 07-DEC-2000.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 29.3%; Score 491.2; DB 4; Length 537;  
Best Local Similarity 98.6%; Pred. No. 2.2e-119;  
RESULT 497  
ID ADM47274 standard; DNA; 617 BP.  
DE Oestrogen regulated protein like NOVX 25b gene.  
PN WO2003083039-A2.  
PD 09-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 26.8%; Score 449.4; DB 11; Length 617;  
Best Local Similarity 97.6%; Pred. No. 2.8e-108;  
RESULT 498  
ID AAF93346 standard; cDNA; 452 BP.  
DE Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.  
PN WO200107611-A2.  
PD 01-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 26.3%; Score 441.2; DB 5; Length 452;  
Best Local Similarity 99.1%; Pred. No. 3.5e-106;  
RESULT 499

ID ACH15238 standard; cDNA; 437 BP.  
DE Human adult brain cDNA #2450.  
FN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA//) DRMANAC R T.  
PA (LABA//) LABAT I.  
PA (STAC//) STACHE-CRAIN B.  
PA (DICK//) DICKSON M C.  
PA (JONE//) JONES L W.  
Query Match 24.1%; Score 404; DB 9; Length 437;  
Best Local Similarity 97.4%; Pred. No. 2.4e-96;  
RESULT 500  
ID AAS78035 standard; cDNA; 484 BP.  
DE Human infant brain cDNA #339.  
FN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA//) DRMANAC R T.  
PA (LABA//) LABAT I.  
PA (STAC//) STACHE-CRAIN B.  
PA (DICK//) DICKSON M C.  
PA (JONE//) JONES L W.  
Query Match 21.1%; Score 353.8; DB 9; Length 409;  
Best Local Similarity 98.1%; Pred. No. 4.6e-83;  
RESULT 502  
ID AAL50356 standard; cDNA; 1411 BP.  
DE Human limbic system associated membrane protein 36-85 coding sequence.  
FN CN1345756-A.  
PD 24-APR-2002.  
PA (SHAN//) SHANGHAI BIOWINDOW GENE DEV INC.  
Query Match 20.5%; Score 343.8; DB 6; Length 1411;  
Best Local Similarity 62.1%; Pred. No. 3.8e-80;  
RESULT 503  
ID AAT42080 standard; cDNA to mRNA; 1238 BP.  
DE Rat LAMP coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.4%; Score 343; DB 2; Length 1238;  
Best Local Similarity 62.0%; Pred. No. 5.8e-80;  
RESULT 504  
ID ABX63560 standard; cDNA; 1195 BP.  
DE Human cDNA #560 differentially expressed in activated vascular tissue.  
FN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND//) BANDMAN O.  
Query Match 20.3%; Score 341.6; DB 8; Length 1195;  
Best Local Similarity 60.1%; Pred. No. 1.3e-79;  
RESULT 505  
ID ADI12674 standard; cDNA; 1195 BP.  
DE Human steroid-induced C3A liver cell cDNA #403.  
FN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 20.3%; Score 341.6; DB 12; Length 1195;  
Best Local Similarity 60.1%; Pred. No. 1.3e-79;  
RESULT 506  
ID AAT42084 standard; cDNA to mRNA; 924 BP.  
DE Human LAMP residues 8-315 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.3%; Score 340.6; DB 2; Length 924;  
Best Local Similarity 63.3%; Pred. No. 2.2e-79;  
RESULT 507  
ID AAT42079 standard; cDNA to mRNA; 977 BP.  
DE Human LAMP residues 8-332 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.3%; Score 340.6; DB 2; Length 977;  
Best Local Similarity 63.3%; Pred. No. 2.2e-79;  
RESULT 508  
ID AAT42081 standard; cDNA to mRNA; 1014 BP.  
DE Rat LAMP coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.3%; Score 340.6; DB 2; Length 1014;  
Best Local Similarity 61.9%; Pred. No. 2.3e-79;  
RESULT 509  
ID ABT17402 standard; DNA; 1017 BP.  
DE Human IG gene related nucleic acid SEQ ID No 28.  
FN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 20.3%; Score 340.6; DB 8; Length 1017;  
Best Local Similarity 63.3%; Pred. No. 2.3e-79;  
RESULT 510  
ID ABT17404 standard; DNA; 1017 BP.  
DE Human IG gene related nucleic acid SEQ ID No 30.  
FN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 20.3%; Score 340.6; DB 8; Length 1017;  
Best Local Similarity 63.3%; Pred. No. 2.3e-79;  
RESULT 511  
ID AAT42086 standard; cDNA to mRNA; 861 BP.  
DE Human LAMP residues 29-315 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.2%; Score 338.6; DB 2; Length 861;  
Best Local Similarity 63.7%; Pred. No. 7.1e-79;  
RESULT 512  
ID AAT42082 standard; cDNA to mRNA; 912 BP.  
DE Human mature LAMP coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.2%; Score 338.6; DB 2; Length 912;  
Best Local Similarity 63.7%; Pred. No. 7.3e-79;  
RESULT 513  
ID AAT42085 standard; cDNA to mRNA; 945 BP.  
DE Rat LAMP residues 1-315 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.1%; Score 337.4; DB 2; Length 945;  
Best Local Similarity 63.1%; Pred. No. 1.5e-78;  
RESULT 514  
ID ABZ72624 standard; cDNA; 1757 BP.  
DE Human GENSET cDNA clone name SLAMP.  
FN WO2003014151-A2.  
PD 20-FEB-2003.  
PA (GEST-) GENSET SA.  
Query Match 20.1%; Score 337.4; DB 8; Length 1757;  
Best Local Similarity 63.8%; Pred. No. 2.1e-78;  
RESULT 515  
ID AAT42083 standard; cDNA to mRNA; 930 BP.  
DE Rat mature LAMP coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 20.1%; Score 337; DB 2; Length 930;  
Best Local Similarity 62.1%; Pred. No. 2e-78;  
RESULT 516  
ID ABT17403 standard; DNA; 1075 BP.  
DE Human IG gene related nucleic acid SEQ ID No 29.

PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 20.0%; Score 335; DB 8; Length 1075;  
Best Local Similarity 63.5%; Pred. No. 7.1e-78;  
RESULT 517  
ID AAT42087 standard; cDNA to mRNA; 861 BP.  
DE Rat LAMP residues 29-315 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 19.9%; Score 333.8; DB 2; Length 861;  
Best Local Similarity 63.4%; Pred. No. 1.3e-77;  
RESULT 518  
ID AAT42116 standard; cDNA to mRNA; 1307 BP.  
DE Rat LAMP clone 6c coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 19.8%; Score 331.8; DB 2; Length 1307;  
Best Local Similarity 63.3%; Pred. No. 5.5e-77;  
RESULT 519  
ID AAT43425 standard; cDNA; 1153 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1507.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 19.4%; Score 325.2; DB 4; Length 1153;  
Best Local Similarity 62.7%; Pred. No. 2.9e-75;  
RESULT 520  
ID AAC19214 standard; cDNA; 333 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 23289.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST) GENSET.  
Query Match 18.8%; Score 316.2; DB 3; Length 333;  
Best Local Similarity 97.0%; Pred. No. 3.7e-73;  
RESULT 521  
ID ABT17405 standard; DNA; 898 BP.  
DE Human IG gene related nucleic acid SEQ ID No 31.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 18.7%; Score 314.6; DB 8; Length 898;  
Best Local Similarity 61.6%; Pred. No. 1.6e-72;  
RESULT 522  
ID AAT42094 standard; cDNA to mRNA; 756 BP.  
DE Human LAMP residues 46-294 coding sequence.  
PN WO9630052 A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 18.1%; Score 303.6; DB 2; Length 756;  
Best Local Similarity 63.5%; Pred. No. 1.2e-69;  
RESULT 523  
ID AAT42095 standard; cDNA to mRNA; 756 BP.  
DE Rat LAMP residues 46-294 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 17.8%; Score 298.2; DB 2; Length 756;  
Best Local Similarity 63.0%; Pred. No. 3.3e-68;  
RESULT 524  
ID AAT78034 standard; cDNA; 443 BP.  
DE DNA encoding novel human diagnostic protein #13838.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 17.7%; Score 296.8; DB 5; Length 443;  
Best Local Similarity 89.6%; Pred. No. 5.9e-68;  
RESULT 525  
ID ABT17401 standard; DNA; 1809 BP.  
DE Human IG gene related nucleic acid SEQ ID No 27.  
PN WO200299040-A2.

PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 16.6%; Score 279; DB 8; Length 1809;  
Best Local Similarity 57.8%; Pred. No. 6.2e-63;  
RESULT 526  
ID ADS82049 standard; DNA; 4891 BP.  
DE Human cancer-associated protein coding sequence #5.  
PN WO2004035789-A1.  
PD 29-APR-2004.  
PA (GLDS) LG LIFE SCI LTD.  
Query Match 16.3%; Score 274.2; DB 13; Length 4891;  
Best Local Similarity 58.6%; Pred. No. 1.9e-61;  
RESULT 527  
ID ABQ82338 standard; cDNA; 1165 BP.  
DE Human NOV12b encoding cDNA SEQ ID NO:25.  
PN WO200262999-A2.  
PD 15-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.2%; Score 272.6; DB 6; Length 1165;  
Best Local Similarity 58.4%; Pred. No. 2.4e-61;  
RESULT 528  
ID ADI28059 standard; cDNA; 1327 BP.  
DE ECMAD Gene clone 7087904CB1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 16.2%; Score 272.6; DB 6; Length 1327;  
Best Local Similarity 58.4%; Pred. No. 2.6e-61;  
RESULT 529  
ID AAC87055 standard; cDNA; 4834 BP.  
DE Nucleotide sequence of human polypeptide PRO6004.  
PN WO200077037-A2.  
PD 21-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 4; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 530  
ID ABK3536 standard; cDNA; 4834 BP.  
DE cDNA encoding human PRO protein, Seq ID No 1.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 6; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 531  
ID ACA05014 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 8; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 532  
ID ACA60544 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 8; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 533  
ID ACA04534 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 DNA.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 8; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 534  
ID ACA68497 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003088063-A1.  
PD 08-MAY-2003.



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Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 553
ID ADC21720 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 554
ID ADC49751 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US200308064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 555
ID ADC48950 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US200308070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 556
ID ADC49467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US200308071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 557
ID . ADC47328 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US200308072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 558
ID ADC47073 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 559
ID ADC77948 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 560
ID ADD06183 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 561
ID ADC77702 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US200308066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 562
ID ADD50665 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 563
ID ADD50911 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 564
ID ADD50392 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 565
ID ADD50146 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 566
ID ADD51157 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 567
ID ADG63810 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 CDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 568
ID ACA66841 standard; cDNA; 4834 BP.
DE CDNA encoding human PRO polypeptide #1.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 569
ID ACD42405 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 570
ID ACD68593 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 CDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 571
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ID ADC48704 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 572  
ID ADE20875 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 573  
ID ADE05719 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 574  
ID ADD74948 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 575  
ID ADD75694 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 576  
ID ADB84926 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 577  
ID ADD86752 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 578  
ID ADE20629 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 579  
ID ADE38926 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 580  
ID ADE05473 standard; cDNA; 4834 BP.

DE Human PRO polynucleotide #1.  
FN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 581  
ID ADD73458 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 582  
ID ADD78298 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 583  
ID ADE21121 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 584  
ID ADD77236 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 585  
ID ADE20383 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 586  
ID ADD75448 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 587  
ID ADD73964 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 588  
ID ADD74210 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 589  
ID ADD75940 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.

PN US2003100718-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 590  
 ID ADD85186 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100721-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 591  
 ID ADE04981 standard; cDNA; 4834 BP.  
 DE Human PRO polynucleotide #1.  
 PN US2003100726-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 592  
 ID ADD75194 standard; cDNA; 4834 BP.  
 DE Human PRO polynucleotide #1.  
 PN US2003100714-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 593  
 ID ADD76738 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100715-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 594  
 ID ADD86506 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100719-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 595  
 ID ADE41224 standard; cDNA; 4834 BP.  
 DE Human secreted/transmembrane polypeptide PRO6004 cDNA.  
 PN US2003104558-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 596  
 ID ADD77974 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100731-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 597  
 ID ADD77482 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100729-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 598  
 ID ADD77728 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100730-A1.

PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 599  
 ID ADD85186 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100725-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 600  
 ID ADD73718 standard; cDNA; 4834 BP.  
 DE Human PRO polynucleotide #1.  
 PN US2003100710-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 601  
 ID ADD74456 standard; cDNA; 4834 BP.  
 DE Human PRO polynucleotide #1.  
 PN US2003100713-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 602  
 ID ADD76984 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100716-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 603  
 ID ADD85678 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003100720-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 604  
 ID ADE05327 standard; cDNA; 4834 BP.  
 DE Human PRO polynucleotide #1.  
 PN US2003100723-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 605  
 ID ADD74702 standard; cDNA; 4834 BP.  
 DE Human PRO polynucleotide #1.  
 PN US2003100724-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 606  
 ID ADG05514 standard; cDNA; 4834 BP.  
 DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
 PN US2003096959-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
 Best Local Similarity 58.4%; Pred. No. 5e-61;  
 RESULT 607  
 ID ADG27068 standard; cDNA; 4834 BP.  
 DE Human PRO polynucleotide #1.  
 PN US2003096962-A1.  
 PD 22-MAY-2003.



PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 608  
ID ADG1131 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 609  
ID ADG11910 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 610  
ID ADF9467 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 611  
ID ADG06563 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 612  
ID ADH38907 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 613  
ID ADG63658 standard; cDNA; 4834 BP.  
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.  
FN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 614  
ID ADG33997 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 615  
ID ADI33467 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 616  
ID ADH69561 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.

Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 617  
ID ADI29722 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 618  
ID ADM27119 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
FN US200404179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 619  
ID ADK66477 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
FN US200404180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 272.6; DB 12; Length 4834;  
Best Local Similarity 58.4%; Pred. No. 5e-61;  
RESULT 620  
ID ABO82337 standard; cDNA; 1196 BP.  
DE Human NOV12a encoding cDNA SEQ ID NO:23.  
FN WO200262999-A2.  
PD 15-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.2%; Score 272.2; DB 6; Length 1196;  
Best Local Similarity 58.3%; Pred. No. 3.2e-61;  
RESULT 621  
ID AEN85384 standard; DNA; 1119 BP.  
DE Human NOV6, KILON-like protein, coding sequence.  
FN WO200255704-A2.  
PD 18-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.1%; Score 271; DB 6; Length 1119;  
Best Local Similarity 58.3%; Pred. No. 6.3e-61;  
RESULT 622  
ID ADB62841 standard; cDNA; 2383 BP.  
DE Human cDNA encoding clone OCBBF20110210.  
FN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 16.1%; Score 271; DB 10; Length 2383;  
Best Local Similarity 58.3%; Pred. No. 9.3e-61;  
RESULT 623  
ID AAC78596 standard; cDNA; 2840 BP.  
DE Human PRO4993 nucleotide sequence SEQ ID NO:611.  
FN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 3; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 624  
ID ACA63979 standard; cDNA; 2840 BP.  
DE Novel human secreted and transmembrane protein PRO4993 cDNA.  
FN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 8; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 625  
ID ACA72143 standard; cDNA; 2840 BP.  
DE Human secreted and transmembrane PRO polypeptide #39 cDNA.  
FN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.



ID ADC42276 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 645  
ID AD849645 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 646  
ID AD835699 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 647  
ID AD816813 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 648  
ID AD873428 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 649  
ID AD872786 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 650  
ID AD817437 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 651  
ID ADF47451 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 652  
ID AD853208 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003216361-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 653  
ID ADG60528 standard; cDNA; 2840 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 654  
ID AD161288 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 655  
ID ACD42944 standard; cDNA; 2840 BP.  
DE Novel human secreted and transmembrane protein PRO4993 cDNA.  
FN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 10; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 656  
ID AD848945 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 657  
ID ADE90046 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 658  
ID ADF61686 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
FN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 659

ID ADF40378 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 660  
ID ADF46174 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 661  
ID ADF24570 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 662  
ID ADF41002 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 663  
ID ADF23946 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 664  
ID ADF33929 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 665  
ID ADF27396 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 666  
ID ADF28032 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 667  
ID ADF41626 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
ID ADF33305 standard; cDNA; 2840 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 669  
ID ADF25671 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 670  
ID ADF26772 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 671  
ID ADF34561 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 672  
ID ADF46798 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 673  
ID ADF50784 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 674  
ID ADF50160 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 675  
ID ADF52032 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 676  
ID ADF49536 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 269.4; DB 12; Length 2840;  
Best Local Similarity 58.2%; Pred. No. 2.7e-60;  
RESULT 677  
ID ADF48912 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.

PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 16.0%; Score 269.4; DB 12; Length 2840;  
RESULT 678  
ID ADG51408 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 16.0%; Score 269.4; DB 12; Length 2840;  
RESULT 679  
ID ADG59352 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 16.0%; Score 269.4; DB 12; Length 2840;  
RESULT 680  
ID ADG62808 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 16.0%; Score 269.4; DB 12; Length 2840;  
RESULT 681  
ID ADM17610 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 16.0%; Score 269.4; DB 12; Length 2840;  
RESULT 682  
ID ADL07444 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 16.0%; Score 269.4; DB 12; Length 2840;  
RESULT 683  
ID ADP28695 standard; DNA; 834 BP.  
DE Human secreted protein encoding sequence SEQ ID #683.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 834;  
RESULT 684  
ID ADH71401 standard; DNA; 926 BP.  
DE Human gene of the invention NOV111 SRQ ID NO:297.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 926;  
RESULT 685  
ID ADH71405 standard; DNA; 927 BP.  
DE Human gene of the invention NOV11k SRQ ID NO:301.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 927;  
RESULT 686  
ID ADH71409 standard; DNA; 946 BP.  
DE Human gene of the invention NOV11m SRQ ID NO:305.  
PN WO2003102155-A2.

PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 946;  
RESULT 687  
ID ADH71393 standard; DNA; 946 BP.  
DE Human gene of the invention NOV11e SRQ ID NO:289.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 946;  
RESULT 688  
ID ADH71395 standard; DNA; 976 BP.  
DE Human gene of the invention NOV11f SRQ ID NO:291.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 976;  
RESULT 689  
ID ADH71415 standard; DNA; 976 BP.  
DE Human gene of the invention NOV11p SRQ ID NO:311.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 976;  
RESULT 690  
ID ADH71389 standard; DNA; 976 BP.  
DE Human gene of the invention NOV11c SRQ ID NO:285.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 976;  
RESULT 691  
ID ADH71397 standard; DNA; 976 BP.  
DE Human gene of the invention NOV11g SRQ ID NO:293.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 12; Length 976;  
RESULT 692  
ID ABS71699 standard; DNA; 1017 BP.  
DE DNA encoding human NOV5b protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 6; Length 1017;  
RESULT 693  
ID ADL35978 standard; cDNA; 1017 BP.  
DE Human NOVX cDNA #12.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (GUOX/) GUO X.  
PA (KEKU/) KEKUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (LILL/) LI L.  
PA (PADI/) PADIGARU M.  
Query Match  
Best Local Similarity 15.5%; Score 260.4; DB 11; Length 1017;  
RESULT 694  
ID ADH71417 standard; DNA; 1030 BP.

DE Human gene of the invention NOV11q SEQ ID NO:313.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.5%; Score 260.4; DB 12; Length 1030;  
Best Local Similarity 59.5%; Pred. No. 3.9e-58;  
RESULT 695  
ID ADH71411 standard; DNA; 1033 BP.  
DE Human gene of the invention NOV11n SEQ ID NO:307.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.5%; Score 260.4; DB 12; Length 1033;  
Best Local Similarity 59.5%; Pred. No. 3.9e-58;  
RESULT 696  
ID ADH71387 standard; DNA; 1033 BP.  
DE Human gene of the invention NOV11b SEQ ID NO:283.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.5%; Score 260.4; DB 12; Length 1033;  
Best Local Similarity 59.5%; Pred. No. 3.9e-58;  
RESULT 697  
ID ADH71413 standard; DNA; 1035 BP.  
DE Human gene of the invention NOV11o SEQ ID NO:309.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.5%; Score 260.4; DB 12; Length 1035;  
Best Local Similarity 59.5%; Pred. No. 3.9e-58;  
RESULT 698  
ID ABS76364 standard; DNA; 1427 BP.  
DE DNA encoding human immunoglobulin superfamily protein IGSFP-9.  
PN WO200272794-A2.  
PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.5%; Score 260.4; DB 6; Length 1427;  
Best Local Similarity 59.5%; Pred. No. 4.6e-58;  
RESULT 699  
ID AA047371 standard; DNA; 2653 BP.  
DE Human LP289 DNA.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 15.5%; Score 260.4; DB 8; Length 2653;  
Best Local Similarity 59.5%; Pred. No. 6.3e-58;  
RESULT 700  
ID ABS71698 standard; DNA; 1018 BP.  
DE DNA encoding human NOV5a protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.4%; Score 258.8; DB 6; Length 1018;  
Best Local Similarity 59.4%; Pred. No. 1e-57;  
RESULT 701  
ID ADL35976 standard; cDNA; 1018 BP.  
DE Human NOVX cDNA #11.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY) MALYANKAR U M.  
PA (SHEN) SHENOY S G.  
PA (SPVT) SPYTEK K A.  
PA (ZRRH) ZERHUSEN B D.  
PA (PATT) PATTURAJAN M.  
PA (GUOX) GUO X.  
PA (KEKU) KEKUDA R.  
PA (GANG) GANGOLLI E A.  
PA (SHIM) SHIMKETS R A.  
PA (TAUP) TAUPIER R J.  
PA (LILL) LI L.  
PA (PADI) PADIGARU M.  
Query Match 15.4%; Score 258.8; DB 11; Length 1018;  
Best Local Similarity 59.4%; Pred. No. 1e-57;

RESULT 702  
ID ADH71399 standard; DNA; 1018 BP.  
DE Human gene of the invention NOV11h SEQ ID NO:295.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.4%; Score 258.8; DB 12; Length 1018;  
Best Local Similarity 59.4%; Pred. No. 1e-57;  
RESULT 703  
ID ABS71700 standard; DNA; 1136 BP.  
DE DNA encoding human NOV5c protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.3%; Score 257.2; DB 6; Length 1136;  
Best Local Similarity 59.3%; Pred. No. 2.9e-57;  
RESULT 704  
ID ADH71403 standard; DNA; 1171 BP.  
DE Human gene of the invention NOV11j SEQ ID NO:299.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.3%; Score 257.2; DB 12; Length 1171;  
Best Local Similarity 59.3%; Pred. No. 2.9e-57;  
RESULT 705  
ID ADH71385 standard; DNA; 1271 BP.  
DE Human gene of the invention NOV11a SEQ ID NO:281.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.3%; Score 257.2; DB 12; Length 1271;  
Best Local Similarity 59.3%; Pred. No. 3e-57;  
RESULT 706  
ID ADH71421 standard; DNA; 1271 BP.  
DE Human gene of the invention NOV11s SEQ ID NO:317.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.3%; Score 257.2; DB 12; Length 1271;  
Best Local Similarity 59.3%; Pred. No. 3e-57;  
RESULT 707  
ID ADH71419 standard; DNA; 1271 BP.  
DE Human gene of the invention NOV11r SEQ ID NO:315.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.2%; Score 255.6; DB 12; Length 1271;  
Best Local Similarity 59.1%; Pred. No. 8.1e-57;  
RESULT 708  
ID AAH87585 standard; DNA; 255 BP.  
DE Human single nucleotide polymorphism containing DNA sequence #2442.  
PN WO9953095-A2.  
PD 21-OCT-1999.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 15.2%; Score 255; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 5.2e-57;  
RESULT 709  
ID AAX10694 standard; DNA; 251 BP.  
DE Human biallelic polymorphic DNA fragment WI-9617.  
PN WO9820165-A2.  
PD 14-MAY-1998.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 14.9%; Score 250.6; DB 2; Length 251;  
Best Local Similarity 99.6%; Pred. No. 7.5e-56;  
RESULT 710  
ID ABK35606 standard; DNA; 1011 BP.  
DE Gene encoding novel human secreted or membrane-associated protein #25.  
PN WO200204600-A2.  
PD 17-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 14.7%; Score 246; DB 6; Length 1011;

Best Local Similarity 58.4%; Pred. No. 2.5e-54;  
RESULT 711  
ID ABS71701 standard; DNA; 1169 BP.  
DE DNA encoding human NOV5d protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.7%; Score 246; DB 6; Length 1169;  
Best Local Similarity 58.4%; Pred. No. 2.7e-54;  
RESULT 712  
ID ADH71407 standard; DNA; 1169 BP.  
DE Human gene of the invention NOV111 SEQ ID NO:303.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.7%; Score 246; DB 12; Length 1169;  
Best Local Similarity 58.4%; Pred. No. 2.7e-54;  
RESULT 713  
ID ABA06475 standard; cDNA; 2813 BP.  
DE Human cDNA SEQ ID NO: 141.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.3%; Score 240.8; DB 4; Length 2813;  
Best Local Similarity 58.3%; Pred. No. 1e-52;  
RESULT 714  
ID ABV83812 standard; cDNA; 2813 BP.  
DE Human polynucleotide SEQ ID NO 141.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 14.3%; Score 240.8; DB 6; Length 2813;  
Best Local Similarity 58.3%; Pred. No. 1e-52;  
RESULT 715  
ID ADH71391 standard; DNA; 760 BP.  
DE Human gene of the invention NOV11d SEQ ID NO:287.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.1%; Score 236.6; DB 12; Length 760;  
Best Local Similarity 59.9%; Pred. No. 6.7e-52;  
RESULT 716  
ID AAD47374 standard; DNA; 2601 BP.  
DE Human LP319b DNA.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 13.9%; Score 234; DB 8; Length 2601;  
Best Local Similarity 58.3%; Pred. No. 6.1e-51;  
RESULT 717  
ID ABK35605 standard; DNA; 1056 BP.  
DE Gene encoding novel human secreted or membrane-associated protein #24.  
PN WO200204600-A2.  
PD 17-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 13.8%; Score 232; DB 6; Length 1056;  
Best Local Similarity 58.1%; Pred. No. 1.3e-50;  
RESULT 718  
ID ADL35982 standard; cDNA; 1168 BP.  
DE Human NOVX cDNA #14.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (GUOX/) GUO X.  
PA (KEKU/) KEKUDA R.  
Query Match 13.8%; Score 231.2; DB 11; Length 1168;  
Best Local Similarity 58.1%; Pred. No. 2.2e-50;  
RESULT 719  
ID ADL35980 standard; cDNA; 1133 BP.  
DE Human NOVX cDNA #13.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (GUOX/) GUO X.  
PA (KEKU/) KEKUDA R.  
Query Match 13.4%; Score 224.8; DB 11; Length 1133;  
Best Local Similarity 59.3%; Pred. No. 1.1e-48;  
RESULT 720  
ID AAS28811 standard; cDNA; 4656 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID NO 57.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.1%; Score 220.6; DB 4; Length 4656;  
Best Local Similarity 57.5%; Pred. No. 2.9e-47;  
RESULT 721  
ID ADB31536 standard; cDNA; 4656 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 57.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.1%; Score 220.6; DB 10; Length 4656;  
Best Local Similarity 57.5%; Pred. No. 2.9e-47;  
RESULT 722  
ID AAS78003 standard; cDNA; 2883 BP.  
DE DNA encoding novel human diagnostic protein #13807.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.0%; Score 217.8; DB 5; Length 2883;  
Best Local Similarity 71.1%; Pred. No. 1.2e-46;  
RESULT 723  
ID ADE08816 standard; DNA; 2883 BP.  
DE Novel DNA-related contig nucleotide sequence #60.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.0%; Score 217.8; DB 10; Length 2883;  
Best Local Similarity 71.1%; Pred. No. 1.2e-46;  
RESULT 724  
ID AAD47372 standard; DNA; 754 BP.  
DE Human LP289 splice variant (LP343) DNA.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 12.6%; Score 211.4; DB 8; Length 754;  
Best Local Similarity 61.1%; Pred. No. 3.1e-45;  
RESULT 725  
ID ADP28686 standard; DNA; 666 BP.  
DE Human secreted protein encoding sequence SEQ ID #684.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.5%; Score 210; DB 12; Length 666;

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Best Local Similarity 60.2%; Pred. No. 6.9e-45;
RESULT 726
ID AAD47373 standard; DNA; 2597 BP.
DE Human LP319a DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 12.4%; Score 208.6; DB 8; Length 2597;
Best Local Similarity 58.1%; Pred. No. 3.2e-44;
RESULT 727
ID AAC02777 standard; cDNA; 352 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 2775.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GSEST ) GENSET.
Query Match 11.5%; Score 193.6; DB 3; Length 352;
Best Local Similarity 82.5%; Pred. No. 1.1e-40;
RESULT 728
ID ABL99899 standard; cDNA; 5666 BP.
DE Human secretory polynucleotide (sptm) 154.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCYL ) INCYTE GENOMICS INC.
Query Match 10.7%; Score 180.4; DB 6; Length 5666;
Best Local Similarity 56.1%; Pred. No. 1.4e-36;
RESULT 729
ID ADG63283 standard; DNA; 540 BP.
DE Human OBCAM gene exon 2.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 10.5%; Score 176.6; DB 10; Length 540;
Best Local Similarity 74.9%; Pred. No. 4.3e-36;
RESULT 730
ID ADQ83739 standard; cDNA; 919 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH ) GENENTECH INC.
PA (WUTD ) WU T D.
PA (ZHOU ) ZHOU Y.
Query Match 10.4%; Score 175; DB 12; Length 919;
Best Local Similarity 58.0%; Pred. No. 1.5e-35;
RESULT 731
ID AAS78037 standard; cDNA; 767 BP.
DE DNA encoding novel human diagnostic protein #13841.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 170.2; DB 5; Length 767;
Best Local Similarity 95.6%; Pred. No. 2.5e-34;
RESULT 732
ID AAF93597 standard; cDNA; 585 BP.
DE Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 163.2; DB 5; Length 585;
Best Local Similarity 62.0%; Pred. No. 1.6e-32;
RESULT 733
ID ABS52769 standard; cDNA; 408 BP.
DE Murine tuberosus sclerosis complex 8 (TSC8) DNA.
PN WO200246475-A2.
PD 13-JUN-2002.
PA (CURA ) CURAGEN CORP.
Query Match 9.5%; Score 160; DB 6; Length 408;
Best Local Similarity 63.7%; Pred. No. 9.2e-32;
RESULT 734
ID AAC10355 standard; cDNA; 20C BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14430.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.

Query Match 8.7%; Score 146; DB 3; Length 200;
Best Local Similarity 100.0%; Pred. No. 3.3e-28;
RESULT 735
ID AAS78038 standard; cDNA; 693 BP.
DE DNA encoding novel human diagnostic protein #13842.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.2%; Score 137.2; DB 5; Length 693;
Best Local Similarity 97.9%; Pred. No. 1.3e-25;
RESULT 736
ID ADQ21981 standard; DNA; 125 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4801.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.6%; Score 110.8; DB 12; Length 125;
Best Local Similarity 97.6%; Pred. No. 5.3e-19;
RESULT 737
ID AAS78592 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #14396.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 107; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
RESULT 738
ID AAS71904 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #7708.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 107; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
RESULT 739
ID AAS78036 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #13840.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 107; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
RESULT 740
ID ABX71182 standard; cDNA; 913 BP.
DE Novel human cDNA sequence #407.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match 6.3%; Score 105.6; DB 8; Length 913;
Best Local Similarity 61.1%; Pred. No. 3.5e-17;
RESULT 741
ID ADQ54463 standard; DNA; 351 BP.
DE Novel canine microarray-related DNA sequence SeqID5765.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ ) PFIZER PROD INC.
Query Match 6.2%; Score 104.6; DB 13; Length 351;
Best Local Similarity 60.8%; Pred. No. 3.9e-17;
RESULT 742
ID AAT42088 standard; cDNA to mRNA; 219 BP.
DE Human LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 6.0%; Score 100; DB 2; Length 219;
Best Local Similarity 67.0%; Pred. No. 5.1e-16;
RESULT 743
ID AAT42089 standard; cDNA to mRNA; 219 BP.
DE Rat LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
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PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 5.7%; Score 95.2; DB 2; Length 219;  
Best Local Similarity 65.6%; Pred. No. 9.6e-15;  
RESULT 744  
ID AAS67246 standard; cDNA; 2678 BP.  
DE DNA encoding novel human diagnostic protein #3050.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.6%; Score 94.4; DB 5; Length 2678;  
Best Local Similarity 57.1%; Pred. No. 5.5e-14;  
RESULT 745  
ID AAS71723 standard; cDNA; 2678 BP.  
DE DNA encoding novel human diagnostic protein #7527.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.6%; Score 94.4; DB 5; Length 2678;  
Best Local Similarity 57.1%; Pred. No. 5.5e-14;  
RESULT 746  
ID AAS64445 standard; cDNA; 3131 BP.  
DE DNA encoding novel human diagnostic protein #249.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.6%; Score 94.4; DB 5; Length 3131;  
Best Local Similarity 57.1%; Pred. No. 6e-14;  
RESULT 747  
ID AAS64798 standard; cDNA; 3131 BP.  
DE DNA encoding novel human diagnostic protein #602.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.6%; Score 94.4; DB 5; Length 3131;  
Best Local Similarity 57.1%; Pred. No. 6e-14;  
RESULT 748  
ID ADM18382 standard; DNA; 2026 BP.  
DE Human chromosome 11qtel subtelomeric DNA probe SEQ ID NO:6.  
FN WO2004029283-A2.  
PD 08-APR-2004.  
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.  
Query Match 5.3%; Score 89; DB 12; Length 2026;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
RESULT 749  
ID ADG63285 standard; DNA; 420 BP.  
DE Human OBCAM gene exon 4.  
FN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 4.7%; Score 78.6; DB 10; Length 420;  
Best Local Similarity 70.5%; Pred. No. 3.3e-10;  
RESULT 750  
ID AAT42090 standard; cDNA to mRNA; 177 BP.  
DE Human LAMP residues 156-204 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 4.6%; Score 77.8; DB 2; Length 177;  
Best Local Similarity 65.0%; Pred. No. 3.5e-10;  
RESULT 751  
ID AAT42091 standard; cDNA to mRNA; 177 BP.  
DE Rat LAMP residues 156-204 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 4.6%; Score 77.8; DB 2; Length 177;  
Best Local Similarity 65.0%; Pred. No. 3.5e-10;  
RESULT 752  
ID ADG63287 standard; DNA; 480 BP.  
DE Human OBCAM gene exon 6.  
FN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.

Query Match 4.6%; Score 76.8; DB 10; Length 480;  
Best Local Similarity 70.8%; Pred. No. 1.1e-09;  
RESULT 753  
ID AAS28866 standard; cDNA; 293 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID NO 112.  
FN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 73; DB 4; Length 293;  
Best Local Similarity 62.9%; Pred. No. 8.3e-09;  
RESULT 754  
ID ABA06681 standard; cDNA; 293 BP.  
DE Human cDNA SEQ ID NO: 347.  
FN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 73; DB 4; Length 293;  
Best Local Similarity 62.9%; Pred. No. 8.3e-09;  
RESULT 755  
ID ABV84018 standard; cDNA; 293 BP.  
DE Human polynucleotide SEQ ID NO 347.  
FN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.3%; Score 73; DB 6; Length 293;  
Best Local Similarity 62.9%; Pred. No. 8.3e-09;  
RESULT 756  
ID ADB31591 standard; cDNA; 293 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 112.  
FN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 73; DB 10; Length 293;  
Best Local Similarity 62.9%; Pred. No. 8.3e-09;  
RESULT 757  
ID ADG63286 standard; DNA; 480 BP.  
DE Human OBCAM gene exon 5.  
FN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 4.3%; Score 71.4; DB 10; Length 480;  
Best Local Similarity 74.4%; Pred. No. 2.8e-08;  
RESULT 758  
ID AAT42092 standard; cDNA to mRNA; 198 BP.  
DE Human LAMP residues 232-297 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 3.8%; Score 64.6; DB 2; Length 198;  
Best Local Similarity 61.3%; Pred. No. 1.1e-06;  
RESULT 759  
ID AAT42093 standard; cDNA to mRNA; 198 BP.  
DE Rat LAMP residues 232-297 coding sequence.  
FN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 3.8%; Score 63.4; DB 2; Length 198;  
Best Local Similarity 60.7%; Pred. No. 2.4e-06;  
RESULT 760  
ID ADG63282 standard; DNA; 270 BP.  
DE Human OBCAM gene exon 1.  
FN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 3.7%; Score 61.6; DB 10; Length 270;  
Best Local Similarity 88.6%; Pred. No. 8.3e-06;  
RESULT 761  
ID ABN40988 standard; DNA; 60 BP.  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:13736.  
FN WO200210449-A2.  
PD 07-FEB-2002.

PA (COMP-) COMPUGEN INC.  
Query Match 3.6%; Score 60; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
RESULT 762  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
FN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 3.5%; Score 58.6; DB 8; Length 2000;  
Best Local Similarity 9.5%; Pred. No. 0.00014;  
RESULT 763  
ID ADG63284 standard; DNA; 420 BP.  
DE Human OBCAM gene exon 3.  
FN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 3.4%; Score 57.6; DB 10; Length 420;  
Best Local Similarity 65.6%; Pred. No. 0.00012;  
RESULT 764  
ID ACN55172 standard; cDNA; 248 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-030-Q6-K6-C8, SEQ:9953.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.4%; Score 57.2; DB 13; Length 248;  
Best Local Similarity 58.0%; Pred. No. 0.00012;  
RESULT 765  
ID ABX47608 standard; cDNA; 399 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #12773.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 3.4%; Score 56.6; DB 8; Length 399;  
Best Local Similarity 57.7%; Pred. No. 0.00021;  
RESULT 766  
ID ABV56779 standard; cDNA; 247 BP.  
DE Human prostate expression marker cDNA 56770.  
FN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 55.6; DB 5; Length 247;  
Best Local Similarity 54.4%; Pred. No. 0.00031;  
RESULT 767  
ID ABK39945 standard; DNA; 6359 BP.  
DE Human chemically pretreated gene sequence #13 strand 2.  
FN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 55; DB 6; Length 6359;  
Best Local Similarity 66.4%; Pred. No. 0.0023;  
RESULT 768  
ID ACH15235 standard; cDNA; 514 BP.  
DE Human adult brain cDNA #2447.  
FN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 3.2%; Score 54.4; DB 9; Length 514;  
Best Local Similarity 62.3%; Pred. No. 0.00093;  
RESULT 769  
ID ABL32788 standard; DNA; 6171 BP.  
DE Human immune system associated gene SEQ ID NO: 761.  
FN WO200200928-A2.

PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 54.4; DB 6; Length 6171;  
Best Local Similarity 61.1%; Pred. No. 0.0033;  
RESULT 770  
ID AAI86998 standard; cDNA; 390 BP.  
DE Human polynucleotide SEQ ID NO 7058.  
FN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 3.2%; Score 53.2; DB 4; Length 390;  
Best Local Similarity 58.0%; Pred. No. 0.0017;  
RESULT 771  
ID AAD05318 standard; cDNA; 671 BP.  
DE Human secreted protein-encoding gene 19 cDNA clone HWLFQ64, SEQ ID NO:29.  
FN WO200134626-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.2%; Score 53.2; DB 4; Length 671;  
Best Local Similarity 60.3%; Pred. No. 0.0022;  
RESULT 772  
ID ABV58693 standard; cDNA; 607 BP.  
DE Human prostate expression marker cDNA 58684.  
FN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 53; DB 5; Length 607;  
Best Local Similarity 56.6%; Pred. No. 0.0024;  
RESULT 773  
ID ABV48356 standard; cDNA; 392 BP.  
DE Human prostate expression marker cDNA 48347.  
FN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.1%; Score 52.8; DB 5; Length 392;  
Best Local Similarity 57.1%; Pred. No. 0.0022;  
RESULT 774  
ID ADH23363 standard; cDNA; 3351 BP.  
DE Fruit fly PAK4 serine/threonine kinase cDNA.  
FN US2003186254-A1.  
PD 02-OCT-2003.  
PA (CELL-) CELL SIGNALING TECHNOLOGY INC.  
Query Match 3.1%; Score 52.8; DB 12; Length 3351;  
Best Local Similarity 58.1%; Pred. No. 0.0064;  
RESULT 775  
ID ABL33589 standard; DNA; 5567 BP.  
DE Human immune system associated gene SEQ ID NO: 1562.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 52.8; DB 6; Length 5567;  
Best Local Similarity 63.3%; Pred. No. 0.0082;  
RESULT 776  
ID ABL92273 standard; DNA; 5567 BP.  
DE Chemically treated DNA repair gene fragment complementary to#41.  
FN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 52.8; DB 6; Length 5567;  
Best Local Similarity 63.3%; Pred. No. 0.0082;  
RESULT 777  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
FN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 3.1%; Score 52.6; DB 8; Length 2000;  
Best Local Similarity 8.4%; Pred. No. 0.0055;  
RESULT 778  
ID ABQ25430 standard; DNA; 579 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12021.  
FN WO200218632-A2.  
PD 07-MAR-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 52.4; DB 6; Length 579;  
Best Local Similarity 60.6%; Pred. No. 0.0033;  
RESULT 779  
ID AB025431 standard; DNA; 579 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12022.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 52.4; DB 6; Length 579;  
Best Local Similarity 60.6%; Pred. No. 0.0033;  
RESULT 780  
ID ACN81600 standard; DNA; 679 BP.  
DE Breast cancer related marker, seq id 2750.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.1%; Score 52.4; DB 11; Length 679;  
Best Local Similarity 55.2%; Pred. No. 0.0036;  
RESULT 781  
ID ABK40004 standard; DNA; 5586 BP.  
DE Human chemically pretreated gene sequence #43 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 52.4; DB 6; Length 5586;  
Best Local Similarity 59.3%; Pred. No. 0.011;  
RESULT 782  
ID ACN52334 standard; cDNA; 571 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-E11, SEQ:7115.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.1%; Score 52.2; DB 13; Length 571;  
Best Local Similarity 57.8%; Pred. No. 0.0038;  
RESULT 783  
ID AAL11399 standard; cDNA; 666 BP.  
DE Human breast cancer expressed polynucleotide 3856.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.1%; Score 52.2; DB 4; Length 666;  
Best Local Similarity 56.8%; Pred. No. 0.0041;  
RESULT 784  
ID ABUL1515 standard; cDNA; 2010 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 3.1%; Score 52.2; DB 4; Length 2010;  
Best Local Similarity 45.6%; Pred. No. 0.0071;  
RESULT 785  
ID AAF72803 standard; DNA; 2057 BP.  
DE Secreted protein gene #5.  
PN WO200107459-A1.  
PD 01-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.1%; Score 52.2; DB 4; Length 2057;  
Best Local Similarity 57.8%; Pred. No. 0.0072;  
RESULT 786  
ID ABS67818 standard; DNA; 3063 BP.  
DE Human receptors and membrane associated protein REMAP-40 gene.  
PN WO200263006-A2.  
PD 15-AUG-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 3.1%; Score 52.2; DB 6; Length 3063;  
Best Local Similarity 64.5%; Pred. No. 0.0088;  
RESULT 787  
ID ABL33948 standard; DNA; 18218 BP.  
DE Human immune system associated gene SEQ ID NO: 1921.

PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 52.2; DB 6; Length 18218;  
Best Local Similarity 60.0%; Pred. No. 0.022;  
RESULT 788  
ID ADS73024 standard; cDNA; 183 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1621.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 3.1%; Score 52; DB 7; Length 183;  
Best Local Similarity 60.7%; Pred. No. 0.0024;  
RESULT 789  
ID ABV58708 standard; cDNA; 484 BP.  
DE Human prostate expression marker cDNA 58699.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.1%; Score 52; DB 5; Length 484;  
Best Local Similarity 58.3%; Pred. No. 0.0039;  
RESULT 790  
ID ABT08076 standard; cDNA; 791 BP.  
DE Human breast specific coding sequence SEQ ID NO: 22.  
PN WO200266607-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 3.1%; Score 52; DB 6; Length 791;  
Best Local Similarity 60.7%; Pred. No. 0.005;  
RESULT 791  
ID ABL32719 standard; DNA; 5739 BP.  
DE Human immune system associated gene SEQ ID NO: 692.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 52; DB 6; Length 5739;  
Best Local Similarity 59.5%; Pred. No. 0.014;  
RESULT 792  
ID ABQ54403 standard; cDNA; 2911 BP.  
DE Human ovarian antigen HAPOB30 cDNA, SEQ ID NO:283.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.1%; Score 51.6; DB 6; Length 2911;  
Best Local Similarity 59.6%; Pred. No. 0.012;  
RESULT 793  
ID AAL16619 standard; cDNA; 3508 BP.  
DE Human secreted protein clone l0311\_8 nucleotide sequence SEQ ID NO:3.  
PN WO200009552-A1.  
PD 24-FEB-2000.  
PA (GEMY) GENETICS INST INC.  
Query Match 3.1%; Score 51.6; DB 3; Length 3508;  
Best Local Similarity 62.3%; Pred. No. 0.014;  
RESULT 794  
ID ADS89723 standard; DNA; 5759 BP.  
DE Oligonucleotide of the invention SEQ ID NO:739.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 13; Length 5759;  
Best Local Similarity 56.5%; Pred. No. 0.017;  
RESULT 795  
ID AB210109 standard; DNA; 8759 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #249.  
PN WO200272722-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 8; Length 8759;  
Best Local Similarity 56.5%; Pred. No. 0.022;  
RESULT 796  
ID AB210237 standard; DNA; 8759 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #377.  
PN WO200272722-A2.

PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 8; Length 8759;  
Best Local Similarity 56.5%; Pred. No. 0.022;  
RESULT 797  
ID ADS4213 standard; DNA; 8759 BP.  
DE Pretreated genomic DNA region 137.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 10; Length 8759;  
Best Local Similarity 56.5%; Pred. No. 0.022;  
RESULT 798  
ID ADE84147 standard; DNA; 8759 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #83.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 10; Length 8759;  
Best Local Similarity 56.5%; Pred. No. 0.022;  
RESULT 799  
ID ADS89513 standard; DNA; 8759 BP.  
DE Oligonucleotide of the invention SEQ ID NO:529.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 13; Length 8759;  
Best Local Similarity 56.5%; Pred. No. 0.022;  
RESULT 800  
ID ABL32784 standard; DNA; 8979 BP.  
DE Human immune system associated gene SEQ ID NO: 757.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 6; Length 8979;  
Best Local Similarity 63.9%; Pred. No. 0.022;  
RESULT 801  
ID ABK31270 standard; DNA; 8979 BP.  
DE Signal transduction associated gene modified DNA #57.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 6; Length 8979;  
Best Local Similarity 63.9%; Pred. No. 0.022;  
RESULT 802  
ID ABL70231 standard; DNA; 8979 BP.  
DE Chemically treated cell signalling DNA sequence#61.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 6; Length 8979;  
Best Local Similarity 63.9%; Pred. No. 0.022;  
RESULT 803  
ID AAS61178 standard; DNA; 8979 BP.  
DE Human gene regulation-associated gene oligonucleotide #133.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.1%; Score 51.6; DB 6; Length 8979;  
Best Local Similarity 63.9%; Pred. No. 0.022;  
RESULT 804  
ID AAT87807 standard; CDNA; 419 BP.  
DE Human polynucleotide SEQ ID NO 7867.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 3.1%; Score 51.4; DB 4; Length 419;  
Best Local Similarity 60.3%; Pred. No. 0.0052;  
RESULT 805  
ID ACN52877 standard; CDNA; 421 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.  
PN US2004123340-A1.  
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.1%; Score 51.4; DB 13; Length 421;  
Best Local Similarity 58.0%; Pred. No. 0.0052;  
RESULT 806  
ID ACN50120 standard; CDNA; 585 BP.  
DE Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-D8, SEQ:4901.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.1%; Score 51.4; DB 13; Length 585;  
Best Local Similarity 58.0%; Pred. No. 0.0062;  
RESULT 807  
ID ABV58626 standard; CDNA; 504 BP.  
DE Human prostate expression marker CDNA 58617.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 51.2; DB 5; Length 504;  
Best Local Similarity 57.5%; Pred. No. 0.0065;  
RESULT 808  
ID ABK43454 standard; CDNA; 894 BP.  
DE DNA encoding novel central nervous system protein #34.  
PN WO200155318-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 51.2; DB 4; Length 894;  
Best Local Similarity 66.1%; Pred. No. 0.0087;  
RESULT 809  
ID ADI53841 standard; CDNA; 894 BP.  
DE CDNA encoding novel human protein seq id 44.  
PN US2004018969-A1.  
PD 29-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 3.0%; Score 51.2; DB 12; Length 894;  
Best Local Similarity 66.1%; Pred. No. 0.0087;  
RESULT 810  
ID AAI83204 standard; CDNA; 386 BP.  
DE Human polynucleotide SEQ ID NO 3264.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 3.0%; Score 51; DB 4; Length 386;  
Best Local Similarity 59.2%; Pred. No. 0.0064;  
RESULT 811  
ID ACN56273 standard; CDNA; 517 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.0%; Score 51; DB 13; Length 517;  
Best Local Similarity 59.2%; Pred. No. 0.0074;  
RESULT 812  
ID ADJ81646 standard; DNA; 10428 BP.  
DE Human cytosine phosphatase SHP1 bisulphited genomic DNA SeqID 6.  
PN JP2004000128-A.  
PD 08-JAN-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 3.0%; Score 51; DB 12; Length 10428;  
Best Local Similarity 59.2%; Pred. No. 0.034;  
RESULT 813  
ID ACN87837 standard; DNA; 643 BP.  
DE Breast cancer related marker, seq id 8987.

PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.0%; Score 50.8; DB 11; Length 643;  
Best Local Similarity 57.8%; Pred. No. 0.0094;  
RESULT 814  
ID ADU41364 standard; DNA; 393 BP.  
DE Human ovarian cancer DNA marker #15254.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.6; DB 5; Length 393;  
Best Local Similarity 57.1%; Pred. No. 0.0082;  
RESULT 815  
ID ABN98845 standard; DNA; 856 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 613.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 3.0%; Score 50.6; DB 6; Length 856;  
Best Local Similarity 54.8%; Pred. No. 0.012;  
RESULT 816  
ID AAC63439 standard; cDNA; 876 BP.  
DE Human secreted protein coding sequence SEQ ID NO: 40.  
PN WO200061779-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 50.6; DB 3; Length 876;  
Best Local Similarity 63.6%; Pred. No. 0.012;  
RESULT 817  
ID AB273647 standard; cDNA; 876 BP.  
DE Secreted protein-encoding gene 367 cDNA clone HUSIR18, SEQ ID NO:377.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 50.6; DB 8; Length 876;  
Best Local Similarity 63.6%; Pred. No. 0.012;  
RESULT 818  
ID ADA98139 standard; cDNA; 876 BP.  
DE Human secreted protein cDNA sequence #233.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 50.6; DB 8; Length 876;  
Best Local Similarity 63.6%; Pred. No. 0.012;  
RESULT 819  
ID AB267241 standard; cDNA; 876 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO 361.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 50.6; DB 10; Length 876;  
Best Local Similarity 63.6%; Pred. No. 0.012;  
RESULT 820  
ID ADD71195 standard; cDNA; 2200 BP.

DE Human intracellular signalling molecule INTSIG-32 cDNA SEQ ID NO:84.  
PN WO2003039348-A2.  
PD 15-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 3.0%; Score 50.6; DB 10; Length 2200;  
Best Local Similarity 70.1%; Pred. No. 0.02;  
RESULT 821  
ID ADE79863 standard; DNA; 2924 BP.  
DE Rat myosin heavy chain coding sequence, SEQ ID 103.  
PN EP1279744-A2.  
PD 29-JAN-2003.  
PA (WARN-) WARNER LAMBERT CO.  
Query Match 3.0%; Score 50.6; DB 10; Length 2924;  
Best Local Similarity 63.6%; Pred. No. 0.023;  
RESULT 822  
ID ABV25005 standard; cDNA; 4990 BP.  
DE Human prostate expression marker cDNA 24996.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.6; DB 5; Length 4990;  
Best Local Similarity 58.2%; Pred. No. 0.03;  
RESULT 823  
ID ABV25400 standard; cDNA; 4990 BP.  
DE Human prostate expression marker cDNA 25391.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.6; DB 5; Length 4990;  
Best Local Similarity 58.2%; Pred. No. 0.03;  
RESULT 824  
ID ACN89861 standard; DNA; 5001 BP.  
DE Breast cancer related marker, seq id 11011.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.0%; Score 50.6; DB 11; Length 5001;  
Best Local Similarity 58.2%; Pred. No. 0.03;  
RESULT 825  
ID ABL92257 standard; DNA; 6029 BP.  
DE Chemically treated DNA repair gene fragment complementary to#33.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.0%; Score 50.6; DB 6; Length 6029;  
Best Local Similarity 57.1%; Pred. No. 0.033;  
RESULT 826  
ID AAD2326 standard; DNA; 6029 BP.  
DE Chemically treated human genomic DNA #16 associated with DNA adducts.  
PN WO200177378-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.0%; Score 50.6; DB 6; Length 6029;  
Best Local Similarity 57.1%; Pred. No. 0.033;  
RESULT 827  
ID ABX41821 standard; cDNA; 272 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #6986.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 3.0%; Score 50.4; DB 8; Length 272;  
Best Local Similarity 60.0%; Pred. No. 0.0077;  
RESULT 828  
ID AAH71505 standard; cDNA; 310 BP.  
DE Human cervical cancer marker nucleic acid 2779.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.4; DB 4; Length 310;  
Best Local Similarity 56.7%; Pred. No. 0.0082;

RESULT 829  
ID ABL33696 standard; DNA; 6668 BP.  
DE Human immune system associated gene SEQ ID NO: 1669.  
PN WO2000200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.0%; Score 50.4; DB 6; Length 6668;  
Best Local Similarity 58.8%; Pred. No. 0.039;  
RESULT 830  
ID ABV19038 standard; cDNA; 201 BP.  
DE Human prostate expression marker cDNA 19029.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.2; DB 5; Length 201;  
Best Local Similarity 59.8%; Pred. No. 0.0075;  
RESULT 831  
ID AAT76782 standard; DNA; 240 BP.  
DE Staphylococcus aureus exfoliative toxin A gene capture probe.  
PN US5627054-A.  
PD 06-MAY-1997.  
PA (USSA-) US SEC OF ARMY.  
Query Match 3.0%; Score 50.2; DB 2; Length 240;  
Best Local Similarity 58.3%; Pred. No. 0.0082;  
RESULT 832  
ID ABV42927 standard; cDNA; 382 BP.  
DE Human prostate expression marker cDNA 42918.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.2; DB 5; Length 382;  
Best Local Similarity 55.4%; Pred. No. 0.01;  
RESULT 833  
ID ABV34060 standard; cDNA; 383 BP.  
DE Human prostate expression marker cDNA 34051.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.2; DB 5; Length 383;  
Best Local Similarity 55.4%; Pred. No. 0.01;  
RESULT 834  
ID ABV18980 standard; cDNA; 384 BP.  
DE Human prostate expression marker cDNA 18971.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.2; DB 5; Length 384;  
Best Local Similarity 48.1%; Pred. No. 0.01;  
RESULT 835  
ID ADT69792 standard; DNA; 384 BP.  
DE Human ovarian cancer DNA marker #2534.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.2; DB 5; Length 384;  
Best Local Similarity 52.6%; Pred. No. 0.01;  
RESULT 836  
ID ADT76128 standard; DNA; 384 BP.  
DE Human ovarian cancer DNA marker #8870.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.2; DB 5; Length 384;  
Best Local Similarity 52.6%; Pred. No. 0.01;  
RESULT 837  
ID ABV48817 standard; cDNA; 448 BP.  
DE Human prostate expression marker cDNA 48808.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50.2; DB 5; Length 448;  
Best Local Similarity 59.8%; Pred. No. 0.011;  
RESULT 838  
ID ABL32540 standard; DNA; 6476 BP.  
DE Human immune system associated gene SEQ ID NO: 513.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.0%; Score 50.2; DB 6; Length 6476;  
Best Local Similarity 62.2%; Pred. No. 0.043;  
RESULT 839  
ID ABV59017 standard; cDNA; 325 BP.  
DE Human prostate expression marker cDNA 59008.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50; DB 5; Length 325;  
Best Local Similarity 61.5%; Pred. No. 0.011;  
RESULT 840  
ID ABV50931 standard; cDNA; 464 BP.  
DE Human prostate expression marker cDNA 50922.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50; DB 5; Length 464;  
Best Local Similarity 63.1%; Pred. No. 0.013;  
RESULT 841  
ID ABV54323 standard; cDNA; 471 BP.  
DE Human prostate expression marker cDNA 54314.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 50; DB 5; Length 471;  
Best Local Similarity 52.4%; Pred. No. 0.013;  
RESULT 842  
ID ACH45627 standard; cDNA; 520 BP.  
DE Human foetal brain cDNA #6352.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 3.0%; Score 50; DB 9; Length 520;  
Best Local Similarity 53.8%; Pred. No. 0.014;  
RESULT 843  
ID AAC79893 standard; cDNA; 680 BP.  
DE Human secreted protein encoding cDNA for gene 45.  
PN WO200055176-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 50; DB 3; Length 680;  
Best Local Similarity 58.9%; Pred. No. 0.016;  
RESULT 844  
ID AAA61261 standard; DNA; 870 BP.  
DE Human secreted protein gene 2 clone HHFBY53.  
PN WO200029422-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 50; DB 3; Length 870;  
Best Local Similarity 59.7%; Pred. No. 0.018;  
RESULT 845  
ID ADA39860 standard; cDNA; 870 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 50; DB 8; Length 870;  
Best Local Similarity 59.7%; Pred. No. 0.018;  
RESULT 846  
ID ACC50464 standard; cDNA; 870 BP.  
DE Human secreted protein coding sequence, SEQ ID 131.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.0%; Score 50; DB 8; Length 870;  
Best Local Similarity 59.7%; Pred. No. 0.018;  
RESULT 847  
ID AD062706 standard; DNA; 1971 BP.  
DE Transcription factor G2550 orthologous sequence, SEQ ID 1173.  
PN WO2004031349-A2.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 3.0%; Score 50; DB 12; Length 1971;  
Best Local Similarity 67.0%; Pred. No. 0.027;  
RESULT 848  
ID ADQ24914 standard; DNA; 3459 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7734.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 3.0%; Score 50; DB 12; Length 3469;  
Best Local Similarity 56.8%; Pred. No. 0.036;  
RESULT 849  
ID ABR80041 standard; DNA; 5387 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 58.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.0%; Score 50; DB 6; Length 5387;  
Best Local Similarity 57.8%; Pred. No. 0.045;  
RESULT 850  
ID ABX56303 standard; DNA; 8243 BP.  
DE Human NOV25b CG93858-02 DNA SEQ ID 85.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 3.0%; Score 50; DB 8; Length 8243;  
Best Local Similarity 49.7%; Pred. No. 0.055;  
RESULT 851  
ID ABJ33999 standard; DNA; 21537 BP.  
DE Human immune system associated gene SEQ ID NO: 1972.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.0%; Score 50; DB 6; Length 21537;  
Best Local Similarity 60.1%; Pred. No. 0.09;  
RESULT 852  
ID ABV49239 standard; cDNA; 311 BP.  
DE Human prostate expression marker cDNA 49230.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 49.8; DB 5; Length 311;  
Best Local Similarity 58.4%; Pred. No. 0.012;  
RESULT 853  
ID ABV57904 standard; cDNA; 376 BP.  
DE Human prostate expression marker cDNA 57895.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 49.8; DB 5; Length 376;  
Best Local Similarity 58.4%; Pred. No. 0.013;  
RESULT 854  
ID ABV54466 standard; cDNA; 381 BP.  
DE Human prostate expression marker cDNA 54457.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 49.8; DB 5; Length 381;  
Best Local Similarity 62.4%; Pred. No. 0.013;  
RESULT 855  
ID ACH39052 standard; cDNA; 465 BP.  
DE Human foetal brain cDNA #419.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 3.0%; Score 49.8; DB 9; Length 465;  
Best Local Similarity 55.9%; Pred. No. 0.015;  
RESULT 856  
ID ACH2893 standard; cDNA; 506 BP.  
DE Human adult ovary cDNA #1273.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 3.0%; Score 49.8; DB 9; Length 506;  
Best Local Similarity 60.4%; Pred. No. 0.015;  
RESULT 857  
ID ABV56485 standard; cDNA; 543 BP.  
DE Human prostate expression marker cDNA 56476.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 49.8; DB 5; Length 543;  
Best Local Similarity 57.3%; Pred. No. 0.016;  
RESULT 858  
ID AAH70126 standard; cDNA; 545 BP.  
DE Human cervical cancer marker nucleic acid 1400.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.0%; Score 49.8; DB 4; Length 545;  
Best Local Similarity 53.9%; Pred. No. 0.016;  
RESULT 859  
ID ACN53724 standard; cDNA; 571 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-K6-H4, SEQ:8505.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.0%; Score 49.8; DB 13; Length 571;  
Best Local Similarity 64.1%; Pred. No. 0.016;  
RESULT 860  
ID AAA26373 standard; cDNA; 1048 BP.  
DE Human secreted protein gene 28 SEQ ID NO:38.  
PN WO200006698-A1.  
PD 10-FEB-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.0%; Score 49.8; DB 3; Length 1048;  
Best Local Similarity 59.6%; Pred. No. 0.022;  
RESULT 861  
ID ADL71434 standard; cDNA; 1048 BP.  
DE Novel human secreted protein cDNA seqid 38.  
PN US2004034196-A1.  
PD 19-FEB-2004.  
PA (KOMA/) KOMATSOUKIS G A.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (DUAN/) DUAN D R.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAPL/) LAPLEUR D W.  
PA (WEIY/) WEI Y.  
Query Match 3.0%; Score 49.8; DB 12; Length 1048;  
Best Local Similarity 59.6%; Pred. No. 0.022;  
RESULT 862  
ID ADH02701 standard; DNA; 1317 BP.  
DE Human elongation factor EEF1A1 cDNA fragment, SEQ ID NO:7.  
PN WO2003104488-A1.  
PD 18-DEC-2003.  
PA (CANC-) CANCER CARE ONTARIO.

Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1317;  
RESULT 863  
ID ACP34510 standard; DNA; 1833 BP.  
DE Gene encoding angiogenesis protein ENO144.  
PN WO2003027285-A1.  
PD 03-APR-2003.  
PA (BION-) BIONOMICS LTD.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 8; Length 1833;  
RESULT 864  
ID ADL35468 standard; DNA; 1833 BP.  
DE Human eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) DNA.  
PN WO2004019893-A2.  
PD 11-MAR-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1833;  
RESULT 865  
ID ADS88611 standard; cDNA; 1833 BP.  
DE Human housekeeping gene cDNA sequence SEQ ID NO:154.  
PN WO2004035785-A1.  
PD 29-APR-2004.  
PA (NIGA-) NGK INSULATORS LTD.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 13; Length 1833;  
RESULT 866  
ID ADJ62805 standard; cDNA; 1837 BP.  
DE Human cDNA differentially expressed in response to docetaxel #75.  
PN US2004018527-A1.  
PD 29-JAN-2004.  
PA (CHAN/) CHANG J C.  
PA (OCON/) O'CONNELL P.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1837;  
RESULT 867  
ID ADP10528 standard; DNA; 1837 BP.  
DE Reference mRNA sequences for marker probe #205.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1837;  
RESULT 868  
ID AAF18296 standard; DNA; 2044 BP.  
DE Lung cancer associated polynucleotide sequence SEQ ID 315.  
PN WO200505180-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 3; Length 2044;  
RESULT 869  
ID AAA95790 standard; cDNA; 2045 BP.  
DE Apoptosis related gene 1 clone HLDOK36.  
PN WO200506752-A2.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 3; Length 2045;  
RESULT 870  
ID AAH33283 standard; cDNA; 2045 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:339.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 4; Length 2045;  
RESULT 871  
ID AAV63189 standard; cDNA; 2496 BP.  
DE cDNA from clone crll62\_25 which encodes a secreted protein.  
PN WO9844113-A1.  
PD 08-OCT-1998.

PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 2; Length 2496;  
RESULT 872  
ID ABQ92039 standard; cDNA; 2496 BP.  
DE Human polynucleotide SEQ ID NO 36.  
PN US2002065394-A1.  
PD 30-MAY-2002.  
PA (JACO/) JACOBS K.  
PA (MCCO/) MCCOY J M.  
PA (LAVA/) LAVALLE E R.  
PA (COLL/) COLLINS-RACIE L A.  
PA (EVAN/) EVANS C.  
PA (MERB/) MERBERG D.  
PA (TREA/) TREACY M.  
PA (SPAU/) SPAULDING V.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 6; Length 2496;  
RESULT 873  
ID ADI03925 standard; DNA; 2496 BP.  
DE Human B7-1.1 polypeptide encoding DNA.  
PN WO2003105887-A1.  
PD 24-DEC-2003.  
PA (AMHP) WYETH.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 2496;  
RESULT 874  
ID AAF91859 standard; cDNA; 3436 BP.  
DE Human secreted protein-encoding gene 2 cDNA clone HDFFB02, SEQ ID NO:12.  
PN WO200118022-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 4; Length 3436;  
RESULT 875  
ID AAS00767 standard; cDNA; 3436 BP.  
DE Human B7-H3 cDNA clone.  
PN WO200118021-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MAYO-) MAYO CLINIC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 4; Length 3436;  
RESULT 876  
ID ADA39737 standard; cDNA; 3436 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 8; Length 3436;  
RESULT 877  
ID ADC73453 standard; DNA; 3436 BP.  
DE Human secreted protein-related DNA - SEQ ID 86.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 10; Length 3436;  
RESULT 878  
ID ABL32345 standard; DNA; 7346 BP.  
DE Human immune system associated gene SEQ ID NO: 318.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 6; Length 7346;  
RESULT 879  
ID ABN80102 standard; DNA; 8712 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 119.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.



Query Match  
Best Local Similarity 3.0%; Score 49.8; DB 6; Length 8712;  
RESULT 880  
ID AA192106 standard; cDNA; 425 BP.  
DE Human polynucleotide SEQ ID NO 12166.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 4; Length 425;  
RESULT 881  
ID ACN60136 standard; cDNA; 481 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 13; Length 481;  
RESULT 882  
ID ADQ22716 standard; DNA; 1486 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5536.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 12; Length 1486;  
RESULT 883  
ID ACC59907 standard; cDNA; 1678 BP.  
DE Human REMAP-20 encoding cDNA SEQ ID NO:56.  
PN WO2003025130-A2.  
PD 27-MAR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 9; Length 1678;  
RESULT 884  
ID ADL63386 standard; DNA; 2161 BP.  
DE Human ovarian cancer DNA marker #21598.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 5; Length 2161;  
RESULT 885  
ID ADG32748 standard; DNA; 2870 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID72.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 10; Length 2870;  
RESULT 886  
ID ADD18806 standard; DNA; 3232 BP.  
DE Human disease related protein DNA sequence SeqID238.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 10; Length 3232;  
RESULT 887  
ID ADH61306 standard; DNA; 3420 BP.  
DE INTSIG encoding DNA 7512389CB1, SEQ ID 23.  
PN WO2004001005-A2.  
PD 31-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 12; Length 3420;  
RESULT 888  
ID ABL33518 standard; DNA; 5520 BP.  
DE Human immune system associated gene SEQ ID NO: 1491.  
PN WO200200928-A2.

PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 6; Length 5520;  
RESULT 889  
ID ABL32677 standard; DNA; 6015 BP.  
DE Human immune system associated gene SEQ ID NO: 650.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 3.0%; Score 49.6; DB 6; Length 6015;  
RESULT 890  
ID AAI87537 standard; cDNA; 366 BP.  
DE Human polynucleotide SEQ ID NO 7597.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 2.9%; Score 49.4; DB 4; Length 366;  
RESULT 891  
ID ABV56666 standard; cDNA; 408 BP.  
DE Human prostate expression marker cDNA 56657.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 2.9%; Score 49.4; DB 5; Length 408;  
RESULT 892  
ID AAI82260 standard; cDNA; 412 BP.  
DE Human polynucleotide SEQ ID NO 2320.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 2.9%; Score 49.4; DB 4; Length 412;  
RESULT 893  
ID ABV45890 standard; cDNA; 438 BP.  
DE Human prostate expression marker cDNA 45881.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 2.9%; Score 49.4; DB 5; Length 438;  
RESULT 894  
ID AAI82206 standard; cDNA; 480 BP.  
DE Human polynucleotide SEQ ID NO 2266.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 2.9%; Score 49.4; DB 4; Length 480;  
RESULT 895  
ID ACH25146 standard; cDNA; 561 BP.  
DE Human adult ovary cDNA #3526.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match  
Best Local Similarity 2.9%; Score 49.4; DB 9; Length 561;  
RESULT 896  
ID ABV58690 standard; cDNA; 579 BP.  
DE Human prostate expression marker cDNA 58681.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 2.9%; Score 49.4; DB 5; Length 579;  
RESULT 897

ID AAL20340 standard; cDNA; 622 BP.  
DE Human breast cancer expressed polynucleotide 12797.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.4; DB 4; Length 622;  
Best Local Similarity 57.4%; Pred. No. 0.022;  
RESULT 98  
ID AAC80551 standard; cDNA; 658 BP.  
DE Human secreted protein gene 21 SEQ ID NO:31.  
PN WO200058467-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 49.4; DB 3; Length 658;  
Best Local Similarity 57.4%; Pred. No. 0.022;  
RESULT 99  
ID AAH35003 standard; cDNA; 788 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2085.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 49.4; DB 4; Length 788;  
Best Local Similarity 58.5%; Pred. No. 0.024;  
RESULT 900  
ID AAS02414 standard; cDNA; 797 BP.  
DE Human secreted protein, cDNA #20.  
PN WO200123546-A1.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 49.4; DB 4; Length 797;  
Best Local Similarity 58.5%; Pred. No. 0.024;  
RESULT 901  
ID ABV28953 standard; cDNA; 1603 BP.  
DE Human prostate expression marker cDNA 28944.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.4; DB 5; Length 1603;  
Best Local Similarity 64.3%; Pred. No. 0.035;  
RESULT 902  
ID ABV22100 standard; cDNA; 1603 BP.  
DE Human prostate expression marker cDNA 22091.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.4; DB 5; Length 1603;  
Best Local Similarity 64.3%; Pred. No. 0.035;  
RESULT 903  
ID ABV23114 standard; cDNA; 1603 BP.  
DE Human prostate expression marker cDNA 23105.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.4; DB 5; Length 1603;  
Best Local Similarity 64.3%; Pred. No. 0.035;  
RESULT 904  
ID ABV27940 standard; cDNA; 1603 BP.  
DE Human prostate expression marker cDNA 27931.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.4; DB 5; Length 1603;  
Best Local Similarity 64.3%; Pred. No. 0.035;  
RESULT 905  
ID AAS31262 standard; cDNA; 2645 BP.  
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID No 76.  
PN WO200155368-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 49.4; DB 4; Length 2645;  
Best Local Similarity 58.5%; Pred. No. 0.045;  
RESULT 906  
ID ABQ66586 standard; cDNA; 2645 BP.

DE Human polynucleotide SEQ ID NO 76.  
PN US2002042386-A1.  
PD 11-APR-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 2.9%; Score 49.4; DB 6; Length 2645;  
Best Local Similarity 58.5%; Pred. No. 0.045;  
RESULT 907  
ID ADC10608 standard; cDNA; 2645 BP.  
DE Human cDNA from extracellular matrix gene 66.  
PN US2003059875-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 49.4; DB 10; Length 2645;  
Best Local Similarity 58.5%; Pred. No. 0.045;  
RESULT 908  
ID ADQ23227 standard; DNA; 3480 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6047.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 49.4; DB 12; Length 3480;  
Best Local Similarity 57.4%; Pred. No. 0.052;  
RESULT 909  
ID ADQ24537 standard; DNA; 3480 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7357.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 49.4; DB 12; Length 3480;  
Best Local Similarity 57.4%; Pred. No. 0.052;  
RESULT 910  
ID AAI88514 standard; cDNA; 389 BP.  
DE Human polynucleotide SEQ ID NO 8574.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 49.2; DB 4; Length 389;  
Best Local Similarity 57.0%; Pred. No. 0.019;  
RESULT 911  
ID AAI88643 standard; cDNA; 396 BP.  
DE Human polynucleotide SEQ ID NO 8703.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 49.2; DB 4; Length 396;  
Best Local Similarity 57.0%; Pred. No. 0.019;  
RESULT 912  
ID AAI87424 standard; cDNA; 429 BP.  
DE Human polynucleotide SEQ ID NO 7484.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 49.2; DB 4; Length 429;  
Best Local Similarity 60.0%; Pred. No. 0.02;  
RESULT 913  
ID ABV58527 standard; cDNA; 442 BP.  
DE Human prostate expression marker cDNA 58518.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.2; DB 5; Length 442;  
Best Local Similarity 57.0%; Pred. No. 0.021;  
RESULT 914  
ID ACH25161 standard; cDNA; 448 BP.  
DE Human adult ovary cDNA #3541.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.  
Query Match 2.9%; Score 49.2; DB 9; Length 448;  
Best Local Similarity 59.1%; Pred. No. 0.021;  
RESULT 915  
ID AAI84689 standard; cDNA; 453 BP.  
DE Human polynucleotide SEQ ID NO 4749.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 49.2; DB 4; Length 453;  
Best Local Similarity 60.4%; Pred. No. 0.021;  
RESULT 916  
ID ABV58840 standard; cDNA; 539 BP.  
DE Human prostate expression marker cDNA 58831.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.2; DB 5; Length 539;  
Best Local Similarity 59.2%; Pred. No. 0.023;  
RESULT 917  
ID ABV56624 standard; cDNA; 544 BP.  
DE Human prostate expression marker cDNA 56615.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.2; DB 5; Length 544;  
Best Local Similarity 60.4%; Pred. No. 0.023;  
RESULT 918  
ID ABV58620 standard; cDNA; 554 BP.  
DE Human prostate expression marker cDNA 58611.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.2; DB 5; Length 554;  
Best Local Similarity 61.9%; Pred. No. 0.023;  
RESULT 919  
ID ABV58414 standard; cDNA; 575 BP.  
DE Human prostate expression marker cDNA 58405.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.2; DB 5; Length 575;  
Best Local Similarity 57.0%; Pred. No. 0.023;  
RESULT 920  
ID AAH71551 standard; cDNA; 621 BP.  
DE Human cervical cancer marker nucleic acid 2825.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49.2; DB 4; Length 621;  
Best Local Similarity 57.0%; Pred. No. 0.024;  
RESULT 921  
ID AAH34312 standard; cDNA; 712 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1394.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 49.2; DB 4; Length 712;  
Best Local Similarity 59.2%; Pred. No. 0.026;  
RESULT 922  
ID ADJ80203 standard; cDNA; 877 BP.  
DE Novel human nucleic acid-associated protein coding sequence #21.  
PN WO2003038052-A2.  
PD 08-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 2.9%; Score 49.2; DB 10; Length 877;  
Best Local Similarity 59.2%; Pred. No. 0.029;  
RESULT 923  
ID AAK58876 standard; cDNA; 1503 BP.  
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3936.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.9%; Score 49.2; DB 4; Length 1503;  
Best Local Similarity 59.6%; Pred. No. 0.038;  
RESULT 924  
ID ABA93758 standard; cDNA; 1537 BP.  
DE Human testis derived cDNA clone tes3\_22124.  
PN WO200198454-A2.  
PD 27-DEC-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 2.9%; Score 49.2; DB 6; Length 1537;  
Best Local Similarity 63.6%; Pred. No. 0.039;  
RESULT 925  
ID AQO22988 standard; DNA; 1576 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 49.2; DB 12; Length 1576;  
Best Local Similarity 57.0%; Pred. No. 0.039;  
RESULT 926  
ID AQO23425 standard; DNA; 2408 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6245.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 49.2; DB 12; Length 2408;  
Best Local Similarity 61.9%; Pred. No. 0.048;  
RESULT 927  
ID ABZ10224 standard; DNA; 2501 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #364.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49.2; DB 8; Length 2501;  
Best Local Similarity 58.0%; Pred. No. 0.049;  
RESULT 928  
ID AQO08601 standard; DNA; 3030 BP.  
DE Clona intestinalis nervous system associated gene SeqID3.  
PN JP2004057127-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 2.9%; Score 49.2; DB 12; Length 3030;  
Best Local Similarity 60.4%; Pred. No. 0.054;  
RESULT 929  
ID AAX33181 standard; DNA; 6644 BP.  
DE Base sequence of the plasmid pRx-ires-bsr.  
PN WO9913073-A2.  
PD 18-MAR-1999.  
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.  
Query Match 2.9%; Score 49.2; DB 2; Length 6644;  
Best Local Similarity 60.4%; Pred. No. 0.081;  
RESULT 930  
ID ABK40051 standard; DNA; 7058 BP.  
DE Human chemically pretreated gene sequence #67 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49.2; DB 6; Length 7058;  
Best Local Similarity 63.6%; Pred. No. 0.083;  
RESULT 931  
ID AAX33182 standard; DNA; 7372 BP.  
DE Base sequence of the plasmid pRx-Bcl-xl-bsr.  
PN WO9913073-A2.  
PD 18-MAR-1999.  
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.  
Query Match 2.9%; Score 49.2; DB 2; Length 7372;  
Best Local Similarity 60.4%; Pred. No. 0.085;  
RESULT 932  
ID AAX33180 standard; DNA; 7797 BP.  
DE Cowpox virus bsr full length gene sequence.  
PN WO9913073-A2.  
PD 18-MAR-1999.  
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.  
Query Match 2.9%; Score 49.2; DB 2; Length 7797;

Best Local Similarity 60.4%; Pred. No. 0.088;

RESULT 933

ID AAX3184 standard; DNA; 7996 BP.

DE Base sequence of the plasmid PRX-Bcl 2-i-hCD 25.

PN WO9913073-A2.

PD 18-MAR-1999.

PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.

Query Match 2.9%; Score 49.2; DB 2; Length 7996;

Best Local Similarity 60.4%; Pred. No. 0.089;

RESULT 934

ID ABR28222 standard; DNA; 11394 BP.

DE DNA transcription associated complementary genomic DNA #48.

PN WO200192565-A2.

PD 06-DEC-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 2.9%; Score 49.2; DB 6; Length 11394;

Best Local Similarity 57.0%; Pred. No. 0.11;

RESULT 935

ID AB210104 standard; DNA; 35962 BP.

DE Haematopoietic cell proliferation disorder related DNA sequence #244.

PN WO20027272-A2.

PD 03-OCT-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 2.9%; Score 49.2; DB 8; Length 35962;

Best Local Similarity 58.0%; Pred. No. 0.19;

RESULT 936

ID AAS07790 standard; DNA; 256 BP.

DE Cervical cancer pre-malignant condition DNA marker #89.

PN WO200142792-A2.

PD 14-JUN-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 4; Length 256;

Best Local Similarity 59.0%; Pred. No. 0.018;

RESULT 937

ID ACN55002 standard; cDNA; 342 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-A9, SEQ:9783.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 2.9%; Score 49; DB 13; Length 342;

Best Local Similarity 57.5%; Pred. No. 0.02;

RESULT 938

ID ABV58528 standard; cDNA; 347 BP.

DE Human prostate expression marker cDNA 58519.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 347;

Best Local Similarity 57.5%; Pred. No. 0.02;

RESULT 939

ID AAI84446 standard; cDNA; 348 BP.

DE Human polynucleotide SEQ ID NO 4506.

PN WO200164835-A2.

PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 49; DB 4; Length 348;

Best Local Similarity 59.9%; Pred. No. 0.021;

RESULT 940

ID AAI85202 standard; cDNA; 390 BP.

DE Human polynucleotide SEQ ID NO 5262.

PN WO200164835-A2.

PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 49; DB 4; Length 390;

Best Local Similarity 58.6%; Pred. No. 0.022;

RESULT 941

ID ACN53426 standard; cDNA; 403 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-F9, SEQ:8207.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.

Query Match

Best Local Similarity 57.5%; Pred. No. 0.022;

RESULT 942

ID ACH23125 standard; cDNA; 426 BP.

DE Human adult ovary cDNA #1505.

PN US2003073623-A1.

PD 17-APR-2003.

PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

Query Match 2.9%; Score 49; DB 9; Length 426;

Best Local Similarity 58.6%; Pred. No. 0.023;

RESULT 943

ID ABV57380 standard; cDNA; 429 BP.

DE Human prostate expression marker cDNA 57371.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 429;

Best Local Similarity 59.9%; Pred. No. 0.023;

RESULT 944

ID ABV56638 standard; cDNA; 469 BP.

DE Human prostate expression marker cDNA 56629.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 469;

Best Local Similarity 58.6%; Pred. No. 0.024;

RESULT 945

ID ACN51887 standard; cDNA; 469 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 2.9%; Score 49; DB 13; Length 469;

Best Local Similarity 57.5%; Pred. No. 0.024;

RESULT 946

ID ACN58415 standard; cDNA; 469 BP.

DE Cotton gynoeceum tissue EST Clone ID: LIB3829-009-Q6-K6-H8, SEQ:13196.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 2.9%; Score 49; DB 13; Length 469;

Best Local Similarity 57.5%; Pred. No. 0.024;

RESULT 947

ID ABV57020 standard; cDNA; 472 BP.

DE Human prostate expression marker cDNA 57011.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 472;

Best Local Similarity 55.6%; Pred. No. 0.024;

RESULT 948

ID ABV54546 standard; cDNA; 541 BP.

DE Human prostate expression marker cDNA 54537.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 541;

Best Local Similarity 58.6%; Pred. No. 0.026;

RESULT 949

ID ACN53890 standard; cDNA; 547 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 49; DB 13; Length 547;  
Best Local Similarity 56.2%; Pred. No. 0.026;  
RESULT 950  
ID ABQ52063 standard; DNA; 553 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38654.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 553;  
Best Local Similarity 62.3%; Pred. No. 0.026;  
RESULT 951  
ID ABQ52062 standard; DNA; 553 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38653.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 553;  
Best Local Similarity 62.3%; Pred. No. 0.026;  
RESULT 952  
ID ADR63596 standard; cDNA; 1041 BP.  
DE Cotton cDNA sequence, SEQ ID 4377.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 2.9%; Score 49; DB 13; Length 1041;  
Best Local Similarity 58.6%; Pred. No. 0.036;  
RESULT 953  
ID ADQ24168 standard; DNA; 1698 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6988.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 49; DB 12; Length 1698;  
Best Local Similarity 61.2%; Pred. No. 0.046;  
RESULT 954  
ID ADM47920 standard; DNA; 1882 BP.  
DE Polynucleotide sequence #338 useful in producing transgenic plants.  
PN US2003233670-A1.  
PD 18-DEC-2003.  
PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCETTI L B.  
Query Match 2.9%; Score 49; DB 12; Length 1882;  
Best Local Similarity 59.9%; Pred. No. 0.048;  
RESULT 955  
ID AAA23441 standard; cDNA; 1954 BP.  
DE cDNA encoding human secreted protein vc51\_1, SEQ ID NO:37.  
PN WO20011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 2.9%; Score 49; DB 3; Length 1954;  
Best Local Similarity 59.9%; Pred. No. 0.049;  
RESULT 956  
ID ACN88781 standard; DNA; 2024 BP.  
DE Breast cancer related marker, seq id 9931.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.9%; Score 49; DB 11; Length 2024;  
Best Local Similarity 58.6%; Pred. No. 0.05;  
RESULT 957  
ID AAZ43781 standard; cDNA; 2685 BP.  
DE Human fetal brain cDNA clone vb6\_1.

PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 2.9%; Score 49; DB 3; Length 2685;  
Best Local Similarity 59.9%; Pred. No. 0.058;  
RESULT 958  
ID ADQ24699 standard; DNA; 2936 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7519.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 49; DB 12; Length 2936;  
Best Local Similarity 57.5%; Pred. No. 0.06;  
RESULT 959  
ID ADQ24532 standard; DNA; 2936 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7352.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 49; DB 12; Length 2936;  
Best Local Similarity 57.5%; Pred. No. 0.06;  
RESULT 960  
ID ABQ54675 standard; cDNA; 1044 BP.  
DE Human ovarian antigen HVCAR76 cDNA, SEQ ID NO:555.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 49; DB 6; Length 3044;  
Best Local Similarity 59.0%; Pred. No. 0.062;  
RESULT 961  
ID ABLJ3662 standard; DNA; 5845 BP.  
DE Human immune system associated gene SEQ ID NO: 1635.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 5845;  
Best Local Similarity 59.9%; Pred. No. 0.086;  
RESULT 962  
ID ADI45710 standard; DNA; 5930 BP.  
DE Human ovarian cancer DNA marker #19600.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 49; DB 5; Length 5930;  
Best Local Similarity 58.6%; Pred. No. 0.086;  
RESULT 963  
ID ABLJ34058 standard; DNA; 6012 BP.  
DE Human immune system associated gene SEQ ID NO: 2031.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 6012;  
Best Local Similarity 59.9%; Pred. No. 0.087;  
RESULT 964  
ID ABLJ2411 standard; DNA; 6161 BP.  
DE Human immune system associated gene SEQ ID NO: 384.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 6161;  
Best Local Similarity 64.6%; Pred. No. 0.088;  
RESULT 965  
ID ABLJ2806 standard; DNA; 6211 BP.  
DE Human immune system associated gene SEQ ID NO: 779.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 6211;  
Best Local Similarity 59.9%; Pred. No. 0.088;  
RESULT 966  
ID ABLJ3050 standard; DNA; 6522 BP.  
DE Human immune system associated gene SEQ ID NO: 1023.  
PN WO200200928-A2.

PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 6522;  
Best Local Similarity 59.9%; Pred. No. 0.09;  
RESULT 967  
ID ABLJ32118 standard; DNA; 11416 BP.  
DE Human immune system associated gene SEQ ID NO: 91.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 11416;  
Best Local Similarity 59.9%; Pred. No. 0.12;  
RESULT 968  
ID ABL70135 standard; DNA; 11416 BP.  
DE Chemically treated cell signalling DNA sequence#13.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 11416;  
Best Local Similarity 59.9%; Pred. No. 0.12;  
RESULT 969  
ID AAS61063 standard; DNA; 11416 BP.  
DE Human gene regulation-associated gene oligonucleotide #10.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 11416;  
Best Local Similarity 59.9%; Pred. No. 0.12;  
RESULT 970  
ID ABLJ34072 standard; DNA; 40862 BP.  
DE Human immune system associated gene SEQ ID NO: 2045.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 49; DB 6; Length 40862;  
Best Local Similarity 59.9%; Pred. No. 0.23;  
RESULT 971  
ID ADI72102 standard; DNA; 299 BP.  
DE Human ovarian cancer DNA marker #4844.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 299;  
Best Local Similarity 56.0%; Pred. No. 0.021;  
RESULT 972  
ID ADL37251 standard; DNA; 299 BP.  
DE Human ovarian cancer DNA marker #11141.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 299;  
Best Local Similarity 56.0%; Pred. No. 0.021;  
RESULT 973  
ID ABV49426 standard; cDNA; 308 BP.  
DE Human prostate expression marker cDNA 49417.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 308;  
Best Local Similarity 57.1%; Pred. No. 0.022;  
RESULT 974  
ID ABV55289 standard; cDNA; 313 BP.  
DE Human prostate expression marker cDNA 55280.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 313;  
Best Local Similarity 63.8%; Pred. No. 0.022;  
RESULT 975  
ID ABV04395 standard; cDNA; 326 BP.  
DE Human prostate expression marker cDNA 4386.  
PN WO200160860-A2.  
PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 326;  
Best Local Similarity 61.2%; Pred. No. 0.022;  
RESULT 976  
ID AAI89034 standard; cDNA; 413 BP.  
DE Human polynucleotide SEQ ID NO 9094.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.8; DB 4; Length 413;  
Best Local Similarity 57.1%; Pred. No. 0.025;  
RESULT 977  
ID AAI91775 standard; cDNA; 421 BP.  
DE Human polynucleotide SEQ ID NO 11835.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.8; DB 4; Length 421;  
Best Local Similarity 60.6%; Pred. No. 0.026;  
RESULT 978  
ID ACN56150 standard; cDNA; 436 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-D9, SEQ:10931.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.8; DB 13; Length 436;  
Best Local Similarity 53.7%; Pred. No. 0.026;  
RESULT 979  
ID ABV19606 standard; cDNA; 446 BP.  
DE Human prostate expression marker cDNA 19597.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 446;  
Best Local Similarity 59.2%; Pred. No. 0.026;  
RESULT 980  
ID AAI80552 standard; cDNA; 448 BP.  
DE Human polynucleotide SEQ ID NO 612.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.8; DB 4; Length 448;  
Best Local Similarity 59.3%; Pred. No. 0.026;  
RESULT 981  
ID ACN45690 standard; cDNA; 486 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-F5, SEQ:471.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.8; DB 13; Length 486;  
Best Local Similarity 62.1%; Pred. No. 0.027;  
RESULT 982  
ID ABV23693 standard; cDNA; 489 BP.  
DE Human prostate expression marker cDNA 23684.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 489;  
Best Local Similarity 59.3%; Pred. No. 0.028;  
RESULT 983  
ID ABV29562 standard; cDNA; 489 BP.  
DE Human prostate expression marker cDNA 29553.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 489;  
Best Local Similarity 59.3%; Pred. No. 0.028;

RESULT 984  
ID ABV58114 standard; cDNA; 510 BP.  
DE Human prostate expression marker cDNA 58105.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.8; DB 5; Length 510;  
Best Local Similarity 59.3%; Pred. No. 0.028;  
RESULT 985  
ID AAC74364 standard; cDNA; 639 BP.  
DE Human secreted protein gene 28 SEQ ID NO:38.  
PN WO200058340-A2.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 48.8; DB 3; Length 639;  
Best Local Similarity 63.8%; Pred. No. 0.032;  
RESULT 986  
ID AAD05366 standard; cDNA; 655 BP.  
DE Human secreted protein-encoding gene 19 cDNA clone HMLFQ64, SEQ ID NO:77.  
PN WO200134626-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 48.8; DB 4; Length 655;  
Best Local Similarity 62.1%; Pred. No. 0.032;  
RESULT 987  
ID AAH34055 standard; cDNA; 673 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1137.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 48.8; DB 8; Length 836;  
Best Local Similarity 59.3%; Pred. No. 0.036;  
RESULT 988  
ID ABG76269 standard; cDNA; 836 BP.  
DE Human GENSET cDNA clone name NBART.  
PN WO2003014151-A2.  
PD 20-FEB-2003.  
PA (GEST) GENSET SA.  
Query Match 2.9%; Score 48.8; DB 8; Length 836;  
Best Local Similarity 59.3%; Pred. No. 0.036;  
RESULT 989  
ID ADQ22074 standard; DNA; 980 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.8; DB 12; Length 980;  
Best Local Similarity 57.1%; Pred. No. 0.039;  
RESULT 990  
ID AAU70895 standard; cDNA; 1813 BP.  
DE cDNA encoding an allelic variant of human Zcytor5.  
PN WO9849307-A1.  
PD 05-NOV-1998.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 2.9%; Score 48.8; DB 2; Length 1813;  
Best Local Similarity 56.1%; Pred. No. 0.053;  
RESULT 991  
ID ABL33879 standard; DNA; 5378 BP.  
DE Human immune system associated gene SEQ ID NO: 1852.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.8; DB 6; Length 5378;  
Best Local Similarity 57.1%; Pred. No. 0.093;  
RESULT 992  
ID ABQ67094 standard; DNA; 83391 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.8; DB 6; Length 83391;  
Best Local Similarity 58.1%; Pred. No. 0.37;  
RESULT 993

ID ADI72391 standard; DNA; 291 BP.  
DE Human ovarian cancer DNA marker #5133.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.6; DB 5; Length 291;  
Best Local Similarity 52.2%; Pred. No. 0.024;  
RESULT 994  
ID ADL37534 standard; DNA; 291 BP.  
DE Human ovarian cancer DNA marker #11424.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.6; DB 5; Length 291;  
Best Local Similarity 52.2%; Pred. No. 0.024;  
RESULT 995  
ID ABV49069 standard; cDNA; 320 BP.  
DE Human prostate expression marker cDNA 49060.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.6; DB 5; Length 320;  
Best Local Similarity 56.5%; Pred. No. 0.025;  
RESULT 996  
ID AA186367 standard; cDNA; 379 BP.  
DE Human polynucleotide SEQ ID NO 6427.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.6; DB 4; Length 379;  
Best Local Similarity 54.9%; Pred. No. 0.027;  
RESULT 997  
ID ACH19935 standard; cDNA; 423 BP.  
DE Human adult lung cDNA #938.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 2.9%; Score 48.6; DB 9; Length 423;  
Best Local Similarity 52.5%; Pred. No. 0.029;  
RESULT 998  
ID ABV38062 standard; cDNA; 425 BP.  
DE Human prostate expression marker cDNA 38053.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.6; DB 5; Length 425;  
Best Local Similarity 57.6%; Pred. No. 0.029;  
RESULT 999  
ID ABV47755 standard; cDNA; 471 BP.  
DE Human prostate expression marker cDNA 47746.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.6; DB 5; Length 471;  
Best Local Similarity 58.7%; Pred. No. 0.031;  
RESULT 1000  
ID ACN54837 standard; cDNA; 489 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D11, SEQ:9618.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.6; DB 13; Length 489;  
Best Local Similarity 57.6%; Pred. No. 0.031;  
RESULT 1001  
ID ABV17965 standard; cDNA; 816 BP.  
DE Human prostate expression marker cDNA 17956.

PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.6; DB 5; Length 816;  
Best Local Similarity 58.7%; Pred. No. 0.04;  
RESULT 1002  
ID ABA93702 standard; cDNA; 835 BP.  
DE Human signal transduction cDNA clone amy2\_10h17.  
PN WO200198454-A2.  
PD 27-DEC-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 2.9%; Score 48.6; DB 6; Length 835;  
Best Local Similarity 61.4%; Pred. No. 0.041;  
RESULT 1003  
ID AAC98083 standard; cDNA; 1377 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:93.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 48.6; DB 3; Length 1377;  
Best Local Similarity 58.3%; Pred. No. 0.053;  
RESULT 1004  
ID ABX92004 standard; cDNA; 1808 BP.  
DE Lung specific nucleic acid (LSNA) #46.  
PN WO200268633-A2.  
PD 06-SEP-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 2.9%; Score 48.6; DB 6; Length 1808;  
Best Local Similarity 58.7%; Pred. No. 0.06;  
RESULT 1005  
ID AB857347 standard; cDNA; 1851 BP.  
DE cDNA encoding human cancer cell growth suppressing protein PP6068.  
PN CN1351080-A.  
PD 29-MAY-2002.  
PA (SHAN-) SHANGHAI INST ONCOLOGY.  
Query Match 2.9%; Score 48.6; DB 6; Length 1851;  
Best Local Similarity 58.7%; Pred. No. 0.061;  
RESULT 1006  
ID AAD06011 standard; DNA; 2034 BP.  
DE Human neuronal apoptosis regulated candidate (NARC) 10C DNA.  
PN WO200131007-A2.  
PD 03-MAY-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.9%; Score 48.6; DB 4; Length 2034;  
Best Local Similarity 56.6%; Pred. No. 0.064;  
RESULT 1007  
ID ABS6722 standard; cDNA; 2034 BP.  
DE Human NARC10 cDNA.  
PN WO200281516-A2.  
PD 17-OCT-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.9%; Score 48.6; DB 8; Length 2034;  
Best Local Similarity 56.6%; Pred. No. 0.064;  
RESULT 1008  
ID ADJ57918 standard; cDNA; 2034 BP.  
DE Human NARC 10C cDNA.  
PN US2004009553-A1.  
PD 15-JAN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.9%; Score 48.6; DB 12; Length 2034;  
Best Local Similarity 56.6%; Pred. No. 0.064;  
RESULT 1009  
ID AD023617 standard; DNA; 2050 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6437.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.6; DB 12; Length 2050;  
Best Local Similarity 60.0%; Pred. No. 0.064;  
RESULT 1010  
ID ABU32778 standard; DNA; 5532 BP.  
DE Human immune system associated gene SEQ ID NO: 751.  
PN WO200200928-A2.

PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.6; DB 6; Length 5532;  
Best Local Similarity 63.0%; Pred. No. 0.11;  
RESULT 1011  
ID ABL32911 standard; DNA; 8946 BP.  
DE Human immune system associated gene SEQ ID NO: 884.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.6; DB 6; Length 8946;  
Best Local Similarity 57.6%; Pred. No. 0.14;  
RESULT 1012  
ID AAS46704 standard; DNA; 14615 BP.  
DE Tumour suppressor gene derived chemically modified sequence #427.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.6; DB 4; Length 14615;  
Best Local Similarity 57.6%; Pred. No. 0.17;  
RESULT 1013  
ID ABX47137 standard; cDNA; 341 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #12302.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 2.9%; Score 48.4; DB 8; Length 341;  
Best Local Similarity 62.3%; Pred. No. 0.029;  
RESULT 1014  
ID AAI67525 standard; cDNA; 367 BP.  
DE Human polynucleotide SEQ ID NO 7585.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.4; DB 4; Length 367;  
Best Local Similarity 64.0%; Pred. No. 0.03;  
RESULT 1015  
ID AAI84785 standard; cDNA; 388 BP.  
DE Human polynucleotide SEQ ID NO 4845.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.4; DB 4; Length 388;  
Best Local Similarity 60.8%; Pred. No. 0.031;  
RESULT 1016  
ID ADL43635 standard; DNA; 388 BP.  
DE Human ovarian cancer DNA marker #17525.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.4; DB 5; Length 388;  
Best Local Similarity 57.1%; Pred. No. 0.031;  
RESULT 1017  
ID AAI89093 standard; cDNA; 415 BP.  
DE Human polynucleotide SEQ ID NO 9153.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.4; DB 4; Length 415;  
Best Local Similarity 65.4%; Pred. No. 0.032;  
RESULT 1018  
ID ABV56837 standard; cDNA; 432 BP.  
DE Human prostate expression marker cDNA 56828.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.4; DB 5; Length 432;  
Best Local Similarity 64.0%; Pred. No. 0.033;  
RESULT 1019  
ID ABX47746 standard; cDNA; 442 BP.



DE Bovine EST associated with lactation/muscle/fat deposition #12911.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 2.9%; Score 48.4; DB 8; Length 442;  
Best Local Similarity 66.0%; Pred. No. 0.033;  
RESULT 1020  
ID ABV56778 standard; cDNA; 451 BP.  
DE Human prostate expression marker cDNA 56769.  
FN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.4; DB 5; Length 451;  
Best Local Similarity 60.8%; Pred. No. 0.034;  
RESULT 1021  
ID ACN45855 standard; cDNA; 608 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-009-Q1-K6-G7, SEQ:636.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.4; DB 13; Length 608;  
Best Local Similarity 57.1%; Pred. No. 0.039;  
RESULT 1022  
ID ACN53565 standard; cDNA; 619 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-C10, SEQ:8346.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.4; DB 13; Length 619;  
Best Local Similarity 57.1%; Pred. No. 0.04;  
RESULT 1023  
ID AA59475 standard; DNA; 1117 BP.  
DE Nucleotide sequence of a soybean type III glutathione-S-transferase.  
FN WO200047728-A2.  
PD 17-AUG-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 2.9%; Score 48.4; DB 3; Length 1117;  
Best Local Similarity 58.6%; Pred. No. 0.053;  
RESULT 1024  
ID ADQ22714 standard; DNA; 1661 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5534.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.4; DB 12; Length 1661;  
Best Local Similarity 68.4%; Pred. No. 0.065;  
RESULT 1025  
ID ADH72103 standard; DNA; 2136 BP.  
DE Human gene of the invention NOV43b SEQ ID NO:999.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 12; Length 2136;  
Best Local Similarity 49.4%; Pred. No. 0.074;  
RESULT 1026  
ID ACAL0119 standard; cDNA; 2153 BP.  
DE Human NOVX polynucleotide #9.  
FN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 8; Length 2153;  
Best Local Similarity 49.4%; Pred. No. 0.074;  
RESULT 1027  
ID ADH72101 standard; DNA; 2153 BP.  
DE Human gene of the invention NOV43a SEQ ID NO:997.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 12; Length 2153;  
Best Local Similarity 49.4%; Pred. No. 0.074;  
RESULT 1028  
ID ADO08270 standard; cDNA; 2153 BP.  
DE Human NOVX polynucleotide #9.  
FN US2004018594-A1.  
PD 29-JAN-2004.  
PA (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CASM/) CASMAN S J.  
PA (CHAP/) CHAPOVAL A.  
PA (EDIN/) EDINGER S R.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUNT/) GUNTHER E.  
PA (GUOX/) GUO X S.  
PA (KEKU/) KEKUDA R.  
PA (LEPL/) LEPLEY D M.  
PA (LILL/) LI L.  
PA (LIUX/) LIU X.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLER C E.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENNA C E A.  
PA (RIEG/) RIEGER D K.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (SPYT/) SPYTEK K A.  
PA (TAUP/) TAUPIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
Query Match 2.9%; Score 48.4; DB 12; Length 2153;  
Best Local Similarity 49.4%; Pred. No. 0.074;  
RESULT 1029  
ID ADQ25384 standard; DNA; 2176 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8204.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.4; DB 12; Length 2176;  
Best Local Similarity 58.2%; Pred. No. 0.075;  
RESULT 1030  
ID ADO22511 standard; DNA; 2179 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5331.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.4; DB 12; Length 2179;  
Best Local Similarity 60.8%; Pred. No. 0.075;  
RESULT 1031  
ID ADQ22185 standard; DNA; 2857 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5005.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.4; DB 12; Length 2857;  
Best Local Similarity 57.8%; Pred. No. 0.086;  
RESULT 1032  
ID AAS68120 standard; cDNA; 3910 BP.  
DE DNA encoding novel human diagnostic protein #3924.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.4; DB 5; Length 3910;

Best Local Similarity 49.4%; Pred. No. 0.1;  
RESULT 1033  
ID ADQ23023 standard; DNA; 4046 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5843.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.4; DB 12; Length 4046;  
Best Local Similarity 58.2%; Pred. No. 0.1;  
RESULT 1034  
ID AA172024 standard; cDNA; 4073 BP.  
DE Human thrombospondin protein, BTL012, coding sequence.  
PN WO200174852-A2.  
PD 11-OCT-2001.  
PA (FARB) BAYER CORP.  
Query Match 2.9%; Score 48.4; DB 6; Length 4073;  
Best Local Similarity 49.4%; Pred. No. 0.1;  
RESULT 1035  
ID ADB54096 standard; DNA; 4316 BP.  
DE Pretreated genomic DNA region 20.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 10; Length 4316;  
Best Local Similarity 62.3%; Pred. No. 0.11;  
RESULT 1036  
ID ADB54224 standard; DNA; 4316 BP.  
DE Pretreated genomic DNA region 148.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 10; Length 4316;  
Best Local Similarity 62.3%; Pred. No. 0.11;  
RESULT 1037  
ID ADS89522 standard; DNA; 4316 BP.  
DE Oligonucleotide of the invention SEQ ID NO:538.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 13; Length 4316;  
Best Local Similarity 62.3%; Pred. No. 0.11;  
RESULT 1038  
ID ADS89248 standard; DNA; 4316 BP.  
DE Oligonucleotide of the invention SEQ ID NO:264.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 13; Length 4316;  
Best Local Similarity 62.3%; Pred. No. 0.11;  
RESULT 1039  
ID ABL32921 standard; DNA; 5195 BP.  
DE Human immune system associated gene SEQ ID NO: 894.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 5195;  
Best Local Similarity 62.3%; Pred. No. 0.12;  
RESULT 1040  
ID ADL9396 standard; cDNA; 5877 BP.  
DE Human G-coupled protein receptor-related gene #44.  
PN US2004006205-A1.  
PD 08-JAN-2004.  
PA (LILU) LI L.  
PA (GERL) GERLACH V.  
PA (LIUX) LIU X.  
PA (MILL) MILLER C E.  
PA (SPYT) SPYTEK K A.  
PA (ZERH) ZERHUSEN B D.  
PA (PENA) PENA C E A.  
PA (SHEN) SHENOY S G.  
PA (ZHON) ZHONG H.  
PA (SMIT) SMITHSON G.  
PA (CASM) CASMAN S J.

(BOLD/) BOLDOG F L.  
PA (VOSS/) VOSS E Z.  
PA (VERN/) VERNET C A.  
PA (MACD/) MACDOUGALL J R.  
PA (RAST/) RASTELLI L.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (MEZE/) MEZES P S.  
PA (FURT/) FURTAK K.  
PA (PATI/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (MALY/) MALYANKAR U M.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (EDIN/) EDINGER S.  
PA (MAZU/) MAZUR A.  
Query Match 2.9%; Score 48.4; DB 12; Length 5877;  
Best Local Similarity 49.4%; Pred. No. 0.12;  
RESULT 1041  
ID ADL16057 standard; DNA; 5935 BP.  
DE G-coupled protein receptor related polypeptide DNA, SEQ ID NO 87.  
PN WO200283841-A2.  
PD 24-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 10; Length 5935;  
Best Local Similarity 49.4%; Pred. No. 0.12;  
RESULT 1042  
ID ABL33679 standard; DNA; 6070 BP.  
DE Human immune system associated gene SEQ ID NO: 1652.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6070;  
Best Local Similarity 54.5%; Pred. No. 0.13;  
RESULT 1043  
ID ABL34579 standard; DNA; 6070 BP.  
DE Human metastasis associated gene SEQ ID NO: 132.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6070;  
Best Local Similarity 54.5%; Pred. No. 0.13;  
RESULT 1044  
ID ABL70372 standard; DNA; 6070 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#131.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6070;  
Best Local Similarity 54.5%; Pred. No. 0.13;  
RESULT 1045  
ID ABQ67130 standard; DNA; 6070 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 160.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6070;  
Best Local Similarity 54.5%; Pred. No. 0.13;  
RESULT 1046  
ID ADS99840 standard; DNA; 6070 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #66.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 2.9%; Score 48.4; DB 7; Length 6070;  
Best Local Similarity 54.5%; Pred. No. 0.13;  
RESULT 1047  
ID ABX56304 standard; DNA; 6343 BP.  
DE Human NOV25c CG56914-03 DNA SEQ ID 87.  
PN WO200281625-A2.  
PD 17-OCT-2002.

PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 8; Length 6343;  
Best Local Similarity 49.4%; Pred. No. 0.13;  
RESULT 1048  
ID ADH72107 standard; DNA; 6343 BP.  
DE Human gene of the invention NOV43d SEQ ID NO:1003.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 12; Length 6343;  
Best Local Similarity 49.4%; Pred. No. 0.13;  
RESULT 1049  
ID ABL33356 standard; DNA; 6577 BP.  
DE Human immune system associated gene SEQ ID NO: 1329.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6577;  
Best Local Similarity 58.2%; Pred. No. 0.13;  
RESULT 1050  
ID ABL70561 standard; DNA; 6577 BP.  
DE Chemically treated cell signalling DNA sequence#226.  
FN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6577;  
Best Local Similarity 58.2%; Pred. No. 0.13;  
RESULT 1051  
ID AA861221 standard; DNA; 6577 BP.  
DE Human gene regulation-associated gene oligonucleotide #176.  
FN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6577;  
Best Local Similarity 58.2%; Pred. No. 0.13;  
RESULT 1052  
ID ABK34027 standard; DNA; 6944 BP.  
DE Human DNA for staging of Astrocytomas, complement, #57.  
FN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 6944;  
Best Local Similarity 62.3%; Pred. No. 0.13;  
RESULT 1053  
ID ADA20447 standard; DNA; 6944 BP.  
DE Prostate tumour related genomic DNA complement sample #56.  
FN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 8; Length 6944;  
Best Local Similarity 62.3%; Pred. No. 0.13;  
RESULT 1054  
ID AD484254 standard; DNA; 6944 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.  
FN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 8; Length 6944;  
Best Local Similarity 62.3%; Pred. No. 0.13;  
RESULT 1055  
ID ADQ22776 standard; DNA; 7281 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5596.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.4; DB 12; Length 7281;  
Best Local Similarity 57.1%; Pred. No. 0.14;  
RESULT 1056  
ID ADS89706 standard; DNA; 7467 BP.  
DE Oligonucleotide of the invention SEQ ID NO:722.  
FN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.9%; Score 48.4; DB 13; Length 7467;  
Best Local Similarity 60.8%; Pred. No. 0.14;  
RESULT 1057  
ID ADK60477 standard; DNA; 8546 BP.  
DE Angiogenesis differentially expressed gene GS-N52.  
FN FR283687-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 2.9%; Score 48.4; DB 12; Length 8546;  
Best Local Similarity 49.4%; Pred. No. 0.15;  
RESULT 1058  
ID ADK60778 standard; DNA; 8546 BP.  
DE Angiogenesis differentially expressed gene GS-N52.  
FN FR283686-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 2.9%; Score 48.4; DB 12; Length 8546;  
Best Local Similarity 49.4%; Pred. No. 0.15;  
RESULT 1059  
ID ADP73100 standard; DNA; 8546 BP.  
DE Angiogenesis inhibitor human DNA sequence, GS-N52.  
FN FR2843753-A1.  
PD 27-FEB-2004.  
PA (GENE/) GENE S.  
PA (ALMS/) AL M S.  
Query Match 2.9%; Score 48.4; DB 12; Length 8546;  
Best Local Similarity 49.4%; Pred. No. 0.15;  
RESULT 1060  
ID ADS09799 standard; DNA; 8546 BP.  
DE Human therapeutic DNA - SEQ ID 36.  
FN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 2.9%; Score 48.4; DB 13; Length 8546;  
Best Local Similarity 49.4%; Pred. No. 0.15;  
RESULT 1061  
ID ABL33068 standard; DNA; 9117 BP.  
DE Human immune system associated gene SEQ ID NO: 1041.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 6; Length 9117;  
Best Local Similarity 62.3%; Pred. No. 0.15;  
RESULT 1062  
ID ADF50896 standard; DNA; 11097 BP.  
DE Chemically modified promoter region of human melastatin gene (SeqID 4).  
FN EPI344832-A1.  
PD 17-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 10; Length 11097;  
Best Local Similarity 62.3%; Pred. No. 0.17;  
RESULT 1063  
ID ADF50894 standard; DNA; 11097 BP.  
DE Chemically modified promoter region of human melastatin gene (SeqID 2).  
FN EPI344832-A1.  
PD 17-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.4; DB 10; Length 11097;  
Best Local Similarity 62.3%; Pred. No. 0.17;  
RESULT 1064  
ID AD008272 standard; cDNA; 15659 BP.  
DE Human NOVX polynucleotide #10.  
FN US2004018594-A1.  
PD 29-JAN-2004.  
PA (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CASM/) CASMAN S J.  
PA (CHAP/) CHAPOVAL A.  
PA (EDIN/) EDINGER S R.

PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUNT/) GUNTHER E.  
PA (GUOX/) GUO X S.  
PA (KEKU/) KEKUDA R.  
PA (LEPL/) LEFLEY D M.  
PA (LILL/) LI L.  
PA (LIUX/) LIU X.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLER C E.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATI/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (RIEG/) RIEGER D K.  
PA (SHEN/) SHENOV S G.  
PA (SHIM/) SHIMKETS R A.  
PA (SPYT/) SPYTEK K A.  
PA (TAUP/) TAUPIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZSRH/) ZERHUSEN B D.  
Query Match 2.9%; Score 48.4; DB 12; Length 15659;  
Best Local Similarity 49.4%; Pred. No. 0.2;  
RESULT 1065  
ID ACA10120 standard; cDNA; 15660 BP.  
DE Human NOVX polynucleotide #10.  
PN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 8; Length 15660;  
Best Local Similarity 49.4%; Pred. No. 0.2;  
RESULT 1066  
ID ADH72105 standard; DNA; 15660 BP.  
DE Human gene of the invention NOV43c SEQ ID NO:1001.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 2.9%; Score 48.4; DB 12; Length 15660;  
Best Local Similarity 49.4%; Pred. No. 0.2;  
RESULT 1067  
ID ABQ86156 standard; DNA; 16908 BP.  
DE Novel human gene. SEQ ID 27.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SWIK ) SMITHKLINE BEECHAM CORP.  
PA (SWIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 2.9%; Score 48.4; DB 6; Length 16908;  
Best Local Similarity 49.4%; Pred. No. 0.21;  
RESULT 1068  
ID ADK60455 standard; DNA; 18207 BP.  
DE Angiogenesis differentially expressed gene GS-N29.  
PN FR2836687-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 2.9%; Score 48.4; DB 12; Length 18207;  
Best Local Similarity 49.4%; Pred. No. 0.22;  
RESULT 1069  
ID ADK60756 standard; DNA; 18207 BP.  
DE Angiogenesis differentially expressed gene GS-N29.  
PN FR2836686-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Query Match 2.9%; Score 48.4; DB 12; Length 18207;  
Best Local Similarity 49.4%; Pred. No. 0.22;  
RESULT 1070  
ID ADP73078 standard; DNA; 18207 BP.  
DE Angiogenesis inhibitor human DNA sequence, GS-N29.  
PN FR2843753-A1.  
PD 27-FEB-2004.

PA (GENE/) GENE S.  
PA (ALMS/) AL M S.  
Query Match 2.9%; Score 48.4; DB 12; Length 18207;  
Best Local Similarity 49.4%; Pred. No. 0.22;  
RESULT 1071  
ID ADQ22570 standard; DNA; 18248 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.4; DB 12; Length 18248;  
Best Local Similarity 49.4%; Pred. No. 0.22;  
RESULT 1072  
ID ABL37453 standard; cDNA; 153 BP.  
DE Human colon tumour antigen polynucleotide SEQ ID NO:1042.  
PN WO200196388-A2.  
PD 20-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 2.9%; Score 48.2; DB 6; Length 153;  
Best Local Similarity 59.3%; Pred. No. 0.022;  
RESULT 1073  
ID AAH70080 standard; cDNA; 268 BP.  
DE Human cervical cancer marker nucleic acid 1354.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.2; DB 4; Length 268;  
Best Local Similarity 51.9%; Pred. No. 0.029;  
RESULT 1074  
ID ACN45531 standard; cDNA; 272 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-K6-E5, SEQ:312.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.2; DB 13; Length 272;  
Best Local Similarity 63.2%; Pred. No. 0.03;  
RESULT 1075  
ID ABV58763 standard; cDNA; 317 BP.  
DE Human prostate expression marker cDNA 58754.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.2; DB 5; Length 317;  
Best Local Similarity 57.7%; Pred. No. 0.032;  
RESULT 1076  
ID ACN50558 standard; cDNA; 325 BP.  
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-K6-E8, SEQ:5339.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.2; DB 13; Length 325;  
Best Local Similarity 62.2%; Pred. No. 0.032;  
RESULT 1077  
ID AAL23694 standard; cDNA; 359 BP.  
DE Human breast cancer expressed polynucleotide 16151.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.2; DB 4; Length 359;  
Best Local Similarity 61.6%; Pred. No. 0.034;  
RESULT 1078  
ID ADL37765 standard; DNA; 385 BP.  
DE Human ovarian cancer DNA marker #11655.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.2; DB 5; Length 385;

Best Local Similarity 53.5%; Pred. No. 0.035;  
RESULT 1079  
ID ADI72626 standard; DNA; 385 BP.  
DE Human ovarian cancer DNA marker #5368.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.2; DB 5; Length 385;  
Best Local Similarity 53.5%; Pred. No. 0.035;  
RESULT 1080  
ID AAI84791 standard; cDNA; 390 BP.  
DE Human polynucleotide SEQ ID NO 4851.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.2; DB 4; Length 390;  
Best Local Similarity 57.7%; Pred. No. 0.035;  
RESULT 1081  
ID AAI83999 standard; cDNA; 411 BP.  
DE Human polynucleotide SEQ ID NO 4059.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.2; DB 4; Length 411;  
Best Local Similarity 60.2%; Pred. No. 0.036;  
RESULT 1082  
ID AAI88617 standard; cDNA; 416 BP.  
DE Human polynucleotide SEQ ID NO 8677.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.2; DB 4; Length 416;  
Best Local Similarity 58.9%; Pred. No. 0.037;  
RESULT 1083  
ID AAI89032 standard; cDNA; 416 BP.  
DE Human polynucleotide SEQ ID NO 9092.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48.2; DB 4; Length 416;  
Best Local Similarity 61.6%; Pred. No. 0.037;  
RESULT 1084  
ID ABV49374 standard; cDNA; 453 BP.  
DE Human prostate expression marker cDNA 49365.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.2; DB 5; Length 453;  
Best Local Similarity 63.2%; Pred. No. 0.038;  
RESULT 1085  
ID ACN57722 standard; cDNA; 492 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-005-Q6-N6-B12, SEQ:12503.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.2; DB 13; Length 492;  
Best Local Similarity 60.2%; Pred. No. 0.04;  
RESULT 1086  
ID ABV57520 standard; cDNA; 504 BP.  
DE Human prostate expression marker cDNA 57511.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48.2; DB 5; Length 504;  
Best Local Similarity 58.9%; Pred. No. 0.04;  
RESULT 1087  
ID ACN55029 standard; cDNA; 518 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-D8, SEQ:9810.  
PN US2004123340-A1.  
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.2; DB 13; Length 518;  
Best Local Similarity 55.3%; Pred. No. 0.041;  
RESULT 1088  
ID ACN60563 standard; cDNA; 585 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-K6-B11, SEQ:15344.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.2; DB 13; Length 585;  
Best Local Similarity 56.7%; Pred. No. 0.043;  
RESULT 1089  
ID ACN62771 standard; cDNA; 594 BP.  
DE Cotton carpel wall/septum EST Clone ID: LIB3831-001-Q1-K6-CS, SEQ:17552.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48.2; DB 13; Length 594;  
Best Local Similarity 61.6%; Pred. No. 0.044;  
RESULT 1090  
ID AAD34114 standard; cDNA; 921 BP.  
DE Human secreted protein-encoding gene 9 cDNA clone HB8NQ42, SEQ ID NO:19.  
PN WO200222654-A1.  
PD 21-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 48.2; DB 6; Length 921;  
Best Local Similarity 63.2%; Pred. No. 0.055;  
RESULT 1091  
ID AAD54409 standard; cDNA; 990 BP.  
DE Lolium perenne defensin a (LpDEPa) cDNA.  
PN WO200288359-A1.  
PD 07-NOV-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 2.9%; Score 48.2; DB 8; Length 990;  
Best Local Similarity 54.1%; Pred. No. 0.057;  
RESULT 1092  
ID AAL57070 standard; DNA; 1040 BP.  
DE Human G-protein coupled receptor GAVE18 DNA sequence.  
PN WO2003042399-A2.  
PD 22-MAY-2003.  
PA (AVET) AVENTIS PHARM INC.  
Query Match 2.9%; Score 48.2; DB 9; Length 1040;  
Best Local Similarity 63.2%; Pred. No. 0.058;  
RESULT 1093  
ID ADG73631 standard; cDNA; 1259 BP.  
DE Human cDNA of the invention SEQ ID NO:16.  
PN CN1369506-A.  
PD 18-SEP-2002.  
PA (SHAN-) SHANGHAI INST ONCOLOGY.  
Query Match 2.9%; Score 48.2; DB 10; Length 1259;  
Best Local Similarity 65.1%; Pred. No. 0.064;  
RESULT 1094  
ID ADF94940 standard; cDNA; 1311 BP.  
DE Human gene 8-derived ACRP30-like cDNA, SEQ ID NO:36.  
PN WO2003031586-A2.  
PD 17-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (BLON-) BLONDEL O.  
PA (RUBE/) RUBEN S M.  
Query Match 2.9%; Score 48.2; DB 10; Length 1311;  
Best Local Similarity 62.2%; Pred. No. 0.065;  
RESULT 1095  
ID ABS53034 standard; DNA; 2038 BP.

DE Arabidopsis thaliana squalene epoxidase polynucleotide #4.  
PN WO200261072-A2.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match 2.9%; Score 48.2; DB 6; Length 2038;  
Best Local Similarity 58.9%; Pred. No. 0.082;  
RESULT 1096  
ID AD023275 standard; DNA; 3056 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6095.  
PN WO200404838-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.9%; Score 48.2; DB 12; Length 3056;  
Best Local Similarity 63.2%; Pred. No. 0.1;  
RESULT 1097  
ID ABL33751 standard; DNA; 7037 BP.  
DE Human immune system associated gene SEQ ID NO: 1724.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.2; DB 6; Length 7037;  
Best Local Similarity 60.2%; Pred. No. 0.15;  
RESULT 1098  
ID ABL32448 standard; DNA; 7238 BP.  
DE Human immune system associated gene SEQ ID NO: 421.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.2; DB 6; Length 7238;  
Best Local Similarity 60.2%; Pred. No. 0.16;  
RESULT 1099  
ID ABL32332 standard; DNA; 8895 BP.  
DE Human immune system associated gene SEQ ID NO: 305.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.2; DB 6; Length 8895;  
Best Local Similarity 58.9%; Pred. No. 0.17;  
RESULT 1100  
ID ABL34492 standard; DNA; 11996 BP.  
DE Human metastasis associated gene SEQ ID NO: 45.  
PN WO20017376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.9%; Score 48.2; DB 6; Length 11996;  
Best Local Similarity 65.1%; Pred. No. 0.2;  
RESULT 1101  
ID ADS99753 standard; DNA; 11996 BP.  
DE Bisulphite treated human gene associated with metastasis #23.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 2.9%; Score 48.2; DB 7; Length 11996;  
Best Local Similarity 65.1%; Pred. No. 0.2;  
RESULT 1102  
ID ACH50958 standard; CDNA; 139 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-002-Q1-N6-E3, SEQ:5739.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 2.9%; Score 48; DB 13; Length 139;  
Best Local Similarity 64.3%; Pred. No. 0.024;  
RESULT 1103  
ID ABX46273 standard; CDNA; 239 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11438.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 2.9%; Score 48; DB 8; Length 239;  
Best Local Similarity 59.6%; Pred. No. 0.031;  
RESULT 1104  
ID ABX42739 standard; CDNA; 241 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #7904.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 2.9%; Score 48; DB 8; Length 241;  
Best Local Similarity 59.6%; Pred. No. 0.031;  
RESULT 1105  
ID ADS72366 standard; CDNA; 269 BP.  
DE Human kidney tumour specific CDNA, SEQ ID 963.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 2.9%; Score 48; DB 7; Length 269;  
Best Local Similarity 56.2%; Pred. No. 0.033;  
RESULT 1106  
ID ABX43930 standard; CDNA; 283 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #9095.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 2.9%; Score 48; DB 8; Length 283;  
Best Local Similarity 64.3%; Pred. No. 0.034;  
RESULT 1107  
ID ABV56758 standard; CDNA; 323 BP.  
DE Human prostate expression marker CDNA 56749.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.9%; Score 48; DB 5; Length 323;  
Best Local Similarity 56.2%; Pred. No. 0.036;  
RESULT 1108  
ID ABX38490 standard; CDNA; 373 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3655.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 2.9%; Score 48; DB 8; Length 373;  
Best Local Similarity 58.3%; Pred. No. 0.039;  
RESULT 1109  
ID AAI89019 standard; CDNA; 386 BP.  
DE Human polynucleotide SEQ ID NO 9079.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48; DB 4; Length 386;  
Best Local Similarity 64.3%; Pred. No. 0.04;  
RESULT 1110  
ID AAI85430 standard; CDNA; 401 BP.  
DE Human polynucleotide SEQ ID NO 5490.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 2.9%; Score 48; DB 4; Length 401;  
Best Local Similarity 55.6%; Pred. No. 0.041;  
RESULT 1111  
ID AAI85304 standard; CDNA; 404 BP.  
DE Human polynucleotide SEQ ID NO 5364.

PN WO2000164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 2.9%; Score 48; DB 4; Length 404;  
 Best Local Similarity 64.3%; Pred. No. 0.041;  
 RESULT 1112  
 ID AA183194 standard; cDNA; 407 BP.  
 DE Human polynucleotide SEQ ID NO 3254.  
 PN WO2000164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 2.9%; Score 48; DB 4; Length 407;  
 Best Local Similarity 64.3%; Pred. No. 0.041;  
 RESULT 1113  
 ID AA183744 standard; cDNA; 408 BP.  
 DE Human polynucleotide SEQ ID NO 3804.  
 PN WO2000164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 2.9%; Score 48; DB 4; Length 408;  
 Best Local Similarity 57.9%; Pred. No. 0.041;  
 RESULT 1114  
 ID ABV59282 standard; cDNA; 452 BP.  
 DE Human prostate expression marker cDNA 59273.  
 PN WO2000160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 2.9%; Score 48; DB 5; Length 452;  
 Best Local Similarity 64.3%; Pred. No. 0.043;  
 RESULT 1115  
 ID AA182085 standard; cDNA; 466 BP.  
 DE Human polynucleotide SEQ ID NO 2145.  
 PN WO2000164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 2.9%; Score 48; DB 4; Length 466;  
 Best Local Similarity 64.3%; Pred. No. 0.044;  
 RESULT 1116  
 ID AA188612 standard; cDNA; 478 BP.  
 DE Human polynucleotide SEQ ID NO 8672.  
 PN WO2000164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 2.9%; Score 48; DB 4; Length 478;  
 Best Local Similarity 64.3%; Pred. No. 0.044;  
 RESULT 1117  
 ID ACN61416 standard; cDNA; 490 BP.  
 DE Cotton gynoeceum tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FING/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 2.9%; Score 48; DB 13; Length 490;  
 Best Local Similarity 49.6%; Pred. No. 0.045;  
 RESULT 1118  
 ID ABV58419 standard; cDNA; 515 BP.  
 DE Human prostate expression marker cDNA 58410.  
 PN WO2000160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 2.9%; Score 48; DB 5; Length 515;  
 Best Local Similarity 56.2%; Pred. No. 0.046;  
 RESULT 1119  
 ID ABV57482 standard; cDNA; 533 BP.  
 DE Human prostate expression marker cDNA 57473.  
 PN WO2000160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 2.9%; Score 48; DB 5; Length 533;  
 Best Local Similarity 56.2%; Pred. No. 0.047;  
 RESULT 1120

ID ABV58372 standard; cDNA; 540 BP.  
 DE Human prostate expression marker cDNA 58363.  
 PN WO2000160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 2.9%; Score 48; DB 5; Length 540;  
 Best Local Similarity 56.2%; Pred. No. 0.047;  
 RESULT 1121  
 ID ABV58085 standard; cDNA; 585 BP.  
 DE Human prostate expression marker cDNA 58076.  
 PN WO2000160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 2.9%; Score 48; DB 5; Length 585;  
 Best Local Similarity 56.2%; Pred. No. 0.049;  
 RESULT 1122  
 ID ADF76609 standard; cDNA; 602 BP.  
 DE Novel human secreted and transmembrane protein cDNA SeqID 283.  
 PN WO2003072035-A2.  
 PD 04-SEP-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 2.9%; Score 48; DB 10; Length 602;  
 Best Local Similarity 60.9%; Pred. No. 0.05;  
 RESULT 1123  
 ID ADJ83210 standard; cDNA; 602 BP.  
 DE Human PRO52174 cDNA, SEQ ID 412.  
 PN WO2004024097-A2.  
 PD 25-MAR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 2.9%; Score 48; DB 12; Length 602;  
 Best Local Similarity 60.9%; Pred. No. 0.05;  
 RESULT 1124  
 ID ADJ91506 standard; cDNA; 602 BP.  
 DE Human immune-related polypeptide PRO52174-encoding cDNA, SEQ ID NO:21.  
 PN WO2004024072-A2.  
 PD 25-MAR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 2.9%; Score 48; DB 12; Length 602;  
 Best Local Similarity 60.9%; Pred. No. 0.05;  
 RESULT 1125  
 ID ADM41666 standard; cDNA; 602 BP.  
 DE PRO52174 cDNA, associated with B-cell activation.  
 PN WO2004024069-A2.  
 PD 25-MAR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 2.9%; Score 48; DB 12; Length 602;  
 Best Local Similarity 60.9%; Pred. No. 0.05;  
 RESULT 1126  
 ID ABV43916 standard; cDNA; 606 BP.  
 DE Human prostate expression marker cDNA 43907.  
 PN WO2000160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 2.9%; Score 48; DB 5; Length 606;  
 Best Local Similarity 58.3%; Pred. No. 0.05;  
 RESULT 1127  
 ID ACN54555 standard; cDNA; 627 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-K6-C2, SEQ:9336.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FING/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 2.9%; Score 48; DB 13; Length 627;  
 Best Local Similarity 64.3%; Pred. No. 0.051;  
 RESULT 1128  
 ID ADP04748 standard; cDNA; 1352 BP.  
 DE Sea squirt cDNA with tissue specific expression in development Seq 343.  
 PN JP200405129-A.  
 PD 26-FEB-2004.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Query Match 2.9%; Score 48; DB 12; Length 1352;

Best Local Similarity 59.6%; Pred. No. 0.075;  
RESULT 1129  
ID ADG32734 standard; DNA; 1483 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID58.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 2.9%; Score 48; DB 10; Length 1483;  
Best Local Similarity 59.6%; Pred. No. 0.079;  
RESULT 1130  
ID AAI72316 standard; cDNA; 1637 BP.  
DE Human transporter protein cDNA.  
PN WO2002026335-A2.  
PD 10-JAN-2002.  
PA (APPL-) APPLERA CORP.  
Query Match 2.9%; Score 48; DB 6; Length 1637;  
Best Local Similarity 58.3%; Pred. No. 0.083;  
RESULT 1131  
ID AAZ90632 standard; DNA; 1690 BP.  
DE Human adipose tissue protein #2 encoding DNA.  
PN JP2000037190-A.  
PD 08-FEB-2000.  
PA (NLSB-) JAPAN TOBACCO INC.  
Query Match 2.9%; Score 48; DB 3; Length 1690;  
Best Local Similarity 64.3%; Pred. No. 0.084;  
RESULT 1132  
ID AAD32523 standard; DNA; 1726 BP.  
DE Human B7-H10 Gene.  
PN WO200202587-A1.  
PD 10-JAN-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 2.9%; Score 48; DB 6; Length 1726;  
Best Local Similarity 59.6%; Pred. No. 0.085;  
RESULT 1133  
ID AAX52252 standard; DNA; 1984 BP.  
DE Protein PRO271 cDNA clone DNA39423-1182.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 2; Length 1984;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1134  
ID ADC78532 standard; cDNA; 1984 BP.  
DE Human PRO271 cDNA.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 3; Length 1984;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1135  
ID ADR18008 standard; cDNA; 1984 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.

PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.9%; Score 48; DB 13; Length 1984;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1136  
ID AAF72410 standard; cDNA; 1985 BP.  
DE Human PRO271 cDNA.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 4; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1137  
ID AAS45938 standard; cDNA; 1985 BP.  
DE Human DNA encoding PRO polypeptide sequence #14.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1138  
ID ACA60174 standard; cDNA; 1985 BP.  
DE Human cDNA for secreted/transmembrane protein PRO271.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1139  
ID ACA89388 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1140  
ID ACA73398 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1141  
ID ACA05713 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1142  
ID ACA66547 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO protein #14.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1143  
ID ACD07574 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH-) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1144  
ID ACF20122 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.



PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1145  
ID AC88596 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1146  
ID ACD21796 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1147  
ID ACF12961 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1148  
ID ACD25064 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1149  
ID ACF00113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1150  
ID ACA72170 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1151  
ID ACD04694 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1152  
ID ACD18155 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1153  
ID ACD08162 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1154  
ID ABX71622 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO271.  
PN US2002132240-A1.  
PD 19-SEP-2002.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1155  
ID ACA88596 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1156  
ID ACA70038 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1157  
ID ACD12260 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1158  
ID ACC74175 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1159  
ID ACD15803 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1160  
ID ACD25371 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1161  
ID ACD17848 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1162  
ID ACC88135 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1163  
ID ACD21489 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;  
RESULT 1164  
ID ACD18556 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1165  
ID ACH06954 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane polypeptide PRO271 cDNA.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1166  
ID ABX98166 standard; cDNA; 1985 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1167  
ID ACD13917 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1168  
ID AC009697 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1169  
ID ACC88442 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1170  
ID ACD21182 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1171  
ID ABX75554 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO271.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1172  
ID ABX97757 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1173  
ID ACA97233 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1174  
ID ACA57696 standard; cDNA; 1985 BP.  
DE Human PRO271 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1175  
ID ACD14224 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1176  
ID ACC91007 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1177  
ID ACC88749 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1178  
ID ACD06946 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US200308353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1179  
ID ACA67397 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1180  
ID ACC81452 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1181  
ID ACC89056 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1182  
ID ACC86412 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1183  
ID ACC89670 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1184  
ID ACC92849 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1185  
ID ACA72477 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1186  
ID ACA88995 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1187  
ID ACA69731 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1188  
ID ACA96874 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1189  
ID ACA90870 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1190  
ID ACA70652 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1191  
ID ACA95162 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1192  
ID ACC86105 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1193  
ID ACC89977 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1194  
ID ACD12585 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1195  
ID ACF19815 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1196  
ID ABX76759 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1197  
ID ABX96191 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1198  
ID ACA73091 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1199  
ID ACA05512 standard; cDNA; 1985 BP.  
DE cDNA encoding human secreted protein PRO271.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1200  
ID ACA68634 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1201  
ID ACA74478 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1202  
ID ACA70345 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1203  
ID ACD14531 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1204  
ID ACD20179 standard; cDNA; 1985 BP.  
DE Human secreted / transmembrane polypeptide PRO271 cDNA.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1205  
ID ACA68203 standard; cDNA; 1985 BP.

DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1206  
ID ABX98668 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1207  
ID ACC81145 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1208  
ID ACA95469 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1209  
ID ACD04387 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032296-A1.  
PD 30-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1210  
ID ACC87828 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032781-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1211  
ID ACF12490 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1212  
ID ACA96205 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1213  
ID ACA64979 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1214  
ID ACA73705 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1215  
ID ACA74117 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032131-A1.

PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1216  
ID ACA96512 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1217  
ID ACD10618 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1218  
ID ACC91314 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1219  
ID ACD02649 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003032301-A1.  
PD 30-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1220  
ID ACC87214 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1221  
ID ACC85798 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032762-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1222  
ID ACA65286 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1223  
ID ACA94103 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1224  
ID ACA97847 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1225  
ID ACA91349 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1226  
ID ACA90563 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1227  
ID ACD16110 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1228  
ID ACD17271 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1229  
ID ACC91928 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1230  
ID ACA74785 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1231  
ID ACA91656 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1232  
ID ACA71300 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1233  
ID ACC90700 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1234  
ID ACA65710 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO protein #14.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1235  
ID ACA54982 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1236

ID ACA94855 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1237  
ID ACD16417 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1238  
ID ACD15496 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1239  
ID ABX16599 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein #14.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 8; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1240  
ID ACA97540 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1241  
ID ACA98989 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1242  
ID ACC91621 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1243  
ID ACD11032 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1244  
ID ACD14882 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1245  
ID ACD19817 standard; cDNA; 1985 BP.  
DE Human secreted / transmembrane polypeptide PRO271 cDNA.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1246  
ID ACD11646 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1247  
ID ACC95775 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1248  
ID ACF16338 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1249  
ID ACF02456 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1250  
ID ACF02763 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1251  
ID ACF21350 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1252  
ID ACF10034 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068743-A1.  
PD 10-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1253  
ID ACF77927 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1254  
ID ACD46632 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068685-A1.  
PD 10-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1255  
ID ACD49395 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.

PN US2003068725-A1.  
PD 10-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1256  
ID ACF28162 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068752-A1.  
PD 10-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1257  
ID ACD88852 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068682-A1.  
PD 10-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1258  
ID ACD84247 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068701-A1.  
PD 10-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1259  
ID ACD99021 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003068755-A1.  
PD 10-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1260  
ID ADA77779 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003073180-A1.  
PD 17-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1261  
ID ACF48763 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1262  
ID ADB29417 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
PA (GETH) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1263  
ID ACD09083 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1264  
ID ACF11876 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1265  
ID ACF41110 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1266  
ID ACF15724 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1267  
ID ACF16031 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1268  
ID ACD31858 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1269  
ID ACF18666 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1270  
ID ACF09113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1271  
ID ACF78234 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1272  
ID ACF51833 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1273  
ID ACF26320 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1274  
ID ACF24113 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1275  
ID ACF63424 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1276  
ID ACF50298 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1277  
ID ACH07769 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1278  
ID ACF13575 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1279  
ID ACD41501 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1280  
ID ACF31914 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1281  
ID ACF23192 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1282  
ID ACF39882 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1283  
ID ACD45404 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.

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PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1293
ID ACF49684 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1294
ID ACF49991 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1295
ID ACD09390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1296
ID ACD08469 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1297
ID ACF12183 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1298
ID ACC94691 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1299
ID ACD22410 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1300
ID ACF15110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1301
ID ACC97205 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1302
ID ADA18273 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039971-A1.
PD 27-FEB-2003.

PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1284
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1285
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1286
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1287
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1288
ID ACD89773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1289
ID ACD84554 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1290
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1291
ID ACF77006 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1292
ID ACF76699 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104548-A1.
PD 05-JUN-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1303  
ID ACP69694 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding transmembrane protein PRO271.  
FN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1304  
ID ACC92235 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1305  
ID ACF13882 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1306  
ID ACF14189 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1307  
ID ACF09420 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1308  
ID ACD45711 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1309  
ID ACD47860 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1310  
ID ACD67591 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1311  
ID ACF25399 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1312  
ID ACF29083 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1313  
ID ACD84861 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1314  
ID ACD83940 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1315  
ID ACD87931 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1316  
ID ACF30618 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1317  
ID ACF32221 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1318  
ID ACH11881 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1319  
ID ACH12188 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1320  
ID ACD40580 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1321  
ID ACF18052 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1322  
ID ACF08499 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1323  
ID ACF31300 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1324  
ID ACF52140 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1325  
ID ACD50009 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1326  
ID ACF38712 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1327  
ID ACF26627 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1328  
ID ACF24727 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1329  
ID ACF46307 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1330

ID ACF27855 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1331  
ID ACD89159 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1332  
ID ACF63731 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1333  
ID ACF60371 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1334  
ID ACH12495 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1335  
ID ACH09918 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1336  
ID ACD03773 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1337  
ID ACD10311 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1338  
ID ACD11953 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
56.2%; Pred. No. 0.091;  
RESULT 1339  
ID ACD83125 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.

RESULT 1349  
ID ACD91000 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1350  
ID ACF30311 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1351  
ID ACD87010 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1352  
ID ACF60064 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1353  
ID ACF46614 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1354  
ID ACF73471 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1355  
ID ADA79571 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1356  
ID ACF17131 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1357  
ID ACF22885 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1358  
ID ACF7885 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049758-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1359  
ID ACF08192 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1360  
ID ACF40496 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1361  
ID ACF53675 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1362  
ID ACD46939 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1363  
ID ACF47842 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1364  
ID ACF47228 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1365  
ID ACF46000 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1366  
ID ACD96089 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1367  
ID ACF52447 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1368  
ID ACF52754 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1369  
ID ACF64747 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1370  
ID ACF76392 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1371  
ID ACF61292 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1372  
ID ACF61599 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1373  
ID ACD30630 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1374  
ID ACD31551 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1375  
ID ACD32472 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1376  
ID ACF17438 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1377  
ID ACF07271 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1387  
ID ADA42393 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1388  
ID ADA81298 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1389  
ID ACD22103 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1390  
ID ACD24450 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1391  
ID ACD39653 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1392  
ID ACD39960 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1393  
ID ACF13268 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1394  
ID ACF03070 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1395  
ID ACD23303 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1396  
ID ACF78541 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1397  
ID ACF11262 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1398  
ID ACF50605 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1399  
ID ACF34100 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1400  
ID ACD46325 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1401  
ID ACD48167 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1402  
ID ACF27548 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1403  
ID ACF24420 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1404  
ID ACD85475 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1405  
ID ACD90080 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068729-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1406  
ID ACD83633 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1407  
ID ACF49070 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1408  
ID ACH07155 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1409  
ID ACH07462 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1410  
ID ACH08076 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1411  
ID ACH11267 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1412  
ID ACH11574 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1413  
ID ACH10225 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1414  
ID ACF01228 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1415  
ID ACF40803 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1416  
ID ACD24143 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1417  
ID ACD31244 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1418  
ID ACF17745 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1419  
ID ACF32528 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1420  
ID ACF40189 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1421  
ID ACF48149 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1422  
ID ACF38098 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1423  
ID ACF25034 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1424  
ID ACF26934 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068730-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1425  
ID ACF29390 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1426  
ID ACD87624 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1427  
ID ACF76085 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1428  
ID ACF49377 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1429  
ID ACF43834 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1430  
ID ACH06179 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1431  
ID ACH06486 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1432  
ID ADA83096 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1433  
ID ACC92542 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;

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RESULT 1434
ID ACC93156 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032136-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1435
ID ACF19201 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US200303036129-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1436
ID ACD12892 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1437
ID ACF06350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1438
ID ACC94384 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054467-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1439
ID ACC97812 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1440
ID ACC94077 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1441
ID ACF42031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054469-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1442
ID ACD30937 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1443
ID ACD42966 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054463-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
RESULT 1444
ID ACD43273 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054466-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1445
ID ACF14803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003059879-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1446
ID ACF01535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1447
ID ACF31607 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064469-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1448
ID ACD67284 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003064453-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1449
ID ACD48474 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064466-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1450
ID ACD48781 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064468-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1451
ID ACF51219 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068760-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1452
ID ACF53982 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068769-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1453
ID ACF25706 standard; cDNA; 1985 BP.
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DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1454  
ID ACF39019 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1455  
ID ACF28776 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1456  
ID ACD90693 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1457  
ID ACD86396 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1458  
ID ACH05258 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1459  
ID ACF65054 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1460  
ID ADB20139 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1461  
ID ACF43527 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1462  
ID ACH08997 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049774-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1463  
ID ACH09304 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1464  
ID ADA78391 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1465  
ID ACF09727 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1466  
ID ACF50912 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1467  
ID ACF23806 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1468  
ID ACD88238 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1469  
ID ACH09611 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1470  
ID ACH10532 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;  
RESULT 1471  
ID ACD11339 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003036126-A1.  
PD 20-FEB-2003.

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Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1472
ID ACF96389 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1473
ID ACC98419 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1474
ID ADA16672 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1475
ID ACF41724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1476
ID ACF16645 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1477
ID ADA13101 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1478
ID ACD32165 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1479
ID ACD30323 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1480
ID ACD41194 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1481
ID ACF07578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049759-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1482
ID ACF30993 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1483
ID ACF77313 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1484
ID ACF10955 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1485
ID ACF32835 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1486
ID ACF26013 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1487
ID ACD83326 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1488
ID ACF23499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1489
ID ACF42913 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1490
ID ACF43220 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
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Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1491  
ID ACH05872 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1492  
ID ACH08690 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1493  
ID ADA41969 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
FN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1494  
ID ACC90284 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1495  
ID ACF10648 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1496  
ID ACC93463 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1497  
ID ACC96082 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1498  
ID ACD24757 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1499  
ID ADA17316 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
FN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;  
RESULT 1500  
ID ACF01842 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.9%; Score 48; DB 9; Length 1985;  
Best Local Similarity 56.2%; Pred. No. 0.091;

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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 06:48:31 ; Search time 5809 Seconds  
(without alignments)  
11001.878 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679

Sequence: 1 gttgtccttcagcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_hic.\*

4: gb\_est3.\*

5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_ges1.\*

9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1119.4	66.7	1808	3	AK045973 Mus muscu
2	1119.4	66.7	1808	3	AK046377 Mus muscu
3	1014.6	60.4	2512	3	CR602526 full-len
4	852	50.7	874	9	AY406347 Homo sapi
5	743.2	44.3	773	9	AY406348 Pan trogl
6	733.4	43.7	1033	4	BM807426 AGENCOURT
7	720.2	42.9	1083	4	BM809227 AGENCOURT
8	709.6	42.3	874	9	AY406349 Mus muscu
9	674	40.1	865	4	BI666583 603291469
10	669.8	39.9	673	7	CR736885 CRT36885
11	664.8	39.6	856	5	BU155617 AGENCOURT
12	645	38.4	1027	1	AL533026 AL533026
13	643	38.3	732	4	BI551784 603197479
14	640	38.1	748	7	CR362539 170004705
15	635.2	37.8	1039	2	BE798585 601581610
16	628.4	37.4	784	4	BI549318 603194765
17	621.2	37.0	870	4	BI913385 603183295
18	619.6	36.9	765	6	CD354474 UI-M-GMO-
19	611	36.4	737	4	BM679797 UI-E-EJ0-
20	602.4	35.9	604	2	AW025115 wu1h04.x
21	598.8	35.7	602	5	BU741589 UI-E-EJ0-
22	594.8	35.4	770	2	AW117456 xd92a06.x
23	590.6	35.2	680	7	CR751151 DKF2p459F
24	567.8	33.8	1450	7	CO635648 Contig266

98	342.2	20.4	425	7	H87092	H87092 Y974904.r1	C 171	234.6	14.0	425	4	BG054945	BG054945 nac92f04.
99	341.8	20.4	870	5	BUS15609	BUS15609 AGENCOURT	C 172	234.6	14.0	430	2	BE857290	BE857290 7g27a07.x
100	340.6	20.3	1017	9	AY406971	AY406971 Homo sapi	C 173	234	13.9	934	7	CN015939	CN015939 AGENCOURT
101	340.4	20.3	1017	9	AY406973	AY406973 Mus muscu	C 174	233.2	13.9	599	7	CN229507	CN229507 RJB072D02
102	339.4	20.2	2768	3	AK030681	AK030681 Mus muscu	C 175	232	13.8	245	7	R88615	R88615 Ym93f06.r1
103	338	20.1	1015	9	AY406972	AY406972 Pan trogl	C 176	231.8	13.8	277	4	BI011319	BI011319 QV2-EN009
104	337.2	20.1	596	4	BM726313	BM726313 UI-E-EJ0-	C 177	225.8	13.4	564	7	CO602836	CO602836 DGB-24911
105	336.6	20.0	579	2	BB644523	BB644523	C 178	225.8	13.4	639	7	CV030684	CV030684 9878 Full1
106	336	20.0	336	1	A1262562	A1262562 QK42f01.x	C 179	225	13.4	660	7	CR543517	CR543517 DKF2p459N
107	333	19.8	2467	7	AK044845	AK044845 Mus muscu	C 180	221.8	13.2	415	5	BY263876	BY263876 BY263876
108	330.2	19.7	478	7	H05429	H05429 Y180n09.r1	C 181	220	13.1	444	1	AA682970	AA682970 ae89a04.b
109	325	19.4	329	5	F06205	F06205 HSC10F041.n	C 182	218	13.0	229	1	AA450172	AA450172 zx43d09.r
110	323.4	19.3	478	5	BY245406	BY245406	C 183	216	12.9	563	5	BQ637244	BQ637244 he07e09.y
111	323.2	19.2	859	6	CD325278	CD325278 AGENCOURT	C 184	215.4	12.8	697	5	BQ021243	BQ021243 UI-H-DH1-
112	322	19.2	772	7	CK776016	CK776016 967158 MA	C 185	213.8	12.7	640	7	CR545244	CR545244 DKF2p459F
113	320	19.1	896	5	BQ890272	BQ890272 AGENCOURT	C 186	213	12.7	672	6	CA444805	CA444805 UI-H-DH1-
114	310.2	18.5	602	2	BB611718	BB611718	C 187	212.4	12.7	867	6	CD300857	CD300857 AGENCOURT
115	310	18.5	2798	3	AK028345	AK028345 Mus muscu	C 188	211.2	12.6	456	5	BY249027	BY249027 BY249027
116	306	18.2	780	7	CK3113831	CK3113831 SB0203882	C 189	210.6	12.5	656	7	CK619540	CK619540 mk25d06.y
117	305.8	18.2	445	5	BY269882	BY269882	C 190	209	12.4	257	2	AW327110	AW327110 20640 MAR
118	302.4	18.0	513	5	BX279850	BX279850	C 191	208.4	12.4	678	5	BU624639	BU624639 UI-H-FG1-
119	302.4	18.0	690	7	CN233126	CN233126 WL8057E10	C 192	208.4	12.4	1148	4	BM466102	BM466102 AGENCOURT
120	302.2	18.0	759	7	CN094277	CN094277 EC2BBA9CA	C 193	207.6	12.4	226	2	AW374585	AW374585 MRI-CT005
121	301.4	18.0	643	5	BU390882	BU390882 603807132	C 194	204.2	12.2	726	5	CK843444	CK843444 UI-R-BJ2-
122	299.2	17.8	704	7	CN228803	CN228803 RJB061B04	C 195	204.2	12.2	726	5	EX912600	EX912600 BX912600
123	297.4	17.7	764	4	BI752729	BI752729 603028343	C 196	204	12.2	357	5	BY303236	BY303236 BY303236
124	292.4	17.4	764	5	BM945665	BM945665 UI-M-EM0-	C 197	203.6	12.1	656	6	CA307492	CA307492 UI-H-F71-
125	291.6	17.4	415	7	R18841	R18841 Y922906.r1	C 198	203.4	12.1	625	2	BB643056	BB643056
126	290.4	17.3	778	7	CN078143	CN078143 EC2BBA14C	C 199	203.4	12.1	771	7	CN528825	CN528825 UI-M-HQ0-
127	290.2	17.3	457	5	BY249728	BY249728	C 200	202.6	12.1	1084	6	CD255729	CD255729 AGENCOURT
128	290	17.3	290	7	F05894	F05894 HSC0PH101.n	C 201	202.2	12.0	538	7	CK842319	CK842319 UI-R-AD0-
129	288.8	17.2	567	2	BF078551	BF078551 228917 MA	C 202	200.2	11.9	719	7	CK465166	CK465166 936244 MA
130	287.6	17.1	481	5	BY256150	BY256150	C 203	200	11.9	786	7	CO811192	CO811192 AGENCOURT
131	286.2	17.0	497	2	BB854833	BB854833	C 204	200	11.9	858	7	CO914076	CO914076 AGENCOURT
132	284.8	17.0	684	5	BU625289	BU625289 UI-H-FG1-	C 205	199.8	11.9	468	2	BF110673	BF110673 7n55n10.x
133	284.2	16.9	578	2	BB856778	BB856778	C 206	198.6	11.8	663	2	BB633037	BB633037
134	280	16.7	627	5	BQ444788	BQ444788 UI-M-ER0-	C 207	198	11.8	519	7	CV038761	CV038761 4136000 B
135	279.8	16.7	677	6	CD217649	CD217649 p9r1n.pk0	C 208	198	11.8	525	4	BG373976	BG373976 UI-R-CV1-
136	277.6	16.5	590	7	CR545391	CR545391 DKF2p459M	C 209	197.6	11.8	537	2	BB770360	BB770360
137	276.2	16.5	297	1	AA037351	AA037351 zc03b06.8	C 210	195.6	11.6	347	7	CN094278	CN094278 EC2BBA9CA
138	272.6	16.2	815	5	BU230452	BU230452 603320607	C 211	194.4	11.6	670	7	CN083622	CN083622 EC2BBA22D
139	272.6	16.2	827	6	CA306798	CA306798 UI-H-F71-	C 212	194.4	11.6	708	7	CN083621	CN083621 EC2BBA22D
140	271.8	16.2	2096	3	AK035218	AK035218 Mus muscu	C 213	193	11.5	559	5	BY476545	BY476545
141	270.2	16.1	1953	3	AK030503	AK030503 Mus muscu	C 214	192.8	11.5	825	5	BP166655	BP166655 BP166655
142	267.6	15.9	858	6	CD325821	CD325821 AGENCOURT	C 215	192	11.4	659	2	AW149545	AW149545 xf39c10.x
143	267.2	15.9	284	7	CR543721	CR543721 DKF2p459H	C 216	191.4	11.4	294	7	W15256	W15256 zc16b07.81
144	264.8	15.8	695	7	CN28731	CN28731 RJB0608E12	C 217	189.4	11.3	764	6	CA350929	CA350929 621861 NC
145	263.6	15.7	683	2	BB318882	BB318882	C 218	188	11.2	611	6	CA355517	CA355517 627428 NC
146	263.6	15.7	2534	3	AK039193	AK039193 Mus muscu	C 219	187.6	11.2	593	7	CK845949	CK845949 968393 MA
147	263	15.7	2330	3	BC080168	BC080168 Xenopus l	C 220	186.8	11.1	565	2	BB663866	BB663866 147903 MA
148	256.8	15.3	754	7	CO043662	CO043662 UI-M-ER0-	C 221	186.8	11.1	880	6	CD303536	CD303536 AGENCOURT
149	256	15.2	257	7	Z39203	Z39203 HSC13G042.n	C 222	186.6	11.1	509	2	BB771080	BB771080
150	255.2	15.2	587	7	CN088583	CN088583 EC2BBA30B	C 223	186.2	11.1	572	6	CB265380	CB265380 1004285 H
151	253	15.1	410	5	BY276506	BY276506	C 224	186	11.1	640	7	CO351229	CO351229 RAOV.FL
152	247	14.7	796	7	CO399311	CO399311 AGENCOURT	C 225	186	11.1	753	1	AI589824	AI589824 tm74g09.x
153	246.8	14.7	442	5	BX112198	BX112198	C 226	185.2	11.0	906	5	BU186468	BU186468 AGENCOURT
154	246.8	14.7	523	2	BE550993	BE550993 7b67a03.x	C 227	184.4	11.0	392	2	BE651010	BE651010 UI-M-BH3-
155	246.4	14.7	849	6	CA472810	CA472810 AGENCOURT	C 228	183	10.9	835	5	EX881962	EX881962 BX881962
156	243.8	14.5	652	7	CN078144	CN078144 EC2BBA14C	C 229	182.8	10.9	527	5	BY243052	BY243052
157	241.8	14.4	653	7	CF180026	CF180026 815076 MA	C 230	181	10.8	755	5	EX913106	EX913106
158	241.6	14.4	434	1	AI360870	AI360870 qy01b10.x	C 231	180.6	10.8	647	7	CV030870	CV030870 10123 Full1
159	240.8	14.3	621	5	BX312928	BX312928	C 232	179.8	10.7	220	7	H16176	H16176 Ym21909.r1
160	240.6	14.3	496	5	BP201259	BP201259	C 233	179.2	10.7	578	2	BE121132	BE121132 UI-R-CA0-
161	240.6	14.3	926	6	CD325412	CD325412 AGENCOURT	C 234	179.2	10.7	836	4	BI733097	BI733097 60354684
162	240.2	14.3	456	6	CD803885	CD803885 UI-M-GV0-	C 235	178	10.6	178	6	CB118055	CB118055 K-EST0164
163	239.8	14.3	502	1	AI796834	AI796834 we22h06.x	C 236	178	10.6	909	5	BU132565	BU132565 603120307
164	239	14.2	511	5	BN493152	BN493152 DKF2p781G	C 237	176.4	10.5	448	4	BG375509	BG375509 UI-R-CV1-
165	238.8	14.2	611	7	CN075612	CN075612 EC2BBA10C	C 238	176.4	10.5	496	2	BF523086	BF523086 UI-R-C2p-
166	238	14.2	282	7	R75391	R75391 M0B0556R.MO	C 239	176	10.5	666	5	BM951674	BM951674 UI-M-EG0-
167	235.6	14.0	788	4	BI767217	BI767217 603057906	C 240	175.6	10.5	2296	3	CR592222	CR592222 Full1-len9
168	235.4	14.0	492	2	AW967001	AW967001 EST379075	C 241	175.2	10.4	795	1	AU080106	AU080106
169	235	14.0	674	6	CD767791	CD767791 AGENCOURT	C 242	174.6	10.4	867	7	CO543917	CO543917 LYEEST116
170	234.8	14.0	258	7	R42884	R42884 Y906h12.g1	C 243	174.4	10.4	572	2	BF407747	BF407747 UI-R-BJ2-

C 244	171.4	10.2	491	5	BQ174475	UI-M-DJ2-	BQ174475	UI-M-DJ2-	C 317	140.4	8.4	585	7	CO628980	DG9-3m14
245	171.4	10.2	862	7	CK397022	AGENCOURT	CK397022	AGENCOURT	318	140.4	8.4	969	6	BY718203	BY718203
246	170.8	10.2	526	7	BB692328	BB692328	BB692328	BB692328	319	140.4	8.4	1447	3	AK018085	Mus muscu
247	170.6	10.2	768	5	BX868437	BX868437	BX868437	BX868437	320	139.8	8.3	380	6	BY606458	BY606458
248	170.2	10.1	434	1	A1279142	qm18e02.x	A1279142	qm18e02.x	321	139.4	8.3	801	5	BU357013	BU357013
249	169.8	10.1	584	5	BP257486	BP257486	BP257486	BP257486	322	139.4	8.3	809	2	BF304194	BF304194
C 250	169.6	10.1	637	6	CB528708	UI-H-F72-	CB528708	UI-H-F72-	323	138.4	8.2	402	5	BY289266	BY289266
251	169	10.1	378	2	BF601149	266043 MA	BF601149	266043 MA	324	138.2	8.2	914	5	BX843874	BX843874
252	169	10.1	470	5	BX954423	DKF2P781K	BX954423	DKF2P781K	325	138	8.2	775	4	BY119955	BY119955
253	167.8	10.0	791	7	CK308721	SB02047A2	CK308721	SB02047A2	326	137.8	8.2	530	5	BY480409	BY480409
254	167.4	10.0	923	1	AL583491	AL583491	AL583491	AL583491	327	137.8	8.2	718	6	CB460692	CB460692
255	167	9.9	617	6	BY730405	BY730405	BY730405	BY730405	328	136.4	8.1	661	6	CA452139	UI-M-F20-
C 256	166.6	9.9	458	7	CO667956	DG33-31f8	CO667956	DG33-31f8	329	136.2	8.1	304	7	CR472042	CR472042
C 257	166.6	9.9	541	5	BY735309	UI-B-DW0-	BY735309	UI-B-DW0-	330	136	8.1	496	7	CK693129	ZF101-F00
258	166.2	9.9	566	7	CF977262	2-84-BD0-	CF977262	2-84-BD0-	331	135.4	8.1	372	6	BY768835	BY768835
259	166	9.9	442	2	BB676735	BB676735	BB676735	BB676735	332	134.6	8.0	386	5	BY263646	BY263646
260	165.6	9.9	535	9	AY409767	Homo sapi	AY409767	Homo sapi	333	134.4	8.0	594	5	BU400899	BU400899
C 261	165.4	9.9	544	6	CA439326	UI-H-D71-	CA439326	UI-H-D71-	334	134.2	8.0	778	7	CK315507	CK315507
C 262	165.4	9.9	580	7	CK089827	EC2BBA32B	CK089827	EC2BBA32B	335	134	8.0	855	5	BP158085	BP158085
263	164.4	9.8	651	6	BY726997	BY726997	BY726997	BY726997	336	130.6	7.8	700	7	CK458398	CK458398
264	164.2	9.8	450	5	BY263302	BY263302	BY263302	BY263302	337	130.6	7.8	801	7	CK303983	CK303983
265	164	9.8	773	4	BG208674	RST28306	BG208674	RST28306	338	129.4	7.7	372	2	BE990143	BE990143
266	163.2	9.7	894	6	CB199088	AGENCOURT	CB199088	AGENCOURT	339	129	7.7	483	7	CR536826	CR536826
C 267	162.4	9.7	424	1	AI556916	UI-R-C2p-	AI556916	UI-R-C2p-	340	128.8	7.7	265	1	AI577248	UI-R-AD0-
268	162.4	9.7	535	9	AY409769	Mus muscu	AY409769	Mus muscu	341	128.6	7.7	807	5	BP168056	BP168056
269	161.8	9.6	434	2	BB676742	BB676742	BB676742	BB676742	342	128.4	7.6	641	2	AM379374	CM2-HT024
270	161.8	9.6	936	5	BQ227365	AGENCOURT	BQ227365	AGENCOURT	343	128.2	7.6	641	2	AM379374	CM2-HT024
C 271	161.6	9.6	402	1	AI072844	UI-R-Y0-1	AI072844	UI-R-Y0-1	344	127.6	7.6	421	5	BB674781	BB674781
272	160.8	9.6	892	5	BP462753	BP462753	BP462753	BP462753	345	126.6	7.5	825	5	BP464677	BP464677
273	160.6	9.6	268	1	AA296886	EST112650	AA296886	EST112650	346	125	7.4	645	6	CA334396	CA334396
274	160.4	9.6	529	2	BB680624	BB680624	BB680624	BB680624	347	124.4	7.4	377	7	CF977263	2-98-A10-
C 275	159.6	9.5	494	1	AA548396	nj14e04.s	AA548396	nj14e04.s	348	124.2	7.4	868	5	BQ672092	AGENCOURT
276	158.8	9.5	481	5	BY247646	BY247646	BY247646	BY247646	349	123.8	7.4	617	4	BJ622933	BJ622933
277	157.4	9.4	169	7	T06151	EST04040 Fe	T06151	EST04040 Fe	350	123.4	7.3	562	5	BU381982	BU381982
278	157.2	9.4	858	2	BF676478	602086277	BF676478	602086277	351	123	7.3	463	1	AI341423	qx91e11.x
279	157	9.4	426	2	BB677725	BB677725	BB677725	BB677725	352	121.4	7.2	312	2	BB387307	BB387307
280	156.4	9.3	739	7	CK679857	ZF101-F00	CK679857	ZF101-F00	353	121.4	7.2	441	2	BE504685	BE504685
281	156.4	9.3	884	5	BU323269	603405983	BU323269	603405983	354	121.4	7.2	711	7	CO669353	DG33-50D1
282	156.2	9.3	464	2	BB311856	BB311856	BB311856	BB311856	355	120	7.1	504	5	BX281785	BX281785
283	155.8	9.3	815	1	AU079716	AU079716	AU079716	AU079716	356	120	7.1	729	2	BB585976	BB585976
284	155.6	9.3	533	2	BB767692	BB767692	BB767692	BB767692	357	119.4	7.1	613	7	CF892168	A0106B07-
285	155.2	9.2	431	5	BY276402	BY276402	BY276402	BY276402	358	119.4	7.1	863	6	CA475514	AGENCOURT
C 286	154.6	9.2	733	7	CO619752	DG9-1D13	CO619752	DG9-1D13	359	119	7.1	801	5	BX852740	BX852740
C 287	153	9.1	520	7	CK618674	mk15a07.Y	CK618674	mk15a07.Y	360	118.8	7.1	508	2	BB703900	BB703900
C 288	152.8	9.1	436	2	BE991815	UI-M-B21-	BE991815	UI-M-B21-	361	118.4	7.1	278	2	BB193864	BB193864
C 289	151.6	9.0	364	1	AI940007	QVO-CT001	AI940007	QVO-CT001	362	117	7.0	552	4	BI337752	BI337752
290	151	9.0	411	5	BY288341	BY288341	BY288341	BY288341	363	116.6	6.9	422	1	AI288864	AI288864
C 291	150.8	9.0	254	7	CR774354	DKF2p459P	CR774354	DKF2p459P	364	116.6	6.9	461	2	BF463934	BF463934
C 292	149.2	8.9	465	1	AI934791	wp89e04.x	AI934791	wp89e04.x	365	115.6	6.9	308	2	BB187802	BB187802
293	149.2	8.9	497	7	CV036959	4134532 B	CV036959	4134532 B	366	115.6	6.9	790	5	BP141505	BP141505
294	149	8.9	547	6	BY727136	BY727136	BY727136	BY727136	367	115.4	6.9	336	5	BY134531	BY134531
295	149	8.9	854	3	AK020998	Mus muscu	AK020998	Mus muscu	368	115	6.8	368	2	BF350775	QVO-HT036
296	148.8	8.9	412	2	BB668189	BB668189	BB668189	BB668189	369	113.8	6.8	281	2	BE985090	BE985090
297	147.4	8.8	429	5	BY272572	BY272572	BY272572	BY272572	370	113.8	6.8	579	7	CK089828	CK089828
298	146.4	8.7	600	6	CA526928	8023-83 M	CA526928	8023-83 M	371	113.6	6.8	514	1	AI285235	AI285235
299	146.2	8.7	862	5	BP462754	BP462754	BP462754	BP462754	372	112.8	6.7	665	9	BX243020	BX243020
300	146	8.7	411	5	BY276562	BY276562	BY276562	BY276562	373	112.4	6.7	528	2	AM490008	AM490008
301	145.8	8.7	409	6	BY607794	BY607794	BY607794	BY607794	374	112.4	6.7	582	7	CO626674	DG9-278a2
302	145.4	8.7	386	6	CB806970	AMGNNUC-N	CB806970	AMGNNUC-N	375	112	6.7	316	1	AI188493	AI188493
303	145	8.6	418	5	BY278505	BY278505	BY278505	BY278505	376	111.2	6.6	446	7	CO352257	CO352257
304	144.8	8.6	703	7	CF530869	UI-N-GH0-	CF530869	UI-N-GH0-	377	110.8	6.6	994	6	CD325921	AGENCOURT
C 305	144.6	8.6	519	1	AA826266	od3e0e4.s	AA826266	od3e0e4.s	378	110.6	6.6	293	2	BB187368	BB187368
306	144.6	8.6	703	5	BU117309	603138889	BU117309	603138889	379	110.6	6.6	422	4	BI390270	BI390270
C 307	144	8.6	511	1	AI15689	mc70a03.x	AI15689	mc70a03.x	380	110.4	6.6	382	9	AY400235	Mus muscu
308	144	8.6	953	5	BU116264	603139651	BU116264	603139651	381	110.4	6.6	417	6	CA884109	CA884109
309	143.4	8.5	878	5	BP165824	BP165824	BP165824	BP165824	382	110.4	6.6	782	8	AZ731274	RPCI-24-1
310	142.2	8.4	535	9	AY409768	Pan trogl	AY409768	Pan trogl	383	110.2	6.6	267	7	R75390	MDB0556 Mou
C 311	141.8	8.4	470	1	AI580850	ta33e0e.x	AI580850	ta33e0e.x	384	110.2	6.6	451	1	AA933871	AA933871
C 312	141.4	8.4	397	2	AW046074	UI-M-BH1-	AW046074	UI-M-BH1-	385	109.4	6.5	525	1	AL919221	AL919221
C 313	141.4	8.4	875	4	BI734218	603351323	BI734218	603351323	386	109	6.5	283	2	BB194430	BB194430
314	141.2	8.4	437	1	AA219849	mv62c03.x	AA219849	mv62c03.x	387	109	6.5	711	5	BU363662	603790080
315	141.2	8.4	853	3	BP164129	BP164129	BP164129	BP164129	388	108.2	6.4	272	1	AV165649	AV165649
316	140.4	8.4	478	6	CA885050	B0115E08-	CA885050	B0115E08-	389	107.2	6.4	514	4	BG814603	daf69d01.

330	106	6.3	276	2	BB304840	BB304840	BB304840	463	80.4	4.8	529	6	CD284927	CD284927	G39161.77
331	106	6.3	705	7	CN108877	EC2CAA32D	CN108877	464	79.8	4.8	272	2	BB255894	BB255894	BB255894
C 332	105.8	6.3	598	1	AI815935	ua43g02.x	AI815935	465	79.6	4.7	221	2	BB306421	BB306421	BB306421
333	105.6	6.3	394	9	AY400233	Homo sapi	AY400233	466	79.4	4.7	583	6	CA353359	CA353359	624860 NC
334	105.6	6.3	394	9	AY400234	Pan trogl	AY400234	467	79.2	4.7	562	5	BG065676	BG065676	DKF2p781K
335	105.4	6.3	525	6	CB720159	AMGNNUC:N	CB720159	C 468	78.8	4.7	560	4	BG065676	BG065676	CH2303H12-
C 336	105.2	6.3	314	7	CN075611	EC2BBA10C	CN075611	469	78.6	4.7	375	5	BY292584	BY292584	BY292584
337	105	6.3	388	2	BB262900	BB262900	BB262900	470	78.6	4.7	442	7	CN081576	CN081576	EC2BBA19C
338	104.6	6.2	651	6	C9557691	AMGNNUC:N	C9557691	471	78.6	4.7	513	3	AK080669	AK080669	Mus muscu
339	104.2	6.2	284	2	BB054624	BB054624	BB054624	472	78.6	4.7	522	3	BB271167	BB271167	BB271167
400	104.2	6.2	473	5	BZ261511	BZ261511	BZ261511	473	78.6	4.7	916	5	BQ672140	BQ672140	AGENCOURT
401	103.8	6.2	761	6	CD755145	AGENCOURT	CD755145	474	78.4	4.7	206	2	BB589469	BB589469	BB589469
402	103.4	6.2	262	1	AV030145	AV030145	AV030145	475	78.2	4.7	336	4	BG199531	BG199531	RST18822
403	103.4	6.2	279	2	BB362555	BB362555	BB362555	476	78.4	4.7	306	4	BG199531	BG199531	RST18822
404	103.4	6.2	327	2	BB320625	BB320625	BB320625	477	78	4.6	457	7	W39242	W39242	zg16ho07.r1
405	102.2	6.1	291	2	BB248659	BB248659	BB248659	478	77.6	4.6	660	5	BM337636	BM337636	BM337636
406	101.2	6.0	412	5	BY274659	BY274659	BY274659	C 478	77.6	4.6	368	7	CN086072	CN086072	EC2BBA26C
C 407	101	6.0	298	1	AA906739	ok78h08.s	AA906739	479	77	4.6	297	6	BY724443	BY724443	BY724443
408	100.8	6.0	283	2	BB265542	BB265542	BB265542	C 480	77	4.6	538	6	C76456	C76456	C76456
409	100.8	6.0	483	8	A2457316	1M0260A07	A2457316	C 481	76.8	4.6	467	4	BI134406	BI134406	UI-M-BH3-
410	100.6	6.0	260	2	BP455798	UI-M-CG0P	BP455798	C 482	76.8	4.6	581	8	BH269028	BH269028	CH230-66P
411	100.6	6.0	260	2	AA918130	UI-M-BH3-	AA918130	C 483	76.8	4.6	779	8	BH292378	BH292378	CH230-44D
C 412	100.2	6.0	359	2	BE156390	QV0-HT036	BE156390	C 484	76.6	4.6	1127	9	GGA200118	GGA200118	Gallus ga
C 413	100	6.0	402	2	AW522667	UI-R-B00-	AW522667	485	76.6	4.6	281	1	AV227016	AV227016	AV227016
414	99.4	5.9	292	2	BB375591	BB375591	BB375591	486	76.6	4.6	492	4	BI359722	BI359722	384371 MA
415	99.2	5.9	489	6	CB726015	AMGNNUC:N	CB726015	C 488	75.6	4.5	960	5	BQ933325	BQ933325	AGENCOURT
C 416	98.6	5.9	207	2	BP469799	UI-M-BH3-	BP469799	C 489	75.2	4.5	433	1	AL921475	AL921475	AL921475
417	98.6	5.9	694	7	CK699353	ZF101-P00	CK699353	C 490	74.4	4.4	202	2	BB380085	BB380085	BB380085
418	98.4	5.9	392	5	BY267956	BY267956	BY267956	C 491	74.2	4.4	526	7	CO634943	CO634943	DG9-96n24
419	97.2	5.8	421	5	BY275639	BY275639	BY275639	492	73.2	4.4	284	3	AK020745	AK020745	Mus muscu
420	97.2	5.8	656	2	BB617916	BB617916	BB617916	493	73.2	4.4	293	2	BB284230	BB284230	BB284230
421	95.8	5.7	763	1	A1247225	mc70a03.y	A1247225	494	72.8	4.3	687	5	BP461989	BP461989	BP461989
422	95.6	5.7	385	5	BY275013	BY275013	BY275013	495	72.8	4.3	893	2	CNS02MVY	CNS02MVY	Tetraodon
423	94.8	5.6	240	2	BB047231	BB047231	BB047231	496	72.6	4.3	339	2	BE826667	BE826667	QV1-EN004
424	94.4	5.6	646	4	B1393264	pppln.pk0	B1393264	497	72.6	4.3	816	5	BU385923	BU385923	603858616
C 425	94.2	5.6	354	2	BE826697	QV1-EN004	BE826697	C 498	72.4	4.3	378	8	AZ089779	AZ089779	RPCI-23-2
426	94.2	5.6	740	7	CO884202	BoxGen.12	CO884202	C 499	72	4.3	334	1	AI422503	AI422503	tf11e04.x
427	93.6	5.6	401	5	BY266910	BY266910	BY266910	500	71.8	4.3	264	1	AV325817	AV325817	AV325817
428	93	5.5	285	2	BB053997	BB053997	BB053997	501	71.8	4.3	274	1	AV338287	AV338287	AV338287
C 429	92.8	5.5	377	2	BF358688	QV1-ET000	BF358688	502	71.8	4.3	474	2	BB682022	BB682022	BB682022
430	92.6	5.5	229	1	AV350601	AV350601	AV350601	503	71.4	4.3	196	1	AV344490	AV344490	AV344490
431	92.4	5.5	302	2	BB389565	BB389565	BB389565	504	71.4	4.3	202	1	AV031929	AV031929	AV031929
432	92	5.5	304	2	BB282896	BB282896	BB282896	505	71.4	4.3	255	2	BB563869	BB563869	BB563869
433	92	5.5	640	9	CC573801	CH240.450	CC573801	506	70.8	4.2	198	1	AV030665	AV030665	AV030665
434	91.4	5.4	374	5	BY294857	BY294857	BY294857	507	70.8	4.2	216	1	AV341533	AV341533	AV341533
C 435	91.4	5.4	452	1	AI262821	qk35h10.x	AI262821	508	70.6	4.2	199	2	BB127593	BB127593	BB127593
436	91	5.4	318	2	BB321476	BB321476	BB321476	509	70.2	4.2	214	1	AV345671	AV345671	AV345671
437	91	5.4	656	2	BB645027	BB645027	BB645027	510	69.6	4.1	742	7	CO395507	CO395507	AGENCOURT
C 438	90.4	5.4	233	2	AW047822	UI-M-BH1-	AW047822	511	69.4	4.1	261	2	BB278160	BB278160	BB278160
439	90.2	5.4	267	2	BB480567	BB480567	BB480567	512	69	4.1	191	2	BB301025	BB301025	BB301025
440	90	5.4	194	4	B1337742	361263 MA	B1337742	513	68.6	4.1	581	7	CO879831	CO879831	BovGen.08
C 441	90	5.4	317	2	BF056760	7K08C03.x	BF056760	514	68.4	4.1	221	2	BB048644	BB048644	BB048644
442	88.6	5.3	700	2	BB652926	BB652926	BB652926	515	68.4	4.1	292	2	BB198259	BB198259	BB198259
C 443	88.4	5.3	733	9	BX190380	Danio rer	BX190380	516	68.2	4.1	313	2	AW430704	AW430704	70599 MAR
444	88.2	5.3	374	2	BB265140	BB265140	BB265140	517	68	4.0	223	2	BB380518	BB380518	BB380518
445	86	5.1	304	2	BB265140	BB265140	BB265140	C 518	67.6	4.0	514	7	CK769283	CK769283	956841 MA
446	85.8	5.1	285	7	CN209637	QV1-EN004	CN209637	519	67.2	4.0	821	5	BU389844	BU389844	603511165
C 447	85.6	5.1	332	2	BB26737	QV1-EN004	BB26737	520	67	4.0	417	1	AV588904	AV588904	AV588904
448	84.8	5.1	625	6	BY729404	BY729404	BY729404	521	66	3.9	226	2	BB048138	BB048138	BB048138
449	84.6	5.0	526	2	BB641806	BB641806	BB641806	522	66	3.9	433	4	BG515406	BG515406	dae04h10.
450	84.4	5.0	320	2	BB312195	BB312195	BB312195	523	65.8	3.9	296	2	BB193169	BB193169	BB193169
C 451	84.4	5.0	479	2	AW524531	UI-R-B00-	AW524531	524	65.8	3.9	726	5	BU395513	BU395513	603404749
452	84	5.0	657	2	BB618284	BB618284	BB618284	525	65.6	3.9	502	4	BG078950	BG078950	H3033H12-
C 453	84	5.0	723	9	AG035406	Pan trogl	AG035406	526	65	3.9	259	2	BB607028	BB607028	BB607028
454	83.8	5.0	2594	3	AK047122	Mus muscu	AK047122	C 527	64.8	3.9	702	9	CNS02PTU	CNS02PTU	Tetraodon
455	83.4	5.0	550	2	BE012499	121990 MA	BE012499	C 528	64.4	3.8	527	1	AA741334	AA741334	Ob30f08.s
456	83.2	5.0	233	1	AV335954	AV335954	AV335954	529	64.4	3.8	558	7	CK875240	CK875240	CK875240
457	82.8	4.9	262	2	BB078578	BB078578	BB078578	530	63.8	3.8	217	2	BB197705	BB197705	BB197705
458	82.4	4.9	728	7	CN530285	UI-M-H00-	CN530285	531	62.6	3.7	226	1	AA776056	AA776056	ae79a07.s
459	82	4.9	272	2	BB596160	BB596160	BB596160	C 532	62.6	3.7	539	1	AL918370	AL918370	AL918370
460	81.8	4.9	392	2	AW291014	UI-H-B12-	AW291014	533	61.8	3.7	201	1	AV227064	AV227064	AV227064
461	81.6	4.9	586	4	BM696801	UI-E-DW0-	BM696801	C 534	61.8	3.7	247	7	CR474371	CR474371	CR474371
C 462	80.6	4.8	1463	8	CC288776	CH261-170	CC288776	535	61.8	3.7	550	7	CR544460	CR544460	DKF2p459F



536	61	200	1	AV028623	AV028623	AV028623	609	54.2	3.2	806	4	BI762516	BI762516	603048638
537	60.8	189	1	AV029446	AV029446	AV029446	610	54.2	3.2	859	6	CB319037	CB319037	AGENCOURT
538	60.8	255	2	BB577810	BB577810	BB577810	c 611	54	3.2	212	4	BG981747	BG981747	MR3-CN014
539	60.4	222	2	BB053503	BB053503	BB053503	c 612	54	3.2	241	4	BG980534	BG980534	MR3-CN014
540	60.4	484	5	BB099260	BB099260	BB099260	c 613	54	3.2	365	6	CB573833	CB573833	AGENCOURT
541	60.2	1008	9	CL093894	ISB1-24C2	CL093894	614	54	3.2	774	1	AJ786997	AJ786997	AJ786997
542	60	702	4	BG695650	NISC-1v20	BG695650	615	54	3.2	1176	5	BM927266	BM927266	AGENCOURT
543	59.6	420	6	CB798880	AMGNOC:N	CB798880	c 616	53.8	3.2	244	2	BF362751	BF362751	RC1-NN007
544	59.6	845	4	BM042630	603615963	BM042630	617	53.8	3.2	276	7	CO181006	CO181006	EC13331.5
545	59	303	1	AI422504	tf11e05.x	AI422504	618	53.8	3.2	276	7	CO195427	CO195427	EC40320.5
546	58.6	276	2	BB268580	BB268580	BB268580	619	53.8	3.2	286	7	CO182679	CO182679	EC23645.5
547	58.6	426	7	CK767772	968132 MA	CK767772	620	53.8	3.2	303	7	CO181557	CO181557	EC14539.5
548	58.6	736	8	AE298621	2M0273104	AE298621	621	53.8	3.2	350	7	CO191915	CO191915	EC32401.5
549	58.4	242	4	BG980478	MR3-CN014	BG980478	622	53.8	3.2	361	5	BUS89906	BUS89906	AGENCOURT
550	58.4	565	7	CO590783	DG3-41K22	CO590783	623	53.8	3.2	382	7	CO181851	CO181851	EC15101.5
551	58.2	376	7	CO182357	EC22490.5	CO182357	624	53.8	3.2	385	7	CO180258	CO180258	EC01131.5
552	58.2	365	7	CO181363	EC14144.5	CO181363	625	53.8	3.2	395	7	CO182619	CO182619	EC23422.5
553	58.2	421	7	CO181992	EC18396.5	CO181992	626	53.8	3.2	398	7	CO193679	CO193679	EC36616.5
554	58.2	504	7	CO193442	EC35796.5	CO193442	627	53.8	3.2	450	7	CO194401	CO194401	EC38508.5
555	58.2	531	7	CO193920	EC36996.5	CO193920	628	53.8	3.2	452	7	CO193143	CO193143	EC35202.5
556	57.8	831	9	CNS011FZ	Drosophil	AI100217	629	53.8	3.2	464	7	CO183541	CO183541	EC35934.5
557	57.4	559	7	CF123525	UI-HF-CHO	CF123525	630	53.8	3.2	487	7	CO195262	CO195262	EC39947.5
558	57	643	8	AQ327238	nxbx0040J	AQ327238	631	53.8	3.2	490	7	CO180558	CO180558	EC02047.5
559	57	841	5	BUS30009	AGENCOURT	BUS30009	632	53.8	3.2	523	7	CO183076	CO183076	EC24521.5
560	56.8	569	5	BP377634	BP377634	BP377634	633	53.8	3.2	524	7	CO182642	CO182642	EC33489.5
561	56.8	574	5	BP321522	BP321522	BP321522	634	53.8	3.2	547	7	CO185170	CO185170	EC39789.5
562	56.8	582	5	BP208357	BP208357	BP208357	635	53.8	3.2	552	7	CO194609	CO194609	EC38890.5
563	56.6	324	7	CO192533	EC33980.5	CO192533	c 636	53.8	3.2	569	8	AQ394216	AQ394216	CITBI-E1-
564	56.6	502	7	CO691339	DG11-30F1	CO691339	637	53.8	3.2	582	4	BG219746	BG219746	RST39511
565	56.6	574	7	CO184164	EC27256.5	CO184164	638	53.8	3.2	759	9	CNS06QXV	AL411257	T7 end of
566	56.6	964	9	CNS05CLJ	Tetraodon	BI311264	639	53.8	3.2	880	6	CD522648	CD522648	AGENCOURT
567	56.4	1389	4	BI911314	603062429	BI911314	640	53.8	3.2	913	7	CK157193	CK157193	FGAS03828
568	56.2	481	7	CO180995	EC13317.5	CO180995	641	53.8	3.2	1511	3	BB432888	BB432888	Mus muscu
569	56.2	1019	5	BQ723771	AGENCOURT	BQ723771	642	53.6	3.2	271	2	BB432888	BB432888	Mus muscu
570	56.2	1119	6	CD050433	AGENCOURT	CD050433	643	53.6	3.2	532	6	CA354283	CA354283	625969 NC
571	56	497	7	CO180052	EC00836.5	CO180052	644	53.6	3.2	551	1	AL036240	AL036240	DKP2P564J
572	56	710	7	CO961229	pe19c10.Y	CO961229	645	53.6	3.2	692	7	CK654124	CK654124	AGENCOURT
573	56	771	5	BUS56340	AGENCOURT	BUS56340	c 646	53.6	3.2	754	9	AG483752	AG483752	Mus muscu
574	56	1472	9	CL490510	SAIL 539	CL490510	647	53.6	3.2	772	5	BUS37238	BUS37238	AGENCOURT
575	55.8	929	9	CNS050XX	Tetraodon	AG320971	648	53.6	3.2	778	4	BI859188	BI859188	603385268
576	55.8	1376	9	CK017071	Mus muscu	CK017071	c 649	53.6	3.2	893	7	CK196964	CK196964	FGAS00543
577	55.4	311	4	BG193769	RST12905	BG193769	650	53.6	3.2	949	6	CD387866	CD387866	AGENCOURT
578	55.4	355	7	CO878692	BovGen .07	CO878692	651	53.4	3.2	226	6	CD765502	CD765502	EST00188
579	55.4	626	8	AZ385580	1M0144G07	AZ385580	652	53.4	3.2	230	4	BF968205	BF968205	602268946
580	55.4	835	5	BUS54638	AGENCOURT	BUS54638	653	53.4	3.2	363	2	BF076420	BF076420	225985 Ma
581	55.4	335	5	BUS54638	AGENCOURT	BUS54638	654	53.4	3.2	422	7	CV525233	CV525233	Md1v4010h
582	55.2	285	6	CB986322	AGENCOURT	CB986322	655	53.4	3.2	582	5	BP283085	BP283085	6237039
583	55.2	318	7	CK974991	24676 125	CK974991	656	53.4	3.2	584	5	BP327099	BP327099	BP327099
584	55.2	991	4	BG435647	602506930	BG435647	657	53.4	3.2	584	5	BP327111	BP327111	BP327111
585	55.2	1175	6	CD504945	CD470-H09	CD504945	658	53.4	3.2	661	1	AV682763	AV682763	AV682763
586	55	230	7	CO885649	BovGen 13	CO885649	659	53.4	3.2	698	1	AV682763	AV682763	AV682763
587	55	647	9	AG044222	Pan trogl	AG044222	660	53.4	3.2	816	5	BUS43005	BUS43005	AGENCOURT
588	55	1043	6	CD385012	AGENCOURT	CD385012	661	53.4	3.2	880	7	CN835143	CN835143	AGENCOURT
589	55	1123	5	BUS02918	AGENCOURT	BUS02918	662	53.4	3.2	884	5	BUS63135	BUS63135	AGENCOURT
590	54.8	262	6	CF333785	laa33a05.	CF333785	c 663	53.4	3.2	885	9	AG566030	AG566030	Mus muscu
591	54.8	400	7	CF578533	AGENCOURT	CF578533	664	53.4	3.2	935	5	BUS60555	BUS60555	AGENCOURT
592	54.8	684	7	CV274449	WS0173.B2	CV274449	665	53.4	3.2	1101	9	CNS00HAY	CNS00HAY	Drosophil
593	54.6	333	3	CB179629	EST0729 Z	CB179629	666	53.2	3.2	195	7	CF546382	CF546382	lae7e03.
594	54.6	246	1	AL040243	DKP2P434I	AL040243	667	53.2	3.2	422	2	AW778899	AW778899	ho16e08.x
595	54.6	348	6	CB829769	r104h12.Y	CB829769	668	53.2	3.2	560	6	CB333937	CB333937	CA23E103I
596	54.6	390	1	AA490022	ab02b04.B	AA490022	669	53.2	3.2	609	6	CA367906	CA367906	934211 MA
597	54.6	434	6	CA399771	EL01N0325	CA399771	670	53.2	3.2	693	7	CK463316	CK463316	934211 MA
598	54.6	478	6	CB179629	EST0729 Z	CB179629	671	53.2	3.2	712	9	CNS04AL2	CNS04AL2	Tetraodon
599	54.6	842	7	CK128791	AGENCOURT	CK128791	672	53.2	3.2	808	7	CF150373	CF150373	AGENCOURT
600	54.6	844	9	CNS0052P	Drosophil	AL056652	673	53.2	3.2	818	5	BUS64240	BUS64240	AGENCOURT
601	54.6	847	7	CK400611	AGENCOURT	CK400611	674	53.2	3.2	864	5	BUS46240	BUS46240	AGENCOURT
602	54.6	1049	4	BG623609	602648818	BG623609	675	53.2	3.2	869	5	BUS93877	BUS93877	AGENCOURT
603	54.6	1056	4	BG032394	602300394	BG032394	676	53.2	3.2	871	5	BUS40167	BUS40167	AGENCOURT
604	54.4	625	7	CF921039	gm1rhw3-2	CF921039	677	53.2	3.2	895	5	BUS88665	BUS88665	AGENCOURT
605	54.4	637	7	CO541834	gm.K005 2	CO541834	678	53.2	3.2	906	5	BUS31084	BUS31084	AGENCOURT
606	54.2	573	7	CF977921	PAR17G1.R	CF977921	c 679	53.2	3.2	1101	9	CNS00KFT	AL077924	Drosophil
607	54.2	736	9	CNS03WTV	Tetraodon	AL264172	680	53.2	3.2	1379	4	BM548276	BM548276	AGENCOURT
608	54.2	749	5	BUS34260	AGENCOURT	BUS34260	681	53	3.2	286	6	CD773252	CD773252	AGENCOURT

682	53	3.2	296	6	CB076532	CB076532 hf44g04.g	755	52.4	3.1	1298	5	BQ277164	BQ277164 AGENCOURT
683	53	3.2	335	2	CF381770	CF381770 lab84b07.	c 756	52.4	3.1	1357	9	CL080800	CL080800 CH216-159
c 684	53	3.2	432	1	AV665533	AV665533 AV665533	c 757	52.4	3.1	1381	9	AG350187	AG350187 Mus muscu
685	53	3.2	659	9	AG083939	AG083939 Pan trogl	758	52.4	3.1	1699	3	HSR01509	HSR01509 Homo sapi
686	53	3.2	837	9	CNS011F1	AL100200 Dreophil	759	52.4	3.1	1795	3	CL513862	CL513862 SAILI 880
687	53	3.2	864	4	CNS177352	CNS177352 Dreophil	c 760	52.4	3.1	1924	4	B1524436	B1524436 603051712
688	53	3.2	938	5	BU960786	BU960786 AGENCOURT	c 761	52.2	3.1	207	7	CF890463	CF890463 TCTR-1266
689	53	3.2	941	7	CK420653	CK420653 AUF Iptrk	c 762	52.2	3.1	211	21	CG981484	CG981484 MRC3-CN014
c 690	53	3.2	999	5	BU4326211	BU4326211 603323486	763	52.2	3.1	214	6	CA689180	CA689180 wlm96-pko
c 691	53	3.2	1015	9	CL135318	CL135318 ISB1-106P	764	52.2	3.1	231	4	BM529684	BM529684 fyl4h03.y
c 692	53	3.2	1293	9	AG346949	AG346949 Mus muscu	765	52.2	3.1	234	7	CO193387	CO193387 EC35693.5
693	52.8	3.1	196	5	BQ786696	BQ786696 saq72a12.	766	52.2	3.1	276	7	CK379421	CK379421 lailld07.
694	52.8	3.1	234	1	AV349585	AV349585 AV349585	767	52.2	3.1	289	5	BU764209	BU764209 saes4a02.
695	52.8	3.1	250	7	CO191457	CO191457 CK30893.5	768	52.2	3.1	290	5	BQ640732	BQ640732 he32e05.y
696	52.8	3.1	279	7	CF559257	CF559257 DKZP0468M	769	52.2	3.1	301	7	CF622338	CF622338 laf02f12.
697	52.8	3.1	295	7	CF630157	CF630157 DKZP0469M	770	52.2	3.1	308	7	CK375298	CK375298 lai48a03.
c 698	52.8	3.1	302	2	BF362739	BF362739 RC1-NN007	771	52.2	3.1	352	7	CO181785	CO181785 lai48a03.
699	52.8	3.1	315	7	CF804740	CF804740 lad78h10.	c 772	52.2	3.1	381	9	CNS03001	AL252730 Tetraodon
c 700	52.8	3.1	317	7	CNS37157	CNS37157 UI-M-HS0-	773	52.2	3.1	387	8	AZ878524	AZ878524 RPCI-23-1
701	52.8	3.1	323	7	CK379820	CK379820 lai59a11.	774	52.2	3.1	400	7	CK384950	CK384950 lah56e09.
702	52.8	3.1	399	4	BG113662	BG113662 602284164	775	52.2	3.1	405	7	CF968846	CF968846 lag73f11.
703	52.8	3.1	650	6	CD773004	CD773004 AGENCOURT	776	52.2	3.1	428	1	AV681953	AV681953 AV681953
704	52.8	3.1	720	7	CV066275	CV066275 WNELJ32B4	777	52.2	3.1	431	6	CB524077	CB524077 UI-N-GK0-
705	52.8	3.1	813	5	BU950671	BU950671 AGENCOURT	778	52.2	3.1	445	7	CK632450	CK632450 AML-AP000
706	52.8	3.1	840	5	BM985947	BM985947 7.C05.T3	779	52.2	3.1	466	7	CK421958	CK421958 AUF_IpSpn
707	52.8	3.1	849	9	AG044091	AG044091 Pan trogl	780	52.2	3.1	473	4	BG622466	BG622466 602647179
708	52.8	3.1	862	6	CA463085	CA463085 AGENCOURT	781	52.2	3.1	548	7	CK983417	CK983417 re24g03.y
709	52.8	3.1	866	5	BU587173	BU587173 AGENCOURT	782	52.2	3.1	573	7	CV223060	CV223060 ta156f08.
710	52.8	3.1	914	5	BU563375	BU563375 AGENCOURT	783	52.2	3.1	584	4	BU519721	BU519721 BJS19721
711	52.8	3.1	945	5	BU851541	BU851541 AGENCOURT	784	52.2	3.1	614	6	CD251677	CD251677 AGENCOURT
712	52.8	3.1	947	6	CB205316	CB205316 AGENCOURT	785	52.2	3.1	635	4	BG107420	BG107420 602277525
713	52.8	3.1	1131	4	BM542918	BM542918 AGENCOURT	786	52.2	3.1	688	7	CV522032	CV522032 0089P0069
714	52.8	3.1	2186	3	CK749590	CK749590 Homo sapi	787	52.2	3.1	710	7	CN590804	CN590804 TJ5000144
715	52.6	3.1	274	7	CV072032	CV072032 ESTP193.Z	c 788	52.2	3.1	712	4	BJS32300	BJS32300 BJS32300
716	52.6	3.1	304	7	CN927725	CN927725 000530ABP	789	52.2	3.1	723	7	CK451264	CK451264 904423.MA
c 717	52.6	3.1	350	5	BX553079	BX553079 BX553079	790	52.2	3.1	743	1	AV757929	AV757929 AV757929
718	52.6	3.1	427	6	CA778567	CA778567 MPL384.9	791	52.2	3.1	819	5	BU534439	BU534439 AGENCOURT
719	52.6	3.1	493	7	CK377070	CK377070 lah97h03.-	792	52.2	3.1	846	5	BU564052	BU564052 AGENCOURT
720	52.6	3.1	504	6	CB678747	CB678747 OSJNEF01F	793	52.2	3.1	906	7	CK159239	CK159239 FGAS04064
721	52.6	3.1	560	4	BG924474	BG924474 HNC27-1-D	794	52.2	3.1	1000	4	BG572421	BG572421 602593463
722	52.6	3.1	659	6	CD771540	CD771540 AGENCOURT	795	52	3.1	169	4	BU703874	BU703874 BJS703874
723	52.6	3.1	731	7	CF924696	CF924696 DD005C04.	796	52	3.1	172	5	BX504780	BX504780 DKF2p686F
724	52.6	3.1	778	5	BU534338	BU534338 AGENCOURT	797	52	3.1	192	1	AA276487	AA276487 Bvg3e10.r
725	52.6	3.1	811	6	CB951950	CB951950 AGENCOURT	798	52	3.1	202	7	CO883666	CO883666 Bvcgen.11
726	52.6	3.1	812	9	AG031898	AG031898 Pan trogl	799	52	3.1	228	7	CK381405	CK381405 lag38a01.
727	52.6	3.1	825	5	BU850748	BU850748 AGENCOURT	800	52	3.1	243	4	BM187410	BM187410 fw17d12.y
728	52.6	3.1	829	7	CK794790	CK794790 AGENCOURT	801	52	3.1	266	1	AA616347	AA616347 vn65b12.x
729	52.6	3.1	856	5	BU934849	BU934849 AGENCOURT	802	52	3.1	403	6	CA366868	CA366868 642552.NC
730	52.6	3.1	1002	6	CB206065	CB206065 AGENCOURT	803	52	3.1	425	7	CF424254	CF424254 lad27b04.
c 731	52.6	3.1	1380	9	AG311242	AG311242 Mus muscu	c 804	52	3.1	461	6	CB348689	CB348689 CAB2SG000
732	52.6	3.1	1920	3	BC047319	BC047319 Homo sapi	805	52	3.1	478	7	CF779197	CF779197 tad24e10.
733	52.4	3.1	160	2	AW318295	AW318295 sg63d05.y	806	52	3.1	500	7	CK406831	CK406831 AUF_Iflvr
734	52.4	3.1	172	7	CF983728	CF983728 IG02 grap	c 807	52	3.1	590	9	BX240864	BX240864 DanTo_rer
735	52.4	3.1	199	4	BJ699239	BJ699239 BJ699239	808	52	3.1	615	4	BG435835	BG435835 602508457
736	52.4	3.1	244	7	CK430436	CK430436 oj49d02.y	809	52	3.1	743	5	BU108854	BU108854 603112530
737	52.4	3.1	293	4	BM155090	BM155090 fv93d10.y	810	52	3.1	852	5	BU946451	BU946451 AGENCOURT
738	52.4	3.1	374	4	BM154585	BM154585 fv86h02.y	c 811	52	3.1	882	7	CK160127	CK160127 FGAS04167
739	52.4	3.1	432	2	AW773386	AW773386 ip06c01.y	812	52	3.1	935	6	CD384935	CD384935 AGENCOURT
740	52.4	3.1	490	7	CO874828	CO874828 Bvgden.03	813	52	3.1	939	7	CN310359	CN310359 170005999
741	52.4	3.1	562	2	AW636413	AW636413 b146d05.w	814	52	3.1	1016	9	CNS01609	AL107211 Dreophil
742	52.4	3.1	579	7	CF752690	CF752690 om.A001.0	815	52	3.1	1331	5	BM904910	BM904910 AGENCOURT
743	52.4	3.1	603	7	CN004672	CN004672 ip21e12.g	816	51.8	3.1	194	5	BJS30627	BU530627 AGENCOURT
744	52.4	3.1	619	7	CO535894	CO535894 tah10e04	817	51.8	3.1	218	7	CO727269	CO727269 UMC-bend
c 745	52.4	3.1	648	8	AZ379719	AZ379719 LM0135K02	818	51.8	3.1	225	4	BG736457	BG736457 rk57d03.y
746	52.4	3.1	803	6	CB318690	CB318690 AGENCOURT	819	51.8	3.1	236	2	AW657557	AW657557 110971.MA
747	52.4	3.1	826	4	BM041903	BM041903 603615963	820	51.8	3.1	252	4	BM531343	BM531343 fx86a07.y
748	52.4	3.1	870	5	BU843763	BU843763 AGENCOURT	c 821	51.8	3.1	269	4	BG980699	BG980699 MR3-CN014
749	52.4	3.1	873	6	CB844849	CB844849 M2PN-0411	c 822	51.8	3.1	278	4	BG983803	BG983803 MR4-CN014
c 750	52.4	3.1	880	7	CK159114	CK159114 FGAS04050	823	51.8	3.1	310	4	BM154701	BM154701 fv88c10.y
751	52.4	3.1	887	5	BU850963	BU850963 AGENCOURT	824	51.8	3.1	311	4	BM154695	BM154695 fv88c02.y
752	52.4	3.1	949	9	CNS002P1	AL097968 Dreophil	825	51.8	3.1	320	4	BM574233	BM574233 fx60g11.y
753	52.4	3.1	1010	6	CD171719	CD171719 AGENCOURT	826	51.8	3.1	320	5	BU709836	BU709836 fx64d03.y
754	52.4	3.1	1148	6	CD500545	CD500545 CDA45-F05	827	51.8	3.1	321	4	BM154709	BM154709 fv88d07.y

828	51.8	3.1	323	4	BM155040	BM155040 fv92g05.y	901	51.6	3.1	963	7	CF780924	CF780924	AGENCOURT
829	51.8	3.1	336	5	BM783539	BM783539 fab30h11.y	c 902	51.6	3.1	968	5	BM381631	BM381631	AGENCOURT
830	51.8	3.1	340	4	BM155408	BM155408 fw04e06.y	c 903	51.6	3.1	969	7	CK426147	CK426147	AUF IpFes
831	51.8	3.1	345	4	BM534831	BM534831 fx71h06.y	904	51.6	3.1	1002	5	BU590111	BU590111	AGENCOURT
832	51.8	3.1	351	1	AL724883	AL724883 AL724883	905	51.6	3.1	1006	5	BU530175	BU530175	AGENCOURT
833	51.8	3.1	354	4	BM154696	BM154696 fv88c03.y	906	51.6	3.1	1035	6	CD246704	CD246704	AGENCOURT
834	51.8	3.1	356	4	BM155084	BM155084 fv93c11.y	907	51.6	3.1	1093	9	CNS04C0C	CNS04C0C	Tetraodon
835	51.8	3.1	358	6	CB721263	CB721263 jnn603C06	908	51.6	3.1	1122	4	BI259611	BI259611	AGENCOURT
836	51.8	3.1	439	1	AV682218	AV682218 AV682218	c 909	51.6	3.1	1333	9	AG390651	AG390651	Mus muscu
837	51.8	3.1	463	1	AV682001	AV682001 AV682001	910	51.6	3.1	1426	4	BM388238	BM388238	AGENCOURT
838	51.8	3.1	503	8	BM08074	BM08074 TTG24-Sp6.1	911	51.4	3.1	201	2	AW102260	AW102260	sd85d10.y
839	51.8	3.1	540	6	CA320990	CA320990 UI-M-FV0-	912	51.4	3.1	232	4	BM280863	BM280863	ki06b01.y
840	51.8	3.1	557	9	CB135710	CB135710 tigr-gss-	913	51.4	3.1	252	4	BM574901	BM574901	fx37e09.y
841	51.8	3.1	563	7	CF805126	CF805126 lad62f08.	914	51.4	3.1	277	6	CD722233	CD722233	oj07b05.y
842	51.8	3.1	599	8	BI16188	BI16188 347E7.TV CI	915	51.4	3.1	334	7	CO194571	CO194571	EC38826.5
843	51.8	3.1	606	6	CD239409	CD239409 FNPUB12	c 916	51.4	3.1	361	1	AI819970	AI819970	wj88h03.x
844	51.8	3.1	610	8	BI17639	BI17639 347E7.TVB C	917	51.4	3.1	366	7	CO722305	CO722305	mdfr30190
845	51.8	3.1	632	7	CV193140	CV193140 km36h05.y	918	51.4	3.1	371	1	AV689111	AV689111	AV689111
846	51.8	3.1	674	6	CD638408	CD638408 AGENCOURT	919	51.4	3.1	372	7	CF331850	CF331850	NACL--08-
847	51.8	3.1	700	6	CD640967	CD640967 AGENCOURT	920	51.4	3.1	401	4	BG108147	BG108147	602280213
848	51.8	3.1	747	9	CNS011RQ	AL100640 Drosophi1	c 921	51.4	3.1	440	4	BG944106	BG944106	ax46e08.x
849	51.8	3.1	748	9	AG031854	AG031854 Pan trogl	922	51.4	3.1	441	4	BM285111	BM285111	kh94h02.y
850	51.8	3.1	780	7	CNS23584	CNS23584 AGENCOURT	923	51.4	3.1	464	5	BQ639526	BQ639526	he16g12.y
851	51.8	3.1	797	5	BU555131	BU555131 AGENCOURT	924	51.4	3.1	475	5	BQ093142	BQ093142	fy94c12.y
852	51.8	3.1	804	5	BU530964	BU530964 AGENCOURT	925	51.4	3.1	476	6	CB721269	CB721269	jnn603D03
853	51.8	3.1	814	5	BU566469	BU566469 AGENCOURT	926	51.4	3.1	487	5	BQ196890	BQ196890	NXLV106.F
854	51.8	3.1	820	6	CA464889	CA464889 AGENCOURT	927	51.4	3.1	557	6	CA779552	CA779552	MPL384.12
855	51.8	3.1	872	7	CK157539	CK157539 FGAS03867	928	51.4	3.1	557	7	CF123296	CF123296	UI-HF-CHO
856	51.8	3.1	877	3	BC040855	BC040855 Homo sapi	929	51.4	3.1	578	5	BP265719	BP265719	BP265719
857	51.8	3.1	920	5	BU563586	BU563586 AGENCOURT	930	51.4	3.1	583	6	CB073419	CB073419	taa32f07.
858	51.8	3.1	973	5	BQ721625	BQ721625 AGENCOURT	931	51.4	3.1	591	4	BI378442	BI378442	BFLG1_000
859	51.8	3.1	982	4	BG288697	BG288697 602385510	932	51.4	3.1	620	6	CA321372	CA321372	UI-M-FV0-
860	51.8	3.1	1084	5	BU189453	BU189453 AGENCOURT	933	51.4	3.1	624	8	BQ622353	BQ622353	602647035
861	51.8	3.1	1126	6	CD523341	CD523341 AGENCOURT	c 934	51.4	3.1	702	8	AQ256508	AQ256508	nbbx0016M
862	51.8	3.1	1452	9	CL125503	CL125503 ISB1-87B2	935	51.4	3.1	720	6	CD641235	CD641235	AGENCOURT
863	51.6	3.1	191	7	CK895966	CK895966 SGP158500	936	51.4	3.1	762	7	CK655134	CK655134	AGENCOURT
864	51.6	3.1	216	4	BU699031	BU699031	937	51.4	3.1	783	7	CNS385817	CNS385817	LE2TR04J2
865	51.6	3.1	220	2	BE014996	BE014996 126931.MA	938	51.4	3.1	789	6	CB571699	CB571699	AGENCOURT
866	51.6	3.1	254	4	BG981471	BG981471 MR3-CN014	939	51.4	3.1	800	5	BU843107	BU843107	AGENCOURT
867	51.6	3.1	300	7	CK428349	CK428349 laj14g03.y	940	51.4	3.1	859	7	CNS39423	CNS39423	AGENCOURT
868	51.6	3.1	309	4	BM186118	BM186118 fv98b09.y	941	51.4	3.1	867	5	BU843011	BU843011	AGENCOURT
869	51.6	3.1	335	7	CF211902	CF211902 CGF100066	942	51.4	3.1	871	6	CB204789	CB204789	AGENCOURT
870	51.6	3.1	347	4	BM130321	BM130321 pb29e10.y	943	51.4	3.1	883	3	CK865669	CK865669	AGENCOURT
871	51.6	3.1	348	7	CK379136	CK379136 la131b08.	944	51.4	3.1	935	5	BQ958308	BQ958308	AGENCOURT
872	51.6	3.1	375	1	AL713177	AL713177 DFP2p866L	945	51.4	3.1	939	7	CNS14330	CNS14330	AGENCOURT
873	51.6	3.1	432	7	CF373277	CF373277 JMT--07-K	946	51.4	3.1	941	6	CB195504	CB195504	AGENCOURT
874	51.6	3.1	438	4	BJ679676	BJ679676	947	51.4	3.1	973	5	BU945046	BU945046	AGENCOURT
875	51.6	3.1	484	5	BM342763	BM342763 fw47902.y	948	51.4	3.1	975	5	BU963322	BU963322	AGENCOURT
876	51.6	3.1	495	5	BM903137	BM903137 NXLV_080	949	51.4	3.1	1011	6	CD388840	CD388840	AGENCOURT
877	51.6	3.1	577	4	BG927541	BG927541 HNC10-1-B	950	51.4	3.1	1014	5	BU565689	BU565689	AGENCOURT
878	51.6	3.1	602	5	BU589676	BU589676 AGENCOURT	c 951	51.4	3.1	1074	8	BZ696936	BZ696936	SP_Ba009
879	51.6	3.1	604	4	BG927528	BG927528 HNC10-1-C	952	51.4	3.1	1101	9	CNS00ED1	CNS00ED1	AGENCOURT
880	51.6	3.1	607	1	AA522011	AA522011 vht8c09.r	953	51.4	3.1	1112	3	BM920193	BM920193	AGENCOURT
881	51.6	3.1	617	4	BI829090	BI829090 603079182	954	51.4	3.1	151	7	BC032411	BC032411	Homo sapi
882	51.6	3.1	627	6	CA330151	CA330151 haa92b01.	c 955	51.2	3.0	151	7	CF203260	CF203260	RR890915N
883	51.6	3.1	643	3	BI870743	BI870743 603392853	c 956	51.2	3.0	185	4	CG980530	CG980530	MR3-CN014
884	51.6	3.1	673	6	CD707049	CD707049 AGENCOURT	c 957	51.2	3.0	193	7	CK615915	CK615915	ou07c12.y
885	51.6	3.1	697	6	CB319237	CB319237 AGENCOURT	c 958	51.2	3.0	213	4	CG981500	CG981500	MR3-CN014
886	51.6	3.1	761	5	BU555158	BU555158 AGENCOURT	c 959	51.2	3.0	201	4	BM265810	BM265810	fw36b10.y
887	51.6	3.1	771	7	CNS31817	CNS31817 AGENCOURT	c 960	51.2	3.0	202	4	BM983780	BM983780	fx4-CN014
888	51.6	3.1	780	9	AL291788	AL291788 Tetraodon	961	51.2	3.0	210	4	BM573150	BM573150	fw02b03.y
889	51.6	3.1	787	9	AG364646	AG364646 Mus muscu	962	51.2	3.0	213	4	BM155328	BM155328	fw02b03.y
890	51.6	3.1	818	5	BU850480	BU850480 AGENCOURT	c 963	51.2	3.0	217	4	CG981736	CG981736	MR3-CN014
891	51.6	3.1	833	5	BU850474	BU850474 AGENCOURT	964	51.2	3.0	218	4	BM154944	BM154944	fv91e06.y
892	51.6	3.1	853	1	AV758844	AV758844	c 965	51.2	3.0	219	1	AL714277	AL714277	AGENCOURT
893	51.6	3.1	855	7	CNS30709	CNS30709 AGENCOURT	966	51.2	3.0	219	4	BI709326	BI709326	fv63b09.y
894	51.6	3.1	856	2	BS909150	BS909150 601501758	967	51.2	3.0	219	4	BM154546	BM154546	fv86d07.y
895	51.6	3.1	866	7	CF765154	CF765154 CES002716	968	51.2	3.0	220	4	BM573836	BM573836	fv04f07.y
896	51.6	3.1	868	5	BU530888	BU530888 AGENCOURT	969	51.2	3.0	225	4	BM154392	BM154392	fv84e06.y
897	51.6	3.1	869	5	BU566247	BU566247 AGENCOURT	970	51.2	3.0	225	4	BM186096	BM186096	fv97h07.y
898	51.6	3.1	902	2	BF575271	BF575271 602133679	971	51.2	3.0	230	4	BM186042	BM186042	fv96h12.y
899	51.6	3.1	926	5	BU554921	BU554921 AGENCOURT	972	51.2	3.0	231	7	COL81733	COL81733	EC4891.5
900	51.6	3.1	932	3	CR648408	CR648408 Tetraodon	973	51.2	3.0	233	5	BQ786705	BQ786705	saq72b12.

974	51.2	3.0	234	4	BM154438	BM154438	fv85b03.y	1047	51	3.0	231	5	5	BX646093	BX646093	DKF7p781E
975	51.2	3.0	235	7	CF317850	CF317850	HD--07-L0	1048	51	3.0	239	6	6	CD000864	CD000864	AGENCOURT
976	51.2	3.0	237	4	BJ679532	BJ679532		1049	51	3.0	248	7	7	CR772335	CR772335	AGENCOURT
977	51.2	3.0	247	4	BM187242	BM187242	fw13g02.y	1050	51	3.0	261	4	4	BJ469921	BJ469921	BM521967
978	51.2	3.0	248	4	B1704970	B1704970	fw60909.y	1051	51	3.0	281	4	4	BM521967	BM521967	ESSU0504
979	51.2	3.0	249	4	BJ682710	BJ682710	fw682710	1052	51	3.0	315	7	7	CR753138	CR753138	DKF7p468E
980	51.2	3.0	254	4	B1705355	B1705355	fr57g11.y	1053	51	3.0	334	7	7	CO195973	CO195973	EC3376.5
981	51.2	3.0	274	4	BM181089	BM181089	fv94a06.y	1054	51	3.0	349	7	7	CO194580	CO194580	EC33842.5
982	51.2	3.0	278	7	CF123167	CF123167	UI-HF-CHO	1055	51	3.0	350	8	8	BH283073	BH283073	CH230-180
983	51.2	3.0	283	6	CB933364	CB933364	ri29a06.y	1056	51	3.0	359	7	7	CN949627	CN949627	000719AVF
984	51.2	3.0	302	7	CF514461	CF514461	CABud0006	1057	51	3.0	368	5	5	BQ635986	BQ635986	hd02h07.y
985	51.2	3.0	304	7	CF613058	CF613058	la32b10.	1058	51	3.0	368	6	6	CB049672	CB049672	NISC_gj12
986	51.2	3.0	312	7	CF382308	CF382308	lac61h10.	1059	51	3.0	368	6	6	CD639770	CD639770	AGENCOURT
987	51.2	3.0	328	5	BUT63409	BUT63409	ea942c02.	1060	51	3.0	383	1	1	AA401292	AA401292	va63g05.r
988	51.2	3.0	336	7	CK372384	CK372384	lai8aa11.	1061	51	3.0	387	6	6	CB955957	CB955957	AGENCOURT
989	51.2	3.0	336	7	CO509976	CO509976	ta991f07.	1062	51	3.0	395	5	5	BM889038	BM889038	kb04e08.y
990	51.2	3.0	340	6	CB084036	CB084036	hq08d08.b	1063	51	3.0	406	7	7	CO184293	CO184293	EC27824.5
991	51.2	3.0	343	7	CK375218	CK375218	lai46h07.	1064	51	3.0	455	1	1	AA269939	AA269939	va64e10.r
992	51.2	3.0	347	5	CB253791	CB253791		1065	51	3.0	457	5	5	BQ527792	BQ527792	NISC_n024
993	51.2	3.0	397	6	CB257961	CB257961	85-E01113	1066	51	3.0	473	1	1	AL037117	AL037117	DKF7p564M
c 994	51.2	3.0	412	7	CV354891	CV354891	MR4-EN007	1067	51	3.0	546	7	7	CF123295	CF123295	UI-HF-CHO
c 995	51.2	3.0	428	6	CA803003	CA803003	sau45g07.	1068	51	3.0	572	7	7	CO873859	CO873859	BovGen_02
996	51.2	3.0	453	4	BG595797	BG595797	CM2-CI077	1069	51	3.0	642	1	1	AV764206	AV764206	AV764206
997	51.2	3.0	467	7	CF980284	CF980284	re03a12.y	1070	51	3.0	642	7	7	CK656065	CK656065	AGENCOURT
998	51.2	3.0	470	4	BM187391	BM187391	fw17a01.y	1071	51	3.0	647	7	7	CF731589	CF731589	UI-M-HAO-
999	51.2	3.0	470	5	BQ093110	BQ093110	fy94a03.y	1072	51	3.0	785	4	4	BI523919	BI523919	603051662
1000	51.2	3.0	488	6	CA811197	CA811197	CA22LI061	1073	51	3.0	834	5	5	BU554800	BU554800	AGENCOURT
1001	51.2	3.0	489	1	AV682229	AV682229		1074	51	3.0	840	5	5	BU530592	BU530592	AGENCOURT
1002	51.2	3.0	527	5	BM943015	BM943015	UI-M-B21-	1075	51	3.0	860	5	5	BU565723	BU565723	AGENCOURT
1003	51.2	3.0	530	4	BM573742	BM573742	fy03b10.y	1076	51	3.0	860	7	7	CF289324	CF289324	AGENCOURT
1004	51.2	3.0	538	1	AL925790	AL925790		1077	51	3.0	861	7	7	CR288979	CR288979	CR288979
1005	51.2	3.0	541	7	CN840817	CN840817	AGENCOURT	1078	51	3.0	862	5	5	BU601053	BU601053	AGENCOURT
1006	51.2	3.0	566	4	BM155067	BM155067	fv93a12.y	1079	51	3.0	895	6	6	CB309933	CB309933	AGENCOURT
1007	51.2	3.0	622	4	BG106619	BG106619	602290443	1080	51	3.0	904	5	5	BU940115	BU940115	AGENCOURT
1008	51.2	3.0	649	2	BF788814	BF788814	602110522	1081	51	3.0	930	5	5	BU589620	BU589620	AGENCOURT
1009	51.2	3.0	650	6	CD767936	CD767936		1082	51	3.0	932	4	4	BM416498	BM416498	OP21593.M
1010	51.2	3.0	657	5	BQ078813	BQ078813	fy81c06.y	1083	51	3.0	944	6	6	CD051079	CD051079	AGENCOURT
1011	51.2	3.0	769	7	CV065944	CV065944	WNEI28f8	1084	51	3.0	951	5	5	BU959950	BU959950	AGENCOURT
1012	51.2	3.0	775	7	CK787487	CK787487	AGENCOURT	1085	51	3.0	973	5	5	BU958938	BU958938	AGENCOURT
1013	51.2	3.0	776	9	CNS009BD	AL053563	Drosophil	1086	51	3.0	1010	6	6	CA976113	CA976113	AGENCOURT
1014	51.2	3.0	779	4	BG539542	BG539542	602568176	1087	51	3.0	1102	4	4	BG564613	BG564613	602584102
1015	51.2	3.0	786	7	CF455765	CF455765	AGENCOURT	1088	51	3.0	1168	9	9	AG347267	AG347267	Mus.muscu
1016	51.2	3.0	794	4	BI695737	BI695737	603345085	1089	51	3.0	1189	5	5	BU508070	BU508070	AGENCOURT
c1017	51.2	3.0	798	9	CNS010HK	AL098978	Drosophil	1090	51	3.0	1189	9	9	CG752264	CG752264	P046-4-G0
1018	51.2	3.0	822	7	CN168497	CN168497	AGENCOURT	1091	51	3.0	1448	9	9	CL073846	CL073846	CH216-130
1019	51.2	3.0	823	5	BU530830	BU530830	AGENCOURT	1092	51	3.0	1531	9	9	CL058486	CL058486	CH216-88C
1020	51.2	3.0	841	2	BF342119	BF342119	602012877	1093	51	3.0	1782	3	3	CR749618	CR749618	Homo.sapi
1021	51.2	3.0	847	5	BU554569	BU554569	AGENCOURT	1094	51	3.0	2172	9	9	CL078016	CL078016	CH216-147
1022	51.2	3.0	872	7	CK022958	CK022958	AGENCOURT	1095	51	3.0	162	5	5	BQ094671	BQ094671	san50d03.
1023	51.2	3.0	891	5	BU521330	BU521330	AGENCOURT	1096	51	3.0	176	4	4	BI497039	BI497039	df131b05.
1024	51.2	3.0	921	5	BU564012	BU564012	AGENCOURT	1097	51	3.0	179	5	5	BX250051	BX250051	BX250051
1025	51.2	3.0	930	5	BU563671	BU563671	AGENCOURT	1098	51	3.0	192	4	4	BM569696	BM569696	ih96b12.y
c1026	51.2	3.0	941	8	A2539217	A2539217	ENTEJ48TF	1099	51	3.0	198	4	4	BG980744	BG980744	MR3-CN014
1027	51.2	3.0	961	4	BM416004	BM416004	OP21087.M	1100	51	3.0	209	7	7	CF546313	CF546313	lae1a04.
1028	51.2	3.0	1004	4	BG252914	BG252914	602365514	1101	51	3.0	213	2	2	AW423994	AW423994	sh59b11.y
1029	51.2	3.0	1005	9	AG417297	AG417297	Mus.muscu	1102	51	3.0	223	5	5	BQ235609	BQ235609	hd83d07.g
c1030	51.2	3.0	1017	8	BM155389	BM155389	ENTO73TF	1103	51	3.0	240	4	4	BM341802	BM341802	fw53a03.y
1031	51.2	3.0	1027	6	CB208525	CB208525	AGENCOURT	1104	51	3.0	251	4	4	BM533329	BM533329	fy16e09.y
1032	51.2	3.0	1085	4	BG027405	BG027405	602296130	1105	51	3.0	258	2	2	BE752483	BE752483	204884.MA
1033	51.2	3.0	1087	7	CK213437	CK213437	ILLUMIGEN	1106	51	3.0	264	1	1	AL598482	AL598482	DKF7p313J
c1034	51.2	3.0	1100	9	CK145579	CK145579	ISBI-146A	1107	51	3.0	271	5	5	BX497273	BX497273	DKF7p779JL
c1035	51.2	3.0	1101	9	CNS00186	AL058835	Drosophil	1108	51	3.0	293	4	4	BM186087	BM186087	fv97g08.y
1036	51.2	3.0	1101	9	CNS008UB	AL069859	Drosophil	1109	51	3.0	317	7	7	CO754046	CO754046	Mdf33020p
1037	51.2	3.0	1609	9	CL080652	CL080652	CH216-159	1110	51	3.0	341	7	7	CR766009	CR766009	DKF7p468F
1038	51.2	3.0	1727	9	CL118815	CL118815	ISBI-7205	1111	51	3.0	354	1	1	AJ790178	AJ790178	AJ790178
1039	51	3.0	196	6	CA819430	CA819430	sau78C12.	1112	51	3.0	396	4	4	BI538310	BI538310	42810.MA
c1040	51	3.0	197	2	BF936477	BF936477	EST459532	1113	51	3.0	419	6	6	BE514524	BE514524	601315968
c1041	51	3.0	197	7	CF314022	CF314022	HD--02-G0	1114	51	3.0	419	6	6	CD102064	CD102064	AGENCOURT
c1042	51	3.0	200	6	CA814321	CA814321	CA48LN09I	c1115	51	3.0	431	7	7	CK304852	CK304852	SB02025B1
1043	51	3.0	202	6	CA819572	CA819572	sau80G01.	1116	51	3.0	442	6	6	CD679816	CD679816	lab08f08.
1044	51	3.0	221	7	CN834008	CN834008	AGENCOURT	1117	51	3.0	474	7	7	CK551618	CK551618	rhw1a0.00
1045	51	3.0	227	4	BI074139	BI074139	kt40e05.y	1118	51	3.0	495	6	6	CA379708	CA379708	65849.NC
1046	51	3.0	228	7	CO182911	CO182911	EC24271.5	1119	51	3.0	496	7	7	CN004590	CN004590	lp20e11.g

1120	50.8	3.0	499	7	C0726605	COT726605 ILLUMIGEN	1193	50.6	3.0	397	7	CF546355	CF546355 lae71h04.
1121	50.8	3.0	516	7	CN833696	CN833696 AGENCOURT	c1194	50.6	3.0	402	2	AW190286	AW190286 xl13d04.x
1122	50.8	3.0	544	7	CF123716	CF123716 UI-HF-CHO	1195	50.6	3.0	408	7	CN048707	CN048707 v2_p1_O13
1123	50.8	3.0	556	7	CV199827	CV199827 km20h10.y	1196	50.6	3.0	409	7	BI899036	BI899036 480889 MA
1124	50.8	3.0	571	5	B0747579	B0747579 UI-M-FAO-	1197	50.6	3.0	409	7	CK384344	CK384344 lah222c05.
1125	50.8	3.0	577	6	CB524184	CB524184 UI-M-GKO-	1198	50.6	3.0	412	6	CB075778	CB075778 lz51b09.b
1126	50.8	3.0	642	4	B1870677	B1870677 603394773	1199	50.6	3.0	414	5	EX504814	EX504814 DKEZp686J
1127	50.8	3.0	651	8	AQ510797	AQ510797 nbxb0048J	1200	50.6	3.0	431	7	CF123177	CF123177 UI-HF-CHO
1128	50.8	3.0	659	6	CD642013	CD642013 AGENCOURT	1201	50.6	3.0	432	1	AJ725854	AJ725854 AJ725854
1129	50.8	3.0	660	1	AV704928	AV704928	1202	50.6	3.0	434	1	AJ791630	AJ791630 AJ791630
1130	50.8	3.0	707	7	CV520959	CV520959 0089P0052	1203	50.6	3.0	434	1	AL719646	AL719646
1131	50.8	3.0	712	7	CF981073	CF981073 re02e06.y	1204	50.6	3.0	436	1	AL729450	AL729450
1132	50.8	3.0	723	1	AV733682	AV733682	1205	50.6	3.0	437	1	AV682737	AV682737
1133	50.8	3.0	741	7	CV491293	CV491293 AGENCOURT	1206	50.6	3.0	444	6	CD239166	CD239166 FNPBLC12
1134	50.8	3.0	781	6	CB318685	CB318685 AGENCOURT	1207	50.6	3.0	446	4	BM319186	BM319186 ki69d11.y
1135	50.8	3.0	815	8	B19681	B19681 F4H19-T7.1	1208	50.6	3.0	450	7	CO888261	CO888261 BovGen.16
1136	50.8	3.0	817	8	BH156712	BH156712 ENTSM49TF	1209	50.6	3.0	451	1	AL721247	AL721247
1137	50.8	3.0	820	4	BF968558	BF968558 602271159	1210	50.6	3.0	451	2	BE883021	BE883021 601510028
1138	50.8	3.0	822	5	B0843256	B0843256 AGENCOURT	1211	50.6	3.0	459	7	CF980375	CF980375 re04b03.y
1139	50.8	3.0	822	9	CNS00911	AL052989 Drosophila	1212	50.6	3.0	462	4	BM569326	BM569326 kj59f02.y
1140	50.8	3.0	830	7	CK395910	CK395910 AGENCOURT	1213	50.6	3.0	463	6	CB445238	CB445238 696490 MA
1141	50.8	3.0	832	5	B0842545	B0842545 AGENCOURT	1214	50.6	3.0	464	4	BM517997	BM517997 ki86e09.y
1142	50.8	3.0	835	5	B0529221	B0529221 AGENCOURT	1215	50.6	3.0	465	4	BM517871	BM517871 ki83f02.y
1143	50.8	3.0	836	5	B0565750	B0565750 AGENCOURT	c1216	50.6	3.0	468	6	CF047285	CF047285 QCR6904.y
1144	50.8	3.0	847	7	CO647224	CO647224 ILLUMIGEN	1217	50.6	3.0	471	4	BI702656	BI702656 fr55h03.y
1145	50.8	3.0	881	7	CK151831	CK151831 FGAS03458	1218	50.6	3.0	475	4	BM567111	BM567111 kj10c09.y
1146	50.8	3.0	886	7	CK157081	CK157081 FGAS03815	1219	50.6	3.0	482	7	CF124659	CF124659 UI-HF-CHO
1147	50.8	3.0	886	7	CK161161	CK161161 FGAS04285	1220	50.6	3.0	501	1	AJ798819	AJ798819
1148	50.8	3.0	891	9	CNS0092JU	AL053767 Drosophila	1221	50.6	3.0	509	6	CB080062	CB080062 hp80f10.b
1149	50.8	3.0	905	7	CN322888	CN322888 AGENCOURT	1222	50.6	3.0	571	5	BP256021	BP256021
1150	50.8	3.0	908	7	CV066886	CV066886 WNEL9e5 W	1223	50.6	3.0	581	5	BP375614	BP375614
1151	50.8	3.0	909	7	CK407058	CK407058 AUF IFLvr	1224	50.6	3.0	584	7	CV053519	CV053519 BNEL100B9
1152	50.8	3.0	926	4	BG575702	BG575702 602598774	1225	50.6	3.0	585	7	CO403863	CO403863 AGENCOURT
1153	50.8	3.0	940	6	CD386618	CD386618 AGENCOURT	1226	50.6	3.0	597	4	BG572394	BG572394 602593434
1154	50.8	3.0	955	2	BE890041	BE890041 601512310	1227	50.6	3.0	606	5	BUI14551	BUI14551 603131443
1155	50.8	3.0	956	6	CD512769	CD512769 AGENCOURT	1228	50.6	3.0	614	6	CB980039	CB980039 CAB70001.y
1156	50.8	3.0	975	3	CR733776	CR733776 Tetraodon	1229	50.6	3.0	617	7	CF370504	CF370504
1157	50.8	3.0	996	9	CNS04XL6	AG311811 Tetraodon	1230	50.6	3.0	624	5	BP382214	BP382214
1158	50.8	3.0	1009	9	AG392861	AG392861 Mus muscu	1231	50.6	3.0	634	7	CK320427	CK320427 L3P07d09
1159	50.8	3.0	1023	5	B0506457	B0506457 AGENCOURT	1232	50.6	3.0	638	4	BG218217	BG218217 RST37944
1160	50.8	3.0	1031	9	CNS0164Y	AL107380 Drosophila	1233	50.6	3.0	642	7	CK456995	CK456995 921256 MA
1161	50.8	3.0	1098	6	CD049441	CD049441 AGENCOURT	1234	50.6	3.0	717	8	AZ849900	AZ849900 2M0151103
1162	50.8	3.0	1101	9	CNS016TQ	AL107192 Drosophila	1235	50.6	3.0	722	7	CV064765	CV064765 WNEL14H5
1163	50.8	3.0	1151	9	AG324438	AG324438 Mus muscu	1236	50.6	3.0	752	6	CD521791	CD521791 AGENCOURT
1164	50.8	3.0	1227	9	AG361182	AG361182 Mus muscu	c1237	50.6	3.0	771	9	AG517090	AG517090 Mus muscu
1165	50.8	3.0	1274	9	AG341312	AG341312 Mus muscu	1238	50.6	3.0	772	5	B0558222	B0558222 AGENCOURT
1166	50.8	3.0	1690	9	CL078351	CL078351 CH216-149	1239	50.6	3.0	801	7	CF289632	CF289632 AGENCOURT
1167	50.8	3.0	4796	3	CR749476	CR749476 Homo sapi	1240	50.6	3.0	803	5	B0565241	B0565241 AGENCOURT
1168	50.8	3.0	157	4	BM513623	BM513623 kx97b03.y	1241	50.6	3.0	806	7	CK128745	CK128745 AGENCOURT
1169	50.6	3.0	169	1	AL697897	AL697897 DKEZp686A	1242	50.6	3.0	809	5	B0843613	B0843613 AGENCOURT
1170	50.6	3.0	191	4	BI705400	BI705400 fr58g02.y	1243	50.6	3.0	813	5	B0842611	B0842611 AGENCOURT
1171	50.6	3.0	193	4	BM530850	BM530850 fy17e12.y	c1244	50.6	3.0	814	7	CK200263	CK200263 FGAS00877
1172	50.6	3.0	194	4	BM154531	BM154531 fv86c02.y	1245	50.6	3.0	816	5	B0564811	B0564811 AGENCOURT
1173	50.6	3.0	196	4	BI705266	BI705266 fr55f03.y	1246	50.6	3.0	826	9	CL043364	CL043364
1174	50.6	3.0	210	4	BM154362	BM154362 fv84b10.y	1247	50.6	3.0	827	9	BH182445	BH182445 O21_O_13-
1175	50.6	3.0	220	5	BQ785757	BQ785757 saq7c03.	1248	50.6	3.0	827	9	CNS07N08	AL619394 T7 end of
1176	50.6	3.0	222	7	CF926234	CF926234 lafe6e09.	1249	50.6	3.0	829	5	B0531959	B0531959 AGENCOURT
1177	50.6	3.0	236	4	BI681181	BI681181 460497 MA	1250	50.6	3.0	832	9	CNS00818	AL051195 Drosophila
1178	50.6	3.0	236	7	CF754919	CF754919 lae09c01.	1251	50.6	3.0	833	5	B0588052	B0588052 AGENCOURT
1179	50.6	3.0	252	6	CB043981	CB043981 NISC gc01	1252	50.6	3.0	833	6	CB963986	CB963986 AGENCOURT
1180	50.6	3.0	287	6	CB343712	CB343712 CA32EN000	1253	50.6	3.0	844	9	AG058605	AG058605 Pan trogl
1181	50.6	3.0	291	7	CO195274	CO195274 EC39963.5	1254	50.6	3.0	845	5	B0537023	B0537023 AGENCOURT
1182	50.6	3.0	318	6	CB984581	CB984581 AGENCOURT	1255	50.6	3.0	853	5	B0588997	B0588997 AGENCOURT
1183	50.6	3.0	337	5	BQ780082	BQ780082 UI-R-FFO-	1256	50.6	3.0	854	5	B0603992	B0603992 AGENCOURT
1184	50.6	3.0	345	2	BE878735	BE878735 601492990	1257	50.6	3.0	859	7	CO808031	CO808031 AGENCOURT
1185	50.6	3.0	346	5	BA476056	BA476056 DKEZp686B	c1258	50.6	3.0	868	7	CK200194	CK200194 FGAS00870
1186	50.6	3.0	348	6	CB704554	CB704554 AMGNNUC:S	1259	50.6	3.0	874	6	CB844981	CB844981 M2PN-0547
1187	50.6	3.0	375	3	AY068947	AY068947 Schmidtea	1260	50.6	3.0	876	7	CK323414	CK323414 AGENCOURT
1188	50.6	3.0	377	1	AL722378	AL722378 NISC gc04	1261	50.6	3.0	881	9	AZ200698	AZ200698 SP_1026 A
1189	50.6	3.0	386	6	CB044394	CB044394 NISC gc04	1262	50.6	3.0	883	9	AL067381	AL067381 CH216-110
1190	50.6	3.0	387	1	AZ043368	AZ043368 mu31c08.r	1263	50.6	3.0	886	9	CNS011SM	AL100672 Drosophila
1191	50.6	3.0	391	4	BJ688931	BJ688931	c1264	50.6	3.0	888	7	BM415362	BM415362 OP20436 M
1192	50.6	3.0	397	5	BQ395470	BQ395470 NISC ng15	c1265	50.6	3.0	888	7	CK160993	CK160993 FGAS04266

1266	50.6	3.0	889	5	B0851997	B0851997	AGENCOURT	1339	50.4	3.0	762	7	CK397238	CK397238	AGENCOURT
1267	50.6	3.0	904	4	B1859386	B1859386	603388113	1340	50.4	3.0	771	5	B0560352	B0560352	AGENCOURT
1268	50.6	3.0	915	4	B6518636	B6518636	602578491	1341	50.4	3.0	777	2	B8875022	B8875022	601487588
1269	50.6	3.0	915	5	B0718652	B0718652	AGENCOURT	1342	50.4	3.0	778	9	AG586300	AG586300	Mus muscu
1270	50.6	3.0	916	5	B0588527	B0588527	AGENCOURT	1343	50.4	3.0	787	5	AG586300	AG586300	AGENCOURT
c1271	50.6	3.0	936	3	B0233428	B0233428	AGENCOURT	1344	50.4	3.0	802	6	CD000230	CD000230	AGENCOURT
1272	50.6	3.0	937	9	CNS00127	CNS00127	Drocephal	1345	50.4	3.0	803	4	BG335466	BG335466	602403936
1273	50.6	3.0	941	5	B0534769	B0534769	AGENCOURT	1346	50.4	3.0	808	5	B0529789	B0529789	AGENCOURT
1274	50.6	3.0	944	5	B0431642	B0431642	AGENCOURT	1347	50.4	3.0	828	8	AZ194425	AZ194425	SP 1026 A
1275	50.6	3.0	955	5	B0533926	B0533926	AGENCOURT	1348	50.4	3.0	844	9	AG129984	AG129984	Par trogl
1276	50.6	3.0	955	5	B0566880	B0566880	AGENCOURT	1349	50.4	3.0	858	9	CNS0127J	CNS0127J	Drocephal
1277	50.6	3.0	956	7	CK423987	CK423987	AUF IpSto	1350	50.4	3.0	873	7	CF455006	CF455006	AGENCOURT
1278	50.6	3.0	960	6	CB597408	CB597408	AGENCOURT	1351	50.4	3.0	877	7	CK159921	CK159921	FGAS04144
c1279	50.6	3.0	962	8	AZ680445	AZ680445	ENTW50TR	1352	50.4	3.0	892	5	B0960887	B0960887	AGENCOURT
1280	50.6	3.0	978	4	B0569662	B0569662	602272040	1353	50.4	3.0	895	6	CB229191	CB229191	AGENCOURT
c1281	50.6	3.0	1005	8	BH164025	BH164025	ENTQU60TF	1354	50.4	3.0	908	6	CD513633	CD513633	AGENCOURT
1282	50.6	3.0	1054	3	AF130104	AF130104	Homo sapi	1355	50.4	3.0	912	5	B0529547	B0529547	AGENCOURT
1283	50.6	3.0	1063	5	B0840218	B0840218	AGENCOURT	1356	50.4	3.0	916	9	CNS06VOC	CNS06VOC	T3 end of
1284	50.6	3.0	1101	9	CNS00FJ7	CNS00FJ7	AGENCOURT	1357	50.4	3.0	923	5	B0533956	B0533956	AGENCOURT
1285	50.6	3.0	1122	4	BG501454	BG501454	602548028	1358	50.4	3.0	972	9	CNS00KMK	CNS00KMK	Drocephal
c1286	50.6	3.0	1124	9	AG288406	AG288406	Mus muscu	1359	50.4	3.0	998	6	CD049247	CD049247	AGENCOURT
1287	50.6	3.0	1150	6	CD249726	CD249726	AGENCOURT	1360	50.4	3.0	1011	5	B0934341	B0934341	AGENCOURT
1288	50.6	3.0	1165	9	CL051682	CL051682	CH216-74F	1361	50.4	3.0	1038	6	CD249177	CD249177	AGENCOURT
c1289	50.6	3.0	1178	9	AG430313	AG430313	Mus muscu	1362	50.4	3.0	1081	5	B0510236	B0510236	AGENCOURT
c1290	50.6	3.0	1260	3	AV108843	AV108843	Zea mays	1363	50.4	3.0	1085	9	CNS016E8	CNS016E8	Drocephal
1291	50.6	3.0	1380	6	CD248372	CD248372	CH261-62P	1364	50.4	3.0	1114	4	BM452203	BM452203	AGENCOURT
1292	50.6	3.0	1908	8	CC230203	CC230203	CH261-62P	1365	50.4	3.0	1161	9	AG365964	AG365964	Mus muscu
1293	50.6	3.0	3517	3	BC030264	BC030264	Homo sapi	1366	50.4	3.0	1205	4	BM544190	BM544190	AGENCOURT
1294	50.6	3.0	3543	3	HS0803534	HS0803534	Homo sapi	1367	50.4	3.0	1291	5	BQ231056	BQ231056	AGENCOURT
1295	50.4	3.0	141	7	CK467264	CK467264	938548 MA	1368	50.4	3.0	1504	3	EC023270	EC023270	Homo sapi
1296	50.4	3.0	164	7	CR548135	CR548135	DKFZp459I	1369	50.4	3.0	1651	9	CL079030	CL079030	CH216-154
1297	50.4	3.0	213	7	CF118240	CF118240	fe351.z1	1370	50.2	3.0	199	5	BQ326520	BQ326520	MR4-CN014
1298	50.4	3.0	261	7	CR763367	CR763367	DKFZp470I	1371	50.2	3.0	201	4	BG981501	BG981501	MR3-CN014
1299	50.4	3.0	270	4	BM281117	BM281117	ki09f12.Y	1372	50.2	3.0	201	6	CA667413	CA667413	leul.pko
1300	50.4	3.0	273	4	B1089262	B1089262	602853209	1373	50.2	3.0	203	7	CN276442	CN276442	170006001
1301	50.4	3.0	278	6	BQ289264	BQ289264	pj27g05.Y	1374	50.2	3.0	208	6	CA802715	CA802715	saualia12.5
1302	50.4	3.0	278	6	CD641261	CD641261	AGENCOURT	1375	50.2	3.0	209	7	CO182797	CO182797	EC24037.5
1303	50.4	3.0	293	4	B1855783	B1855783	603382721	1376	50.2	3.0	211	2	BE013113	BE013113	122910 MA
1304	50.4	3.0	296	1	A1856737	A1856737	eb41e07.Y	1377	50.2	3.0	214	4	BM265899	BM265899	fw37b09.Y
1305	50.4	3.0	306	1	AA789781	AA789781	vt79c07.r	1378	50.2	3.0	216	4	BM155135	BM155135	fw09b04.Y
1306	50.4	3.0	307	6	CD722153	CD722153	oj06b12.Y	1379	50.2	3.0	220	2	CF383299	CF383299	lac39C02.
1307	50.4	3.0	378	1	AV760102	AV760102	AGENCOURT	1380	50.2	3.0	223	5	BQ276953	BQ276953	AGENCOURT
1308	50.4	3.0	382	6	CA987506	CA987506	AGENCOURT	1381	50.2	3.0	239	4	BM532471	BM532471	fy08e08.Y
1309	50.4	3.0	408	6	CB770419	CB770419	AMGNNUC:S	1382	50.2	3.0	241	4	BM186126	BM186126	fv98c06.Y
1310	50.4	3.0	419	5	B0530428	B0530428	AGENCOURT	1383	50.2	3.0	243	7	CO193787	CO193787	EC36808.5
1311	50.4	3.0	419	6	CB934821	CB934821	laa44h01.	1384	50.2	3.0	252	7	CF212181	CF212181	CGF100066
1312	50.4	3.0	430	6	CB075623	CB075623	hz49c09.b	1385	50.2	3.0	270	7	CK625724	CK625724	mj13e12.Y
1313	50.4	3.0	435	4	BM283047	BM283047	ki44d10.Y	1386	50.2	3.0	271	6	CA802092	CA802092	saui0a04.
1314	50.4	3.0	466	4	BM567650	BM567650	sak77a05.	1387	50.2	3.0	296	2	BE059362	BE059362	saui1907.Y
1315	50.4	3.0	471	5	B0851050	B0851050	AGENCOURT	1388	50.2	3.0	301	7	CF123294	CF123294	UI-HF-CHO
1316	50.4	3.0	480	5	BQ398528	BQ398528	NISC_mo08	1389	50.2	3.0	301	7	CF123294	CF123294	UI-HF-CHO
c1317	50.4	3.0	493	7	CF314113	CF314113	HD--02-10	1390	50.2	3.0	313	4	B1839345	B1839345	f666d05.Y
1318	50.4	3.0	500	2	BF882334	BF882334	IL3-ET011	1391	50.2	3.0	346	6	CB705495	CB705495	AMGNNUC:S
1319	50.4	3.0	500	4	BG571546	BG571546	602592845	1392	50.2	3.0	346	6	CF546293	CF546293	lae70e12.
1320	50.4	3.0	501	6	CA336663	CA336663	NISC_1v03	1393	50.2	3.0	347	6	CB705238	CB705238	AMGNNUC:Y
1321	50.4	3.0	518	7	CK431061	CK431061	oj57d12.Y	1394	50.2	3.0	365	4	B1941631	B1941631	sc80f10.Y
1322	50.4	3.0	531	1	AL712171	AL712171	DKFZp686D	1395	50.2	3.0	374	7	CO878391	CO878391	BovGen.06
1323	50.4	3.0	538	1	AV757416	AV757416	AV757416	1396	50.2	3.0	377	7	CO195922	CO195922	EC43542.5
1324	50.4	3.0	568	7	CV285468	CV285468	ta47h02.	1397	50.2	3.0	378	7	CF124412	CF124412	UI-HF-CHO
c1325	50.4	3.0	571	5	BQ522127	BQ522127	NISC_n114	1398	50.2	3.0	386	2	BF037097	BF037097	601456863
1326	50.4	3.0	579	6	CB607201	CB607201	AMGNNUC:S	1399	50.2	3.0	442	4	CF612777	CF612777	lafo6b12.
1327	50.4	3.0	582	5	BP249933	BP249933	AGENCOURT	1400	50.2	3.0	444	4	BI380861	BI380861	HS 5231 A
1328	50.4	3.0	595	8	BH189680	BH189680	001_K_11-	1401	50.2	3.0	420	1	AL711793	AL711793	KDP2p686B
1329	50.4	3.0	595	9	CNS07TEW	CNS07TEW	T3_end of	1402	50.2	3.0	426	7	CK421093	CK421093	AUF IpSpn
1330	50.4	3.0	607	1	AL729731	AL729731	AGENCOURT	1403	50.2	3.0	427	2	BF793360	BF793360	602554790
1331	50.4	3.0	641	1	AV735039	AV735039	AGENCOURT	1404	50.2	3.0	442	1	AV763658	AV763658	AGENCOURT
1332	50.4	3.0	643	5	BQ747828	BQ747828	UI-M-FA0-	1405	50.2	3.0	449	4	BI380861	BI380861	HS 5231 A
1333	50.4	3.0	662	7	CF350633	CF350633	r153c08.Y	1406	50.2	3.0	457	8	AQ752942	AQ752942	FLS 5231 A
1334	50.4	3.0	682	4	BM734248	BM734248	ki12e12.Y	1407	50.2	3.0	471	7	CF307986	CF307986	ABF--01-J
1335	50.4	3.0	693	7	CO581501	CO581501	ILLUMIGEN	1408	50.2	3.0	483	7	CF315792	CF315792	HD--04-N1
c1336	50.4	3.0	732	9	AG546088	AG546088	Mus muscu	1409	50.2	3.0	490	1	AV756619	AV756619	AV756619
1337	50.4	3.0	741	7	CN842216	CN842216	AGENCOURT	1410	50.2	3.0	525	5	BP683189	BP683189	AGENCOURT
c1338	50.4	3.0	743	9	AG285887	AG285887	Mus muscu	1411	50.2	3.0	525	7	CV066363	CV066363	WNEU3al W

1412	50.2	538	1	AL727686	AL727686	1485	50	3.0	346	2	BF751308	BF751308 RC3-BN042
1413	50.2	601	6	CD239085	FNPBK001	1486	50	3.0	350	2	BF806065	BF806065 MRI-CI018
1414	50.2	603	1	AV732976	AV732976	1487	50	3.0	354	7	CK428760	CK428760 laj16b02.
1415	50.2	604	5	BP271854	BP271854	1488	50	3.0	361	7	CK004628	CK004628 AGENCOURT
1416	50.2	609	6	CD239279	FNPBMF09	1489	50	3.0	363	7	CV194197	CV194197 SnsSTbaa9
1417	50.2	609	6	CD239341	FNPEND08	1490	50	3.0	372	7	CF801074	CF801074 rj1ld08.y
1418	50.2	653	9	CNS02M1D	Tetraodon	1491	50	3.0	375	2	AW827214	AW827214 xn09f12.y
1419	50.2	693	1	AV734099	AV734099	1492	50	3.0	390	7	CF425690	CF425690 lad3a05.
1420	50.2	754	6	BUS37749	AGENCOURT	1493	50	3.0	392	5	BQ290505	BQ290505 NXR0045.B
1421	50.2	754	6	CD523365	AGENCOURT	1494	50	3.0	402	7	CO192753	CO192753 EC34419.5
1422	50.2	759	8	B12963	T23D1-T7.1	1495	50	3.0	405	5	BU055967	BU055967 UI-M-FP0-
1423	50.2	781	9	AG592717	Mus muscu	1496	50	3.0	406	6	CB975383	CB975383 CAB3006-
1424	50.2	782	5	EX422198	EX422198	1497	50	3.0	408	5	BQ126842	BQ126842 i119h05.y
1425	50.2	802	9	AV757528	AV757528	1498	50	3.0	408	7	CK565162	CK565162 dor12a2.D
1426	50.2	802	9	AG452709	Mus muscu	1499	50	3.0	424	1	AA597163	AA597163 vo35h02.r
1427	50.2	840	7	CV486146	AGENCOURT	1500	50	3.0	424	7	CK233937	CK233937 re21f12.y
1428	50.2	847	6	CD250700	AGENCOURT							
1429	50.2	864	5	BU850507	AGENCOURT							
1430	50.2	868	7	CK158040	FGAS03924							
1431	50.2	875	7	CK159714	FGAS04120							
1432	50.2	880	9	AG439347	Mus muscu							
1433	50.2	883	5	BU181547	AGENCOURT							
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1435	50.2	899	7	CK157998	FGAS03920							
1436	50.2	915	7	CK160067	FGAS04160							
1437	50.2	927	5	BQ920326	AGENCOURT							
1438	50.2	927	7	CK403949	AUF Ifhdk							
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1457	50.2	1727	9	CL114085	ISB1-59J1							
1458	50.2	1730	9	CL078531	CH216-151							
1459	50.2	2677	3	BC040828	BC040828 Mus muscu							
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1461	50	148	7	CO726601	CO726601 ILLUMIGEN							
1462	50	149	7	CF124930	CF124930 UI-HF-CHO							
1463	50	157	2	AW268072	AW268072 xr92d05.x							
1464	50	170	7	CO417512	Mdfz3012p							
1465	50	172	7	CO165849	FLDI 57-B							
1466	50	179	5	BQ077081	fz12d12.y							
1467	50	180	7	CK377194	lah99e05.							
1468	50	192	7	CF315538	HD--04-H2							
1469	50	217	6	CA673076	CA673076 wlsu2.pk0							
1470	50	222	4	BL671666	fs51c07.y							
1471	50	239	5	BQ093422	fy97f10.y							
1472	50	241	7	CF123101	UI-HF-CHO							
1473	50	248	7	CF969088	lag05b05.							
1474	50	249	2	BS666137	BS666137 149188 MA							
1475	50	256	4	BG651431	sad46f04.							
1476	50	264	4	BM155516	w606h05.y							
1477	50	281	6	CA934992	sau62c06.							
1478	50	284	7	CF804419	lad72e02.							
1479	50	289	6	CA668025	wlsu1.pk0							
1480	50	301	5	BU563515	AGENCOURT							
1481	50	303	4	BG514981	dag27a10.							
1482	50	309	9	CF319405	tigr-ges-							
1483	50	321	7	CF331988	NACU--08-							
1484	50	324	2	AW306965	sf51a09.y							

## ALIGNMENTS

## RESULT 1

AK045973

## LOCUS DEFINITION

AK045973 1808 bp mRNA linear HTC 03-APR-2004  
Mus musculus adult male corpora quadrigemina cDNA, RIKEN  
full-length enriched library, clone:B230328N06 product:NEUROTRIMIN  
PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.

## ACCESSION

AK045973.1 GI:26337738

## VERSION

HTC; CAP trapper.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

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Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
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RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer

## JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

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20499374

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11042159

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RIKEN integrated sequence analysis (RISA) system--384-format  
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## JOURNAL

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6 (bases 1 to 1808)

AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayaehida, K., Hayata, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
	Direct Submission	
TITLE	Submitted (16-JUL-2001) Yoshihide Hayaehizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]	
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
COMMENT	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. Location/Qualifiers	
	1. 1808 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM_DB:B230328N06" /db_xref="taxon:10090" /clone="B230328N06" /sex="male" /tissue_type="corpora quadrigemina" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stages="adult" 204. .1238	
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	Query Match 66.7%; Score 1119.4; DB 3; Length 1808; Best Local Similarity 83.1%; Pred. No. 1.8e-278; Matches 1417; Conservative 0; Mismatches 251; Indels 37; Gaps 11;	
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	109 AAGAAAG 168 179 AAAAAAG 238	
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	829 TGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGA 888 899 TGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGA 958	
	889 ATTCCAGTGGTACAAAGGATGACAAAAGCTGATTGAAGGAAAGAAAGGGGTGAAGTGGGA 948 959 ATTTCAATGGTTCAAAGGATGACAAAAGCTGGTCTGAAGGAAAGAAAGGGAGTCAAAGTGGGA 1018	
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	1129 GTCGCTCTTCTGTGCTTGTGACCTGCTTCTCAAAATTTTGTGAGTGGCCTATTTCCAC 1188 1199 CTTCCCTCTTCTGTGCTTGTGACCTGCTTCTCAAAATTTTGTGAGTGGCCTTCTCCCTGC 1258	
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	1249 ACCAATCAGATATATACAAATGAAATTTAGAAGAAACACAGCCTTCATGGGACAGAAATTTG 1308	





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Qy 1479 GTGTGGGCAAGGCTCAGCTCTCTGCCCCAC-AGAGTGCCCCACGCTGGAAACATTTCTGGA 1537  
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Qy 1595 CCAAGCTGCGGCTGCGGCACTTTGTAGACTGTGCAACCGCTGTTGTTGTTGTAAC 1654  
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Qy 1655 GTGAATAAAGAGAGCAAAAAAAA 1679  
Db 1728 GTGAATACTGGAGGAGAAAAAAA 1752

RESULT 3  
CR602526  
LOCUS full-length cdna clone CS0DN005YD20 of Adult brain of Homo sapiens  
DEFINITION  
ACCESSION CR602526  
VERSION CR602526.1 GI:50483333  
KEYWORDS HTC; CNSLT cdna  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2512)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cdna libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 2512)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

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Query Match      60.4%; Score 1014.6; DB 3; Length 2512;
Best Local Similarity 90.4%; Pred. No. 2.8e-251;
Matches 1145; Conservative 0; Mismatches 4; Indels 118; Gaps 1;

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Qy 591 TTAGCCTCACCTGCATAGCAACTGTGTAGACAGAGCCTACGGTTACTTTGGAGACACATCT 650
Db 161 TTAGCCTCACCTGCATAGCAACTGTGTAGACAGAGCCTACGGTTACTTTGGAGACACATCT 220
Qy 651 CTCCCAAGCGGTGGCTTTGTGAGTGAAGACGATATCTTGGAAATTCAGGGCATCACCC 710
Db 221 CTCCCAAGCGGTGGCTTTGTGAGTGAAGACGATATCTTGGAAATTCAGGGCATCACCA 280
Qy 711 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGAGCTGGCCGCCCGCTGGTAC 770
Db 281 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGAGCTGGCCGCCCGCTGGTAC 340
Qy 771 GGAGAGTAAAGGTACCGTGAATATCCACCATATCTTCCAGAGCCCAAGGGTACAGGTG 830
Db 341 GGAGAGTAAAGGTACCGTGAATATCCACCATATCTTCCAGAGCCCAAGGGTACAGGTG 400
Qy 831 TCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAAT 890
Db 401 TCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAAT 460
Qy 891 TCCAGTGTGACAAGGATGACAAA----- 914
Db 461 TCCAGTGTGACAGGATGACAAAAGAGCTGAATCTCATTACAGTTGGTTATGATGGG 520
Qy 915 ----- 914
Db 521 AAAGCTTCCTCCCATGGTGGACGAATGGTGTCAAAACGGCCAGTGGGATCAATCAGCCT 580
Qy 915 -----GACTGATTGAAGGAAGAGGGGTGAAGTGGNAAC 952
Db 581 GACTTGTCTCGCAGAAATCTCCGCACTGATTGAAGGAAGAGGGGTGAAAAGTGGAAAAC 640
Qy 953 AGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTGAACATGACTATGGGAACCTAC 1012
Db 641 AGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTGAACATGACTATGGGAACCTAC 700
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Db 761 GCGCCGCTCAGGAGGTGAGCAACGGCAGCTCGAGGAGGGCAGGCTGCTGCTGCTGCTG 820
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Qy 1193 GAAAGGCTGCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1252
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Qy 1553 TTCAATCAGTCCCATAGACAGAAATGAGACCTTCGGCCCAAGGTGGCGCTGCGG 1612
Db 1241 TTCAATCAGTCCCATAGACAGAAATGAGACCTTCGGCCCAAGGTGGCGCTGCGG 1300
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Qy 1673 AAAAAA 1679
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LOCUS      874 bp      DNA      linear      GSS 12-DEC-2003
DEFINITION Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION  AY406347
VERSION    AY406347.1 GI:39762321
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 874)
            Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT    This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
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Best Local Similarity 99.3%; Pred. No. 2.9e-209;
Matches 868; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
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Qy	361	TGCTGGGAATGACAAGTGGTGGTGGCTGGATCTCGGTGGTCTCTTGAGCAACACCCAAAC	420
Ds	61	TGCTGGGAATGACAAGTGGTGGTGGATCTCGGTGGTCTCTTGAGCAACACCCAAAC	120
Qy	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACCTGCTC	480
Ds	121	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACCTGCTC	180
Qy	481	GGTGACAGACAAACACCAACCAAGACCTCTAGGTCCACCTCATTTGGCAAGTATCTCC	540
Ds	181	GGTGACAGACAAACACCAACCAAGACCTCTAGGTCCACCTCATTTGGCAAGTATCTCC	240
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Ds	241	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	300
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Ds	301	CTGCATAGCAACTGGTAGACAGACCTACGGTTACTTTGGAGACACATCTCTCCAAACC	360
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Qy	715	GCAGTACAGGGACTACGAGTGCAGTGGCTCCAATGACGTGGCCCGCCGGTGGTACGGAG	774
Ds	421	GCAGTACAGGGACTACGAGTGCAGTGGCTCCAATGACGTGGCCCGCCGGTGGTACGGAG	480
Qy	775	AGTAAAGGTCAACCGTGAACCTATCCACCATACATTTTCAGAAAGCCAAAGGTTACAGGTGTCCC	834
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Qy	835	CGTGGGACAAAGGGGACACTGACAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAGATTCCA	894
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RESULT 5

AY406348

LOCUS

DEFINITION

ACCESSION

VERSION

SOURCE

ORGANISM

AY406348

Pan troglodytes HCM2527 gene, linear

AY406348

AY406348.1

GSS

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.	
AUTHORS		1 (bases 1 to 773) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)	
TITLE		Gene trios	
JOURNAL		Science 302 (5652), 1960-1963 (2003)	
PUBMED		14671302	
REFERENCE		2 (bases 1 to 773) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.	
COMMENT		Location/Qualifiers	
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		Matches 761; Conservative 0; Mismatches 6; Indels 6; Gaps 1;	
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Qy	361	TGCTGGGAATGACAAGTGGTGGCTGGATCTCGGTGGTCTCTTGAGCAACACCCAAAC	420
Ds	61	TGCTGGGAATGACAAGTGGTGGCTGGATCTCGGTGGTCTCTTGAGCAACACCCAAAC	120
Qy	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACCTGCTC	480
Ds	121	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACCTGCTC	180
Qy	481	GGTGACAGACAAACACCAAGACCTCTAGGTCCACCTCATTTGGCAAGTATCTCC	540
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Qy	658	---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA	714
Ds	361	CGCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA	420
Qy	715	GCAGTACAGGGACTACGAGTGCAGTGGCTCCAATGACGTGGCCCGCCGGTGGTACGGAG	774
Ds	421	GCAGTACAGGGACTACGAGTGCAGTGGCTCCAATGACGTGGCCCGCCGGTGGTACGGAG	480
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Ds	481	AGTAAAGGTCAACCGTGAACCTATCCACCATACATTTTCAGAAAGCCAAAGGTTACAGGTGTCCC	540
Qy	835	CGTGGGACAAAGGGGACACTGACAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAGATTCCA	894
Ds	541	CGTGGGACAAAGGGGACACTGACAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAGATTCCA	600

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Qy 895 GTGGTACAGGATGACAAAAGACTGATTGAAGAGAAAGAAAGGGGTGAAAGTGGAAAACAG 954
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Db 661 ACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACAC 720
Qy 1015 TTGGGTGGCCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTG 1067
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RESULT 6
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LOCUS AGENCOURT_6581928 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471935
5', mRNA sequence.
ACCESSION BM807426.1 GI:19124249
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ruben Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1981 row: c column: 08
High quality sequence stop: 639.

FEATURES
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/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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## ORIGIN

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Query Match 43.7%; Score 733.4; DB 4; Length 1033;
Best Local Similarity 92.5%; Pred. No. 1.6e-178;
Matches 830; Conservative 0; Mismatches 26; Indels 41; Gaps 4;

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Db 301 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTTGCGTGG 360
Qy 1023 CCTCCAAAGAGCTGGGGCCACACCAATGCCAGCATCATGCTATTT----- 1066
Db 361 CCTCCAAAGAGCTGGGGCCACACCAATGCCAGCATCATGCTATTTGAAAGTGAAGAACTACAG 420
Qy 1067 -----GGTCCAGGCCCGCTCAGCAGAGGTGAGCAACGGCAGCTCGAGGA 1109
Db 421 CCCTGACCCCTTGGAAAGGTCAGGGCCGCTCAGCAGAGGTGAGCAACGGCAGCTCGAGGA 480
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Qy 1170 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCAACCACCAACACACAGC 1229
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Qy 1230 AATGGCAACCCGACAGCAACCAATCAGATATATACAAATGAATTAAGAGAAACACAGC 1289
Db 601 AATGGCAACCCGACAGCAACCAATCAGATATATACAAATGAATTAAGAGAAACACAGC 660
Qy 1290 CTCATGGGACAGAAATTTGAGGGGGGGAACAAGAAATACCTTTGGGGGGGAAAGAGTTT 1349
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Db 721 AAAAA--GAATTCGAAATGCTTTGCAGATATTTAGGTACAAATGGAGTTTCTTTTCCCA 778
Qy 1410 AACGGGAAGAACACAGCACACACC--GGCTTGGACCCACTGCAAGCTGCATCGTGAACCTC 1468
Db 779 AACGGGAAGAACACAGCACACACC--GGCTTGGACCCACTGCAAGCTGCATCGTGAACCTC 838
Qy 1469 TTTGGTCCAGTGTGGG-----CAAGGGCTCAGCTCTCTGCCCCACAGAGTGCCCC 1520
Db 839 TTTGGGGGGCAATGAGGGGGGCAAGGGGGTTCATCTCTTCTGCCCCACAGAGTGGCCCC 895

RESULT 7
BM809227 1083 bp mRNA linear EST 05-MAR-2002
LOCUS AGENCOURT_6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
5', mRNA sequence.
ACCESSION BM809227
VERSION BM809227.1 GI:19126050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LICM1971 row: h column: 14

High quality sequence stop: 656.

#### FEATURES

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/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5468221"  
/tissue\_type="amelanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NTH MGC 41"  
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 42.9%; Score 720.2; DB 4; Length 1083;  
Best Local Similarity 91.7%; Pred. No. 4.3e-175;  
Matches 853; Conservative 0; Mismatches 34; Indels 43; Gaps 7;  
  
QY 663 TTGGCTTTGTGAGTGAAGCAAACTTTGGAAATTCAGGGCATCACCCGGAGAGTCAG 722  
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QY 723 GGGACTACGAGTGAGTCCCTCAATGACGCGCGCCCGTGTACGGAGAGTAAAGG 782  
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QY 783 TCACCGTGAACATATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGAC 842  
DB 121 TCACCGTGAACATATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGAC 180  
  
QY 843 AAAAGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACA 902  
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QY 903 AGGATGACAAAGACTGATTCGAGGAGAAAGGGTGAAAGTGGAAACAGACTTTCC 962  
DB 241 AGGATGACAAAGACTGATTCGAGGAGAAAGGGTGAAAGTGGAAACAGACTTTCC 300  
  
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QY 1023 CCTCAAAAGTGGGCGCACACCAATATGCGAGATCATGCTATTT----- 1066  
DB 361 CCTCAAAAGTGGGCGCACACCAATATGCGAGGTGAGCAACGGCAGCTCGAGGA 420  
  
QY 1067 -----GGTCCAGCGCGCTCAGCGGCTGAGCAACGGCAGCTCGAGGA 1109  
DB 421 CCCTGACCCCTTGGAAAGGTTCCAGCGCGCTCAGCGGCTGAGCAACGGCAGCTCGAGGA 480  
  
QY 1110 GGGCAGGCTGGCTGTGGCTGTGCTCTTCTGGTCTTGACACTGTGCTTCAAAATTTGAT 1169  
DB 481 GGGCAGGCTGGCTGTGGCTGTGCTCTTCTGGTCTTGACACTGTGCTTCAAAATTTGAT 540  
  
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QY 1230 AATGCAACACCGACAGCAACCAATTCAGATATATACAAATGAAATTAGAAGAAACACAGC 1289  
DB 601 AATGCAACACCGACAGCAACCAATTCAGATATATACAAATGAAATTAGAAGAAACACAGC 660  
  
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DB 661 CTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAGAGTTT 720  
QY 1349 TAAAAAGAAATTCAAAATTG-CCTTCAGATATTTAGGTACATGAGTTTCTTTTCC 1407  
DB 721 TAAAAAGAAATTCAAAATTGCCCCCTTCGACATATTTAGGTACATGAGTTTCTTTAT 780  
QY 1408 CAAACGGGAAGAACACAGCA----CACCCGGCTTGGACCCCACTCAAGCTCATCGTCA 1463  
DB 781 CCAAAACGGGAAGAAACACAGCACACCGGGCTTGGACCCCACTCAAGCTCATCGTCC 840  
QY 1464 ACCTCTTTTGTGGCAGTGTGGG-CAAGGGCTCAGCC-TCTGTGCCACAGAGTGCCCCCA 1521  
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QY 1522 --CGTGAACATTTCTGAGCTGGCCATCCC 1549  
DB 901 ACGTGGAAACATTTCTGGAATGGGCCCATCC 930  
  
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LOCUS Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY406349  
VERSION AY406349.1 GI:39762323  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 874)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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source 1..874.  
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/db\_xref="taxon:10090"  
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Matches 779; Conservative 0; Mismatches 89; Indels 6; Gaps 1;  
  
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DB 1 GTGCACAAATTGACAAACCGAGTCACCCGGTGGCTGGCTAAACCGCAGTACCATCTCTA 60  
  
QY 361 TGCTGGGAATGACAAGTGGTCCCTGGATCCTCGGTGGTCTCTTGAGCAACACCCCAAC 420  
DB 61 TGCTGGAAATGACAAGTGGTGGCTAGATCCTCGTGGTCTCTCTGATTAACCCAGAC 120  
  
QY 421 GCAGTACAGCATCGAGATCCAGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480





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650  CCTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAG 709
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660  CGGTTGGCTTTGTGAGTGAAGACGAA 685
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RESULT 10
CR736885 673 bp mRNA linear EST 27-AUG-2004
LOCUS
DEFINITION
IMAGp971B1852 ; IMAGE:789137 5', mRNA sequence.
ACCESSION
CR736885
VERSION
CR736885.1 GI:51585450
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 673)
Ebert L., Heil O., Hennig S., Korn B., Neubert P., Partsch E.,
Peters M., Radehof U. and Schneider D.
I.M.A.G.E. cDNA Clone Collection
Unpublished (2004)
COMMENT
Contact: Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGp971B1852.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACGCTATGAC.
FEATURES
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Best Local Similarity 99.7%; Pred. No. 4.4e-162;
Matches 671; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1005 GGAATACACTTGGTGGCTCCACAGCTGGGCCACCAATGCCAGCATCTAT 1064
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QY 1065 TTGGTCCAGGCGCCCTCAGCAGGTGAGCAACGGCAGCTCGAGGAGGCGCGTCT 1124
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DB 121 TTGGTCCAGGCGCCCTCAGCAGGTGAGCAACGGCAGCTCGAGGAGGCGCGTCT 180
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QY 1125 GGCTGCTCCCTTCTGCTGTGACCTGCTCTCAAAATTTGATGTGAGTGCCACTTCC 1184
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DB 181 GGCTGCTCCCTTCTGCTGTGACCTGCTCTCAAAATTTGATGTGAGTGCCACTTCC 240
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QY 1185 CCACCCGGGAAGGCTGGCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1244
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DB 301 AGCAACCAATCAGATATATACAAATGAAATTAGAGAAGAACACAGCCTCATGGGACAGAA 360
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QY 1305 TTTGAGGGAGGGGNAACAAGAATACTTTTGGGGGAAAAAGAGTTTAAAAAAGAAATTGAA 1364
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DB 361 TTTGAGGGAGGGGNAACAAGAATACTTTTGGGGGAAAAAGAGTTTAAAAAAGAAATTGAA 420
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QY 1365 AATTGCTTTCAGATATTTAGGTACAATGAGTGTCTTTTCCCAACGGGAAGAACACA 1424
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DB 421 AATTGCTTTCAGATATTTAGGTACAATGAGTGTCTTTTCCCAACGGGAAGAACACA 480
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LOCUS
DEFINITION
AGENCOURT 7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
5', mRNA sequence.
ACCESSION
BUI55617
VERSION
BUI55617.1 GI:22669149
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 856)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@email.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3527 row: m column: 16
High quality sequence stop: 593.
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 39.6%; Score 664.8; DB 5; Length 856;
Best Local Similarity 97.6%; Pred. No. 9.2e-161;
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Db 94 AGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAAGCTATGGACACGTCGACGGT 153
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Db 154 CCGGAGGGGAGAGCGCCACCTCAGTGCACCTATTGACAACCGGGTCACCCGGGTGGC 213
Qy 334 CTGGCTAAACCGCAGCACCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCTCTCG 393
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Qy 394 CTGGCTCTCTCTGAGCAACACCCAAACGACATACGATCAGATCCAGAACGTCGGATGT 453
Db 274 CTGGCTCTCTCTGAGCAACACCCAAACGACATACGATCAGATCCAGAACGTCGGATGT 333
Qy 454 GTATGACAGGGCCCTTACACTGCTCGGTGCAGACAGACAACCAACCAAGACCTCTAG 513
Db 334 GTATGACAGGGCCCTTACACTGCTCGGTGCAGACAGACAACCAACCAAGACCTCTAG 393
Qy 514 GGTCCACCTCATTTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGATATCTCAT 573
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Qy 694 AATTGAGGACATCACCCGGGAGCAGTACGGGACTACAGTGCAGTGCCTCAATGAGT 753
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RESULT 12
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LOCUS AL533026 Homo sapiens ADULT BRAIN Homo sapiens cdna clone
DEFINITION CS00N005YD20 5-PRIME, mRNA sequence.
ACCESSION AL533026
VERSION AL533026.3 GI:45707932
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1027)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:31070858.
Contact: Genoscope
```

Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 6387.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DN005DB10QPl&c=6387.f.

FEATURES  
source

Location/Qualifiers  
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

## ORIGIN

Query Match 38.4%; Score 645; DB 1; Length 1027;  
Best Local Similarity 86.8%; Pred. No. 1.3e-155;  
Matches 806; Conservative 1; Mismatches 1; Indels 121; Gaps 4;  
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Qy 591 TTAGCCTCACTGCATAGCAACTGGTAGACAGACGCTACGGTTACTTTGGAGACACATCT 650  
Db 162 TTAGCCTCACTGCATAGCAACTGGTAGACAGACGCTACGGTTACTTTGGAGACACATCT 221  
Qy 651 CTCCTCAAGCGTTGGCTTTGTGAGTGAAGCAAGTAATCTTGGAAATTCAGGCGCATCACCC 710  
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Qy 711 GGGAGCAGTCAGGGGACTACAGTGCAGTGCCTCCAATGAGCTGCGCGCCCGTGGTAC 770  
Db 282 GGGAGCAGTCAGGGGACTACAGTGCAGTGCCTCCAATGAGCTGCGCGCCCGTGGTAC 341  
Qy 771 GGAGGTAAAGGTACCGTGAACTATCCACATACATTTGAGAAGCCCAAGGGTACAGGTG 830  
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Qy 915 -----GACTGATTGAAGGAAAGAGGGGTGAAAGTGAAGAAC 952  
Db 582 GACTTGTCTGCAGAAATCTCTCCGACTGATTGAAGGAAAGAGGGGTGAAGTGAAGAAC 641  
Qy 953 AGACCTTTCTCTCAAAACTCATCTTCTCAATGCTCTGTAACATGACTATGGGAACATAC 1012  
Db 642 AGACCTTTCTCTCAAAACTCATCTTCTCAATGCTCTGTAACATGACTATGGGAACATAC 701  
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Db 702 ACTTGCGTGGCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCA 761  
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Db 762 GGCCTCGTCAGGAGTGGACAAACGGACGTCGAGGGGAGGCTGGTCTGGCTGCTG 821  
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Qy 1193 GAAAGGCTGGCCGACACACCAACCAACACAAACAGCAATGGCAACACCGACAGCAACCA 1252  
Db 881 GAAAGGCTGGCCGACACACCAACCAACCAACAGC-ATGGCAACACCGACAGCAACCA 939  
Qy 1253 ATCAGATATATACAAATGAAATAGAGAAACACAGCTCATGGACAGAAATTTGAGGG 1312  
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Qy 1313 AGGGGAACAAAGAAATACTTTTGGGGGAAA 1341  
Db 1000 AGGGG-ACAAAGATACTTTTGGGGGAAA 1027

RESULT 13  
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LOCUS 603197479F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5277115 5',  
mRNA sequence.  
ACCESSION BI551784  
VERSION BI551784.1 GI:15439096  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 732)  
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11699 row: m column: 20  
High quality sequence stop: 732.  
Location/Qualifiers  
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/note="Organ: brain; Vector: pBluescriptR (modified  
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(gtcgag); Oligo-dT primed using primer  
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insert size 2.5 kb and normalized to 80T 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this  
is a NIH\_MGC Library."

FEATURES  
source

RESULT 14  
CN362539  
LOCUS 17000470517655 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN362539  
VERSION CN362539.1 GI:47362473  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 748)  
TITLE Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation

Best Local Similarity 99.4%; Pred. No. 3.9e-155;  
Matches 676; Conservative 0; Mismatches 1; Indels 3; Gaps 3;  
Qy 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCACAAAGCTTGAGAGCAACAC 60  
Db 54 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCACAAAGCTTGAGAGCAACAC 113  
Qy 61 AATCTATCAGGAAGAAAGAAAAACCGAACTCTGACAAAAAAGAGAA-AAAAGAA 119  
Db 114 AATCTATCAGGAAGAAAGAAAAACCGAACTCTGACAAAAAAGAGAA-AAAAGAA 173  
Qy 120 GAAGAAAAAATCATGAAACCATCCAGCCAAAAAATGCAAAATTCATCTCTTTGGGCAA 179  
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Qy 180 TCTTCACGGGGCTGGCTGCTGTGTCTCTTCCAAAGGAGTCCCGTGGCGAGCGAGATG 239  
Db 234 TCTTCACGGGGCTGGCTGCTGTGTCTCTTCCAAAGGAGTCCCGTGGCGAGCGAGATG 293  
Qy 240 CCACCTTCCCAAAAGCTATGGACAAACGTACGGTCCGGCAGGGGAGAGCGCCACCTCA 299  
Db 294 CCACCTTCCCAAAAGCTATGGACAAACGTACGGTCCGGCAGGGGAGAGCGCCACCTCA 353  
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Qy 480 CGGTGCAGACAGCAACACCCAAAGACCTCTTAGGGTCCACCTCATTTGTGCAAGTATCTC 539  
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Db 654 CCTCATAGCAACTGGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAA 713  
Qy 659 GCGGTTGCGTTTGTGAGTGA 678  
Db 714 GCGG-TGGCTTTGTGAGTGA 732

## ORIGIN

Query Match 38.3%; Score 643; DB 4; Length 732;

230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@eron.com  
Insert Length: 748 Std Error: 0.00.  
Location/Qualifiers

## FEATURES

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derived from H1, H7 and H9 cells"  
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/note="oligo dt primed, full-length enriched cDNA library  
from embryoid body outgrowths derived from hES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

## ORIGIN

Query Match 38.1%; Score 640; DB 7; Length 748;  
Best Local Similarity 100.0%; Pred. No. 2.4e-154;  
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 169 CCGGCGGGGAGAGCGCCACCTCAGGTGCACATATTACAAACCGGGTCACCCGGGTGGC 228  
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Db 229 CTGGCTAAACCGCAGCACCACCTCTATGCTGGGAATGACAAGTGGTGGCTTCCTCG 288  
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Qy 394 CGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATCAGATCCAGACGTTGATGT 453  
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Db 289 CGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATCAGATCCAGACGTTGATGT 348  
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Qy 454 GTATGACGAGGCGCTTACCTCTGCTGCGTGACAGACACCAACCCAAAGACCTCTAG 513  
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Qy 514 GGTCCACCTCATTTGCGAAGTATCTCCAAATTTGAGAGATTTCTTCAGATATCTCCAT 573  
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Qy 574 TAAAGAAGGGAACAATATTAGCTCACCCTGATAGCAACTGGTAGACGAGCCTACGGT 633  
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Qy 634 TACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGACGAATCTTGG 693  
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Db 529 TACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGACGAATCTTGG 588  
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Qy 694 AATTGAGGAGATCACCAGGAGCAGTCAGGGGACCTACGAGTGCAGTGCCTCCAATGAGT 753  
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Db 589 AATTGAGGAGATCACCAGGAGCAGTCAGGGGACCTACGAGTGCAGTGCCTCCAATGAGT 648  
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Qy 754 GGCCTGGCTGGTACGGAGAGTAAAGGTACCGTGAACCTATCCACCATCATTTTCAGA 813  
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Db 649 GGCCTGGCTGGTACGGAGAGTAAAGGTACCGTGAACCTATCCACCATCATTTTCAGA 708  
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Qy 814 AGCCAAGGGTACAGGTGTCCTGGTGGGACAAAGGGGACA 853  
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Db 709 AGCCAAGGGTACAGGTGTCCTGGTGGGACAAAGGGGACA 748  
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## RESULT 15

BE798585 1039 bp mRNA linear EST 20-SEP-2000  
LOCUS 601581610F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:393595 5',  
DEFINITION mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BE798585  
BE798585.1 GI:10219783  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgi.nci.nih.gov/.  
1 (bases 1 to 1039)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-f@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCM779 row: d column: 04  
High quality sequence stop: 849.  
Location/Qualifiers

## FEATURES

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EcoRI; cDNA made by oligo-dT priming. Directionally  
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adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 37.8%; Score 635.2; DB 2; Length 1039;  
Best Local Similarity 97.6%; Pred. No. 4.5e-153;  
Matches 656; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

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Db 65 CAGGTGCACATTTGACAAACCGGGTCACCCGGTGGCTGGCTAAACCGCAGCACCATCCT 124  
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Db 125 CTATGCTGGGAATGACAAGTGGTGGCTGGATCTCTGGGTGGTCTCTTGAGCAACACCCA 184  
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Qy 418 AACCGAGTACAGATTCAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACCTG 477  
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Db 185 AACCGAGTACAGATTCAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACCTG 244  
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Qy 478 CTCGGTGCAGACACACACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATC 537  
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Qy 538 TCCCAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCT 597  
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Qy 598 CACCTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCA 657  
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Db 365 CACCTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCA 424  
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Qy 658 AGCGGTTGGCTTTCTGAGTGAAGACGAATATCTTCAAAATTCAGGGCATCACCCGGGAGCA 717  
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Db 425 AGCGGTTGGCTTTCTGAGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCA 484  
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Db	605	GGGACAAAAGGGGACACTGCGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTG	664
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Qy	955	ACCTTTCCTCTC	966
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Job time : 6000 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 06:59:01 ; Search time 308 Seconds  
(without alignments)  
8919.833 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679

Sequence: 1 gttgtccttcagcaaac.....ataaaagagcaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1661.4	99.0	1693	4	US-09-700-397-2
2	1032	61.5	1032	4	US-09-700-397-1
3	939	55.9	939	4	US-09-700-397-5
4	343	20.4	1238	2	US-08-414-657D-3
5	343	20.4	1238	3	US-09-135-080-3
6	341.6	20.3	1195	4	US-09-976-594-403
7	340.6	20.3	924	2	US-08-414-657D-7
8	340.6	20.3	977	2	US-08-414-657D-1
9	340.6	20.3	977	3	US-09-135-080-1
10	340.6	20.3	1014	2	US-08-414-657D-5
11	340.6	20.3	1014	3	US-09-135-080-7
12	338.6	20.2	861	2	US-08-414-657D-9
13	338.6	20.2	912	2	US-08-414-657D-6
14	337.4	20.1	945	2	US-08-414-657D-8
15	333.8	19.9	861	2	US-08-414-657D-10
16	316.2	18.8	333	4	US-09-513-999C-23289
17	303.6	18.1	756	2	US-08-414-657D-17
18	301	17.9	309	4	US-09-621-976-3309
19	298.2	17.8	756	2	US-08-414-657D-18
20	281	16.7	1030	4	US-09-949-016-4587
21	193.6	11.5	352	4	US-09-513-999C-2775
22	174.4	10.4	182	4	US-09-621-976-967
23	146	8.7	200	4	US-09-513-999C-14430
24	105.6	6.3	913	4	US-09-774-528-410
25	100	6.0	219	2	US-08-414-657D-11
26	95.2	5.7	219	2	US-08-414-657D-12
27	87	5.2	438	4	US-09-621-976-8385

28	78.6	4.7	113538	4	US-09-949-016-16329	Sequence 16329, A
29	77.8	4.6	177	2	US-08-414-657D-13	Sequence 13, Appl
30	77.8	4.6	177	2	US-08-414-657D-14	Sequence 14, Appl
c	76.8	4.6	601	4	US-09-949-016-163724	Sequence 163724, A
32	65.6	3.9	198	2	US-08-414-657D-15	Sequence 15, Appl
33	63.4	3.8	198	2	US-08-414-657D-16	Sequence 16, Appl
34	50.4	3.0	612	4	US-09-902-540-1357	Sequence 1357, Ap
35	50.2	3.0	240	1	US-08-628-417-6	Sequence 6, Appl
36	50.2	3.0	1039	4	US-09-902-540-1280	Sequence 1280, Ap
37	49.8	3.0	1048	4	US-09-489-847-38	Sequence 38, Appl
38	48.8	2.9	1813	3	US-09-071-224-3	Sequence 3, Appl
39	48.4	2.9	147	4	US-09-621-976-10383	Sequence 10383, A
40	48.4	2.9	1117	3	US-09-247-373B-33	Sequence 33, Appl
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51	47.8	2.8	441	4	US-09-601-537-10	Sequence 10, Appl
52	47.8	2.8	4121	4	US-09-601-537-9	Sequence 9, Appl
53	47.6	2.8	147	4	US-09-621-976-10254	Sequence 10254, A
54	47.6	2.8	2447	2	US-09-014-969-14	Sequence 14, Appl
55	47.6	2.8	2674	3	US-09-817-180-1	Sequence 1, Appl
56	47.6	2.8	2674	4	US-10-003-295-1	Sequence 1, Appl
57	47.4	2.8	1696	4	US-09-835-811-1	Sequence 1, Appl
58	47.4	2.8	1738	4	US-09-918-509A-27	Sequence 27, Appl
c	47.2	2.8	76164	4	US-09-949-016-12288	Sequence 12288, A
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62	46.8	2.8	2608	4	US-09-904-615-16	Sequence 16, Appl
63	46.6	2.8	569	4	US-09-461-325-44	Sequence 44, Appl
64	46.6	2.8	569	4	US-10-012-542-44	Sequence 44, Appl
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69	46.6	2.8	674	4	US-09-604-287A-465	Sequence 465, App
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74	46.6	2.8	1411	3	US-09-496-692-5	Sequence 5, Appl
75	46.6	2.8	1411	4	US-10-000-273-5	Sequence 5, Appl
76	46.6	2.8	3275	3	US-09-370-838-151	Sequence 151, App
77	46.6	2.8	3275	4	US-09-854-133-151	Sequence 151, App
78	46.4	2.8	140	1	US-08-628-417-5	Sequence 5, Appl
79	46.4	2.8	193	4	US-09-621-976-10543	Sequence 10543, A
80	46.4	2.8	578	3	US-09-602-877A-95	Sequence 95, Appl
c	46.4	2.8	1020	4	US-09-328-475C-43	Sequence 43, Appl
82	46.4	2.8	1034	4	US-09-311-021-105	Sequence 105, App
83	46.4	2.8	2246	3	US-09-363-708-3	Sequence 3, Appl
84	46.4	2.8	2246	4	US-09-083-587-3	Sequence 3, Appl
85	46.4	2.8	2280	3	US-08-813-150-1	Sequence 1, Appl
86	46.4	2.8	2280	4	US-09-546-553-1	Sequence 1, Appl
87	46.4	2.8	3438	4	US-10-164-595-29	Sequence 29, Appl
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90	46.2	2.8	1024	4	US-09-328-475C-50	Sequence 50, Appl
91	46	2.7	4064	4	US-09-873-737A-3	Sequence 3, Appl
92	45.8	2.7	249	4	US-09-621-976-1322	Sequence 1322, Ap
93	45.8	2.7	365	4	US-09-621-976-16042	Sequence 16042, A
94	45.8	2.7	601	4	US-09-949-016-47248	Sequence 47248, A
c	45.8	2.7	903	5	FCT-US95-06406A-21	Sequence 21, Appl
96	45.8	2.7	1447	3	US-09-443-041A-27	Sequence 27, Appl
97	45.8	2.7	2394	4	US-09-800-729-33	Sequence 33, Appl
98	45.8	2.7	5481	4	US-09-949-016-12049	Sequence 12049, A
c	45.8	2.7	5484	4	US-09-949-016-15589	Sequence 15589, A
100	45.8	2.7	12797	4	US-09-949-016-13123	Sequence 13123, A

101	45.8	2.7	96327	4	US-09-949-016-16541	Sequence 16541, A	c 174	44.6	2.7	396	4	US-09-970-966-33	Sequence 33, Appl
102	45.6	2.7	282	4	US-09-621-976-18648	Sequence 18648, A	175	44.6	2.7	601	4	US-09-949-016-204599	Sequence 204599,
c 103	45.4	2.7	260	2	US-08-520-678A-29	Sequence 29, Appl	176	44.6	2.7	601	4	US-09-949-016-204600	Sequence 204600,
c 104	45.4	2.7	260	3	US-08-897-126-29	Sequence 29, Appl	177	44.6	2.7	601	4	US-09-949-016-204601	Sequence 204601,
105	45.4	2.7	1098	3	US-09-248-335-35	Sequence 35, Appl	178	44.6	2.7	601	4	US-09-949-016-204602	Sequence 204602,
106	45.4	2.7	2146	4	US-10-003-332-3	Sequence 3, Appl	179	44.6	2.7	601	4	US-09-949-016-204603	Sequence 204603,
c 107	45.4	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl	180	44.6	2.7	601	4	US-09-949-016-204604	Sequence 204604,
c 108	45.4	2.7	54246	4	US-09-949-016-16206	Sequence 16206, A	181	44.6	2.7	601	4	US-09-949-016-204605	Sequence 204605,
c 109	45.4	2.7	22452	4	US-09-949-016-12968	Sequence 12968, A	182	44.6	2.7	601	4	US-09-949-016-204606	Sequence 204606,
110	45.2	2.7	176	4	US-09-621-976-13903	Sequence 13903, A	183	44.6	2.7	708	4	US-09-270-767-13081	Sequence 13081, A
111	45.2	2.7	359	4	US-09-621-976-16008	Sequence 16008, A	184	44.6	2.7	2184	3	US-08-955-918C-1	Sequence 1, Appl
112	45.2	2.7	362	4	US-09-621-976-16019	Sequence 16019, A	185	44.6	2.7	2184	3	US-08-697-766A-1	Sequence 1, Appl
113	45.2	2.7	362	4	US-09-621-976-16010	Sequence 16010, A	186	44.6	2.7	2184	3	US-09-244-805-29	Sequence 29, Appl
c 114	45.2	2.7	396	4	US-09-640-173-53	Sequence 53, Appl	187	44.6	2.7	2527	3	US-09-653-839-9	Sequence 9, Appl
c 115	45.2	2.7	396	4	US-09-713-550-53	Sequence 53, Appl	188	44.6	2.7	2806	4	US-10-202-619-9	Sequence 9, Appl
c 116	45.2	2.7	396	4	US-09-825-294-53	Sequence 53, Appl	189	44.6	2.7	2806	4	US-09-949-016-17521	Sequence 17521, A
c 117	45.2	2.7	396	4	US-09-970-966-53	Sequence 53, Appl	190	44.6	2.7	87734	4	US-09-949-016-17196	Sequence 17196, A
c 118	45.2	2.7	537	4	US-09-720-201A-4	Sequence 4, Appl	191	44.6	2.7	118143	4	US-09-621-976-13933	Sequence 13933, A
c 119	45.2	2.7	644	4	US-09-720-201A-6	Sequence 6, Appl	192	44.4	2.6	127	4	US-09-442-054A-42	Sequence 42, Appl
c 120	45.2	2.7	1091	4	US-09-328-965-1	Sequence 1, Appl	193	44.4	2.6	196	4	US-09-442-054A-42	Sequence 42, Appl
121	45.2	2.7	1273	4	US-09-270-767-14731	Sequence 14731, A	c 194	44.4	2.6	196	4	US-08-520-678A-22	Sequence 22, Appl
c 122	45.2	2.7	9589	1	US-07-925-695-1	Sequence 1, Appl	c 195	44.4	2.6	356	2	US-08-897-126-22	Sequence 22, Appl
c 123	45.2	2.7	9589	1	US-07-925-695-2	Sequence 2, Appl	c 196	44.4	2.6	356	2	US-09-787-292-3	Sequence 3, Appl
124	45	2.7	371	4	US-09-621-976-16048	Sequence 16048, A	c 197	44.4	2.6	582	4	US-09-949-016-38491	Sequence 38491, A
125	45	2.7	1459	4	US-09-537-654-3	Sequence 3, Appl	198	44.4	2.6	601	4	US-09-949-016-170716	Sequence 170716,
126	45	2.7	1798	3	US-09-797-906-1	Sequence 1, Appl	199	44.4	2.6	601	4	US-09-949-016-170759	Sequence 170759,
127	45	2.7	2010	1	US-07-864-475A-4	Sequence 4, Appl	200	44.4	2.6	601	4	US-09-949-016-170802	Sequence 170802,
c 128	45	2.7	2010	1	US-08-468-249A-4	Sequence 4, Appl	201	44.4	2.6	601	4	US-09-949-016-170843	Sequence 170843,
c 129	44.8	2.7	224	2	US-08-731-272A-26	Sequence 26, Appl	202	44.4	2.6	601	4	US-09-245-041-10	Sequence 10, Appl
130	44.8	2.7	357	4	US-09-621-976-16058	Sequence 16058, A	203	44.4	2.6	601	4	US-09-831-238-10	Sequence 10, Appl
131	44.8	2.7	554	4	US-09-696-169A-14	Sequence 14, Appl	204	44.4	2.6	1051	3	US-09-358-055B-10	Sequence 10, Appl
132	44.8	2.7	601	4	US-09-949-016-170715	Sequence 170715, A	205	44.4	2.6	1051	4	US-09-831-238-10	Sequence 10, Appl
133	44.8	2.7	601	4	US-09-943-016-170715	Sequence 170715, A	206	44.4	2.6	1051	4	US-09-831-238-10	Sequence 10, Appl
134	44.8	2.7	601	4	US-09-949-016-170758	Sequence 170758, A	207	44.4	2.6	1134	3	US-09-248-335-29	Sequence 29, Appl
135	44.8	2.7	601	4	US-09-949-016-170801	Sequence 170801, A	208	44.4	2.6	1141	4	US-09-800-729-78	Sequence 78, Appl
136	44.8	2.7	601	4	US-09-949-016-170842	Sequence 170842, A	209	44.4	2.6	2327	4	US-10-066-130-20	Sequence 20, Appl
137	44.8	2.7	601	4	US-09-949-016-182153	Sequence 182153, A	210	44.4	2.6	2674	4	US-10-066-130-19	Sequence 19, Appl
138	44.8	2.7	601	4	US-09-949-016-182154	Sequence 182154, A	211	44.4	2.6	2771	4	US-10-066-130-18	Sequence 18, Appl
139	44.8	2.7	1000	3	US-09-018-584A-34	Sequence 34, Appl	212	44.4	2.6	4456	3	US-09-035-443-1	Sequence 1, Appl
140	44.8	2.7	1000	4	US-09-199-542B-108	Sequence 108, App	213	44.4	2.6	5860	4	US-10-066-130-17	Sequence 17, Appl
141	44.8	2.7	1000	4	US-09-784-423-34	Sequence 34, Appl	c 214	44.4	2.6	9646	3	US-08-811-566-1	Sequence 1, Appl
142	44.8	2.7	1212	3	US-09-182-145-34	Sequence 34, Appl	c 215	44.4	2.6	9646	3	US-09-034-756-1	Sequence 1, Appl
c 143	44.8	2.7	1212	3	US-09-182-145-35	Sequence 35, Appl	c 216	44.4	2.6	9646	3	US-08-811-566-5	Sequence 5, Appl
144	44.8	2.7	1641	1	US-08-300-903A-8	Sequence 8, Appl	c 217	44.4	2.6	12980	3	US-09-034-756-5	Sequence 5, Appl
145	44.8	2.7	1641	4	US-08-988-137-8	Sequence 8, Appl	c 218	44.2	2.6	12980	3	US-09-621-976-18062	Sequence 18062, A
146	44.8	2.7	1641	4	US-10-385-072-8	Sequence 8, Appl	219	44.2	2.6	195	4	US-09-621-976-18062	Sequence 18062, A
147	44.8	2.7	1771	4	US-09-907-794A-158	Sequence 158, App	220	44.2	2.6	272	4	US-09-270-767-11902	Sequence 11902, A
148	44.8	2.7	1771	4	US-09-866-028-36	Sequence 36, Appl	221	44.2	2.6	318	4	US-09-621-976-10247	Sequence 10247, A
149	44.8	2.7	1771	4	US-09-905-135A-158	Sequence 158, App	222	44.2	2.6	1066	1	US-08-157-101A-4	Sequence 4, Appl
150	44.8	2.7	1771	4	US-09-902-775A-158	Sequence 158, App	223	44.2	2.6	1193	3	US-09-372-422A-23	Sequence 23, Appl
151	44.8	2.7	1771	4	US-09-906-700-158	Sequence 158, App	224	44.2	2.6	1801	4	US-09-709-103-3	Sequence 3, Appl
152	44.8	2.7	1771	4	US-09-944-457-36	Sequence 36, Appl	225	44.2	2.6	1801	4	US-09-439-410A-3	Sequence 3, Appl
153	44.8	2.7	1771	4	US-09-903-603A-158	Sequence 158, App	226	44.2	2.6	1925	4	US-09-148-545-128	Sequence 128, App
154	44.8	2.7	1771	4	US-09-904-920A-158	Sequence 158, App	227	44.2	2.6	2202	3	US-09-465-558-59	Sequence 59, Appl
155	44.8	2.7	1771	4	US-09-909-064-158	Sequence 158, App	c 228	44.2	2.6	670689	4	US-09-949-016-12505	Sequence 12505, A
156	44.8	2.7	1771	4	US-09-905-381A-158	Sequence 158, App	c 229	44.2	2.6	670689	4	US-09-949-016-14207	Sequence 14207, A
157	44.8	2.7	1771	4	US-09-906-638-158	Sequence 158, App	c 230	44	2.6	123	4	US-09-621-976-12330	Sequence 12330, A
158	44.8	2.7	6671	1	US-08-280-443-1	Sequence 1, Appl	231	44	2.6	186	4	US-09-513-999C-18897	Sequence 18897, A
159	44.8	2.7	6671	1	US-08-457-459-1	Sequence 1, Appl	232	44	2.6	240	4	US-09-621-976-1324	Sequence 1324, Ap
160	44.8	2.7	6671	1	US-08-555-678-1	Sequence 1, Appl	233	44	2.6	601	4	US-09-949-016-204598	Sequence 204598,
161	44.8	2.7	6671	5	PCT-US95-02275-1	Sequence 1, Appl	234	44	2.6	882	4	US-09-311-021-107	Sequence 107, App
162	44.8	2.7	36075	4	US-09-949-016-16571	Sequence 16571, A	235	44	2.6	1342	4	US-09-489-847-89	Sequence 89, Appl
163	44.8	2.7	36075	4	US-09-949-016-16572	Sequence 16572, A	236	44	2.6	1882	3	US-09-370-253-1	Sequence 1, Appl
164	44.8	2.7	3625	4	US-09-949-016-16573	Sequence 16573, A	237	44	2.6	1921	2	US-08-557-128-11	Sequence 11, Appl
165	44.8	2.7	37133	4	US-09-949-016-16569	Sequence 16569, A	238	44	2.6	2269	3	US-09-394-645-1	Sequence 1, Appl
166	44.8	2.7	37133	4	US-09-949-016-16570	Sequence 16570, A	239	44	2.6	2269	3	US-09-243-560B-1	Sequence 1, Appl
167	44.8	2.7	74881	4	US-09-949-016-15545	Sequence 15545, A	240	44	2.6	6409	4	US-09-967-908A-1	Sequence 1, Appl
168	44.8	2.7	74914	4	US-09-949-016-12286	Sequence 12286, A	241	44	2.6	6409	4	US-10-159-151-1	Sequence 1, Appl
c 169	44.8	2.7	133358	4	US-09-949-016-12286	Sequence 12286, A	242	43.8	2.6	1248	4	US-09-489-847-101	Sequence 101, App
c 170	44.8	2.7	133360	4	US-09-949-016-12651	Sequence 12651, A	243	43.8	2.6	1636	4	US-09-578-194-6	Sequence 6, Appl
c 171	44.6	2.7	396	4	US-09-640-173-33	Sequence 33, Appl	244	43.8	2.6	1781	4	US-09-818-512-1	Sequence 1, Appl
c 172	44.6	2.7	396	4	US-09-713-550-33	Sequence 33, Appl	245	43.8	2.6	1872	3	US-09-801-052-1	Sequence 1, Appl
c 173	44.6	2.7	396	4	US-09-825-294-33	Sequence 33, Appl	246	43.8	2.6	1872	4	US-10-020-121-1	Sequence 1, Appl

247	43.8	2.6	2082	2	US-08-785-310A-2	Sequence 2, Appli	320	42.6	2.5	558	4	US-09-043-861-3	Sequence 3, Appli
248	43.8	2.6	2262	4	US-09-311-021-171	Sequence 171, App	321	42.6	2.5	601	4	US-09-949-016-161729	Sequence 161729,
c 249	43.8	2.6	31842	4	US-09-949-016-15123	Sequence 15123, A	322	42.6	2.5	2218	4	US-09-016-434-1157	Sequence 1157, Ap
250	43.6	2.6	121	3	US-09-297-535-20	Sequence 20, Appl	323	42.6	2.5	2218	4	US-10-329-668-7	Sequence 7, Appli
251	43.6	2.6	246	4	US-09-621-976-13617	Sequence 13617, A	324	42.6	2.5	2276	4	US-09-205-258-183	Sequence 183, App
c 252	43.6	2.6	396	4	US-09-640-173-16	Sequence 16, Appl	325	42.6	2.5	3334	4	US-09-668-119-2	Sequence 2, Appli
c 253	43.6	2.6	396	4	US-09-713-550-16	Sequence 16, Appl	326	42.6	2.5	5096	4	US-09-949-016-15105	Sequence 15105, A
c 254	43.6	2.6	396	4	US-09-825-294-16	Sequence 16, Appl	c 327	42.6	2.5	17836	4	US-09-949-016-16167	Sequence 16167, A
c 255	43.6	2.6	396	4	US-09-970-966-16	Sequence 16, Appl	c 328	42.6	2.5	39690	4	US-09-949-016-15079	Sequence 15079, A
256	43.6	2.6	550	4	US-09-10-147B-5	Sequence 5, Appli	329	42.4	2.5	194	4	US-09-621-976-9596	Sequence 9596, Ap
257	43.6	2.6	1507	3	US-09-453-323-1	Sequence 1, Appli	330	42.4	2.5	331	4	US-09-621-976-16100	Sequence 16100, A
258	43.6	2.6	2407	3	US-09-370-807-7	Sequence 7, Appli	331	42.4	2.5	1445	3	US-09-814-951A-1	Sequence 1, Appli
259	43.6	2.6	2407	3	US-09-921-259-7	Sequence 7, Appli	332	42.4	2.5	1474	3	US-08-821-994-64	Sequence 64, Appl
260	43.6	2.6	2634	3	US-09-463-238-3	Sequence 3, Appli	333	42.4	2.5	4548	4	US-09-571-479C-5	Sequence 5, Appli
261	43.6	2.6	18026	4	US-09-949-016-13309	Sequence 13309, A	c 334	42.4	2.5	44848	4	US-09-435-739-42	Sequence 42, Appl
262	43.6	2.6	41736	4	US-09-949-016-17091	Sequence 17091, A	c 335	42.4	2.5	44848	4	US-09-988-113-42	Sequence 42, Appl
263	43.4	2.6	552	4	US-09-461-325-111	Sequence 111, App	336	42.4	2.5	61664	4	US-09-949-016-13308	Sequence 13308, A
264	43.4	2.6	552	4	US-10-012-542-111	Sequence 111, App	c 337	42.4	2.5	113379	4	US-09-949-016-17561	Sequence 17561, A
265	43.4	2.6	552	4	US-10-115-123-111	Sequence 111, App	c 338	42.4	2.5	113379	4	US-09-949-016-17562	Sequence 17562, A
266	43.4	2.6	1296	4	US-09-461-325-29	Sequence 29, Appl	339	42.2	2.5	105	4	US-09-621-976-13820	Sequence 13820, A
267	43.4	2.6	1296	4	US-10-012-542-29	Sequence 29, Appl	340	42.2	2.5	298	4	US-09-621-976-3871	Sequence 3871, Ap
268	43.4	2.6	1296	4	US-10-115-123-29	Sequence 29, Appl	c 341	42.2	2.5	370	4	US-09-513-999C-497	Sequence 497, App
269	43.4	2.6	2625	4	US-09-270-767-10080	Sequence 10080, A	c 342	42.2	2.5	370	4	US-09-471-276-222	Sequence 222, App
270	43.4	2.6	2665	3	US-08-971-089-5	Sequence 5, Appli	c 343	42.2	2.5	601	4	US-09-949-016-168357	Sequence 168357,
271	43.4	2.6	3715	4	US-09-234-245-1	Sequence 1, Appli	c 344	42.2	2.5	601	4	US-09-949-016-168358	Sequence 168358,
272	43.4	2.6	49931	4	US-09-949-016-13727	Sequence 13727, A	345	42.2	2.5	601	4	US-09-949-016-193087	Sequence 193087,
273	43.4	2.6	49931	4	US-09-949-016-13728	Sequence 13728, A	346	42.2	2.5	601	4	US-09-949-016-193088	Sequence 193088,
274	43.4	2.6	49931	4	US-09-949-016-13729	Sequence 13729, A	347	42.2	2.5	601	4	US-09-949-016-193180	Sequence 193180,
275	43.4	2.6	225127	4	US-09-949-016-16480	Sequence 16480, A	348	42.2	2.5	601	4	US-09-949-016-193181	Sequence 193181,
c 276	43.2	2.6	196	4	US-09-644-460-40	Sequence 40, Appl	349	42.2	2.5	601	4	US-09-949-016-193273	Sequence 193273,
277	43.2	2.6	358	4	US-09-621-976-927	Sequence 927, App	350	42.2	2.5	601	4	US-09-949-016-193274	Sequence 193274,
278	43.2	2.6	601	4	US-09-949-016-48516	Sequence 48516, A	351	42.2	2.5	601	4	US-09-949-016-193366	Sequence 193366,
279	43.2	2.6	601	4	US-09-949-016-48521	Sequence 48521, A	352	42.2	2.5	601	4	US-09-949-016-193367	Sequence 193367,
c 280	43.2	2.6	601	4	US-09-949-016-186016	Sequence 186016,	353	42.2	2.5	746	3	US-09-013-810-1	Sequence 1, Appli
281	43.2	2.6	763	4	US-09-743-207-3	Sequence 3, Appli	354	42.2	2.5	990	4	US-09-800-729-79	Sequence 79, Appl
282	43.2	2.6	812	3	US-09-091-097-3	Sequence 7, Appli	355	42.2	2.5	1023	1	US-08-252-566B-16	Sequence 16, Appl
283	43.2	2.6	931	4	US-09-482-273-31	Sequence 31, Appl	356	42.2	2.5	1114	3	US-09-152-060-41	Sequence 41, Appl
284	43.2	2.6	2434	4	US-09-489-847-67	Sequence 67, Appl	357	42.2	2.5	1277	4	US-09-270-767-25838	Sequence 25838, A
c 285	43.2	2.6	4419	4	US-09-620-312D-187	Sequence 187, App	358	42.2	2.5	1454	3	US-09-372-422A-19	Sequence 19, Appl
286	43.2	2.6	16600	4	US-09-949-016-13332	Sequence 13332, A	359	42.2	2.5	3116	4	US-09-311-021-187	Sequence 187, App
287	43.2	2.6	16600	4	US-09-949-016-13333	Sequence 13333, A	360	42.2	2.5	3556	4	US-09-270-767-10439	Sequence 10439, A
c 288	43.2	2.6	16600	4	US-09-949-016-13175	Sequence 13175, A	361	42.2	2.5	86213	4	US-09-949-016-17240	Sequence 17240, A
c 289	43.2	2.6	90724	4	US-09-949-016-16601	Sequence 16601, A	362	42.2	2.5	86213	4	US-09-949-016-17241	Sequence 17241, A
c 290	43.2	2.6	96922	4	US-09-949-016-17061	Sequence 17061, A	363	42.2	2.5	86213	4	US-09-949-016-17242	Sequence 17242, A
291	43	2.6	144	1	US-08-702-344-26	Sequence 26, Appl	364	42.2	2.5	86213	4	US-09-949-016-17243	Sequence 17243, A
292	43	2.6	166	4	US-09-621-976-18390	Sequence 18390, A	365	42.2	2.5	118868	4	US-09-949-016-15746	Sequence 15746, A
293	43	2.6	347	4	US-09-621-976-16026	Sequence 16026, A	c 366	42.2	2.5	225127	4	US-09-949-016-16480	Sequence 16480, A
294	43	2.6	635	1	US-08-455-633A-35	Sequence 35, Appl	c 367	42.2	2.5	678533	4	US-09-949-016-14577	Sequence 14577, A
295	43	2.6	635	1	US-08-416-336-5	Sequence 5, Appli	c 368	42.2	2.5	563	4	US-09-949-016-14578	Sequence 14578, A
296	43	2.6	635	5	PCT-US94-05354-35	Sequence 35, Appl	369	42	2.5	639	4	US-09-621-976-19183	Sequence 19183, A
297	43	2.6	711	4	US-09-270-767-9609	Sequence 9609, Ap	370	42	2.5	639	4	US-09-482-273-49	Sequence 49, Appl
c 298	43	2.6	711	4	US-09-270-767-24891	Sequence 24891, A	371	42	2.5	1013	4	US-09-322-409-6	Sequence 6, Appli
c 299	43	2.6	1545	4	US-09-559-023-1	Sequence 1, Appli	c 372	42	2.5	1013	4	US-09-322-409-8	Sequence 8, Appli
300	43	2.6	1733	3	US-09-073-569-1	Sequence 1, Appli	373	42	2.5	1013	4	US-09-451-527-6	Sequence 6, Appli
301	43	2.6	2091	3	US-09-813-818-1	Sequence 1, Appli	c 374	42	2.5	1013	4	US-09-451-527-8	Sequence 8, Appli
302	43	2.6	2091	3	US-10-199-333-1	Sequence 1, Appli	375	42	2.5	1582	3	US-08-545-196B-10	Sequence 10, Appl
303	43	2.6	2091	4	US-10-199-333-1	Sequence 1, Appli	376	42	2.5	1582	3	US-08-545-196B-12	Sequence 12, Appl
304	43	2.6	2186	3	US-09-360-545-66	Sequence 66, Appl	377	42	2.5	1736	3	US-09-182-816-22	Sequence 22, Appl
305	43	2.6	2233	1	US-08-496-631-1	Sequence 1, Appli	c 378	42	2.5	1736	3	US-09-182-816-24	Sequence 24, Appl
306	43	2.6	4086	4	US-09-702-705-1801	Sequence 1801, Ap	379	42	2.5	1736	3	US-09-471-528-22	Sequence 22, Appl
307	43	2.6	4086	4	US-09-736-457-1801	Sequence 1801, Ap	c 380	42	2.5	1736	3	US-09-471-528-24	Sequence 24, Appl
308	43	2.6	4086	4	US-09-949-016-48518	Sequence 48518, A	381	42	2.5	1736	3	US-09-634-530-22	Sequence 22, Appl
309	43	2.6	12521	4	US-09-949-016-15988	Sequence 15988, A	c 382	42	2.5	1736	3	US-09-634-530-24	Sequence 24, Appl
310	42.8	2.5	177	4	US-09-621-976-1047	Sequence 1047, Ap	383	42	2.5	1927	3	US-09-316-536-66	Sequence 66, Appl
311	42.8	2.5	194	4	US-09-621-976-801	Sequence 801, App	384	42	2.5	5749	4	US-09-949-016-15441	Sequence 15441, A
312	42.8	2.5	601	4	US-09-949-016-48517	Sequence 48517, A	385	42	2.5	5749	4	US-09-949-016-15442	Sequence 15442, A
313	42.8	2.5	601	4	US-09-949-016-48518	Sequence 48518, A	386	42	2.5	13184	4	US-09-949-016-16573	Sequence 16573, A
314	42.8	2.5	601	4	US-09-949-016-48519	Sequence 48519, A	387	42	2.5	101349	4	US-09-949-016-17433	Sequence 17433, A
315	42.8	2.5	1378	3	US-09-149-476-208	Sequence 208, App	388	41.8	2.5	130	4	US-09-621-976-12892	Sequence 12892, A
316	42.8	2.5	2271	4	US-09-205-258-243	Sequence 243, Appl	c 389	41.8	2.5	227	2	US-08-530-678A-28	Sequence 28, Appl
317	42.8	2.5	2323	3	US-09-149-476-24	Sequence 24, Appl	c 390	41.8	2.5	227	3	US-08-897-126-28	Sequence 28, Appl
c 318	42.8	2.5	209210	4	US-09-949-016-15094	Sequence 15094, A	391	41.8	2.5	250	4	US-09-621-976-18893	Sequence 18893, A
319	42.6	2.5	323	4	US-09-621-976-10374	Sequence 10374, A	392	41.8	2.5	601	4	US-09-949-016-184918	Sequence 184918,

393	41.8	2.5	601	4	US-09-949-016-185073	Sequence 185073,	466	41.4	2.5	3410	4	US-09-688-489-110	Sequence 110, App
394	41.8	2.5	601	4	US-09-949-016-201490	Sequence 201490,	467	41.4	2.5	3410	4	US-09-679-426-110	Sequence 110, App
395	41.8	2.5	1008	4	US-09-780-641-1	Sequence 1, Appli	468	41.4	2.5	3410	4	US-09-759-143-110	Sequence 110, App
396	41.8	2.5	1192	4	US-09-439-554-23	Sequence 23, Appl	469	41.4	2.5	3410	4	US-09-651-236-110	Sequence 110, App
397	41.8	2.5	1361	4	US-09-489-847-64	Sequence 64, Appl	c 470	41.4	2.5	129778	4	US-09-949-016-12191	Sequence 12191, A
398	41.8	2.5	1461	3	US-08-722-126A-4	Sequence 4, Appli	c 471	41.4	2.5	129778	4	US-09-949-016-17075	Sequence 17075, A
399	41.8	2.5	1461	5	PCT-US95-04258-4	Sequence 4, Appli	472	41.4	2.5	123438	4	US-09-949-016-14349	Sequence 14349, A
400	41.8	2.5	1558	1	US-08-467-607-2	Sequence 2, Appli	473	41.4	2.5	132438	4	US-09-949-016-14350	Sequence 14350, A
401	41.8	2.5	1558	2	US-08-469-362-2	Sequence 2, Appli	474	41.4	2.5	151089	4	US-09-949-016-14348	Sequence 14348, A
402	41.8	2.5	1558	2	US-08-850-392-2	Sequence 1, Appli	c 475	41.4	2.5	151295	4	US-09-949-016-14568	Sequence 14568, A
403	41.8	2.5	1662	4	US-08-668-037A-13	Sequence 13, Appl	c 476	41.4	2.5	151295	4	US-09-949-016-14569	Sequence 14569, A
c 404	41.8	2.5	15666	4	US-09-949-016-15929	Sequence 15929, A	c 477	41.4	2.5	151295	4	US-09-949-016-14570	Sequence 14570, A
c 405	41.8	2.5	149543	4	US-09-949-016-15947	Sequence 15947, A	c 478	41.4	2.5	151295	4	US-09-949-016-14571	Sequence 14571, A
406	41.8	2.5	194937	4	US-09-949-016-17032	Sequence 17032, A	c 479	41.4	2.5	151295	4	US-09-949-016-14572	Sequence 14572, A
407	41.8	2.5	194937	4	US-09-949-016-17033	Sequence 17033, A	c 480	41.4	2.5	154605	4	US-09-949-016-11894	Sequence 11894, A
408	41.6	2.5	117	1	US-08-702-344-3	Sequence 3, Appli	481	41.4	2.5	237241	4	US-09-949-016-16101	Sequence 16101, A
409	41.6	2.5	164	4	US-09-621-976-16692	Sequence 16692, A	c 482	41.4	2.5	393753	4	US-09-949-016-14573	Sequence 14573, A
410	41.6	2.5	231	4	US-09-621-976-16317	Sequence 16317, A	c 483	41.4	2.5	393753	4	US-09-949-016-14574	Sequence 14574, A
411	41.6	2.5	242	4	US-09-621-976-16320	Sequence 16320, A	484	41.4	2.5	524032	4	US-09-949-016-16928	Sequence 16928, A
412	41.6	2.5	242	4	US-09-621-976-16324	Sequence 16324, A	485	41.4	2.5	524032	4	US-09-949-016-16929	Sequence 16929, A
c 413	41.6	2.5	253	2	US-08-520-678A-25	Sequence 25, Appl	486	41.4	2.5	524032	4	US-09-949-016-16930	Sequence 16930, A
c 414	41.6	2.5	253	3	US-08-897-126-25	Sequence 25, Appl	487	41.4	2.5	524032	4	US-09-949-016-16931	Sequence 16931, A
c 415	41.6	2.5	270	2	US-08-520-678A-30	Sequence 30, Appl	488	41.4	2.5	529885	4	US-09-949-016-14340	Sequence 14340, A
c 416	41.6	2.5	270	3	US-08-897-126-30	Sequence 30, Appl	489	41.4	2.5	529885	4	US-09-949-016-14341	Sequence 14341, A
c 417	41.6	2.5	601	4	US-09-949-016-37086	Sequence 37086, A	490	41.4	2.5	529885	4	US-09-949-016-14342	Sequence 14342, A
c 418	41.6	2.5	601	4	US-09-949-016-37087	Sequence 37087, A	491	41.4	2.5	529885	4	US-09-949-016-14343	Sequence 14343, A
c 419	41.6	2.5	601	4	US-09-949-016-161063	Sequence 161063, A	492	41.4	2.5	529885	4	US-09-949-016-14344	Sequence 14344, A
c 420	41.6	2.5	601	4	US-09-949-016-161064	Sequence 161064, A	493	41.4	2.5	529885	4	US-09-949-016-14345	Sequence 14345, A
421	41.6	2.5	664	4	US-09-904-615-66	Sequence 66, Appl	494	41.4	2.5	529885	4	US-09-949-016-14346	Sequence 14346, A
422	41.6	2.5	949	4	US-09-489-847-35	Sequence 35, Appl	495	41.4	2.5	529885	4	US-09-949-016-14347	Sequence 14347, A
423	41.6	2.5	1297	4	US-09-800-729-80	Sequence 80, Appl	c 496	41.4	2.5	818128	4	US-09-949-016-14546	Sequence 14546, A
424	41.6	2.5	1308	4	US-10-151-832-1	Sequence 1, Appli	c 497	41.4	2.5	818128	4	US-09-949-016-14547	Sequence 14547, A
425	41.6	2.5	1414	4	US-09-501-115-5	Sequence 5, Appli	c 498	41.4	2.5	818128	4	US-09-949-016-14548	Sequence 14548, A
426	41.6	2.5	1746	4	US-09-485-529-57	Sequence 57, Appl	c 499	41.4	2.5	818128	4	US-09-949-016-14549	Sequence 14549, A
427	41.6	2.5	1768	4	US-09-485-529-13	Sequence 13, Appl	c 500	41.4	2.5	818128	4	US-09-949-016-14550	Sequence 14550, A
428	41.6	2.5	1817	1	US-08-473-981A-5	Sequence 5, Appli	c 501	41.4	2.5	818128	4	US-09-949-016-14551	Sequence 14551, A
429	41.6	2.5	1817	2	US-08-474-087-5	Sequence 5, Appli	c 502	41.4	2.5	818128	4	US-09-949-016-14552	Sequence 14552, A
430	41.6	2.5	2671	6	5168051-9	Patent No. 5168051	c 503	41.4	2.5	818128	4	US-09-949-016-14553	Sequence 14553, A
431	41.6	2.5	2671	6	5168051-9	Patent No. 5168051	c 504	41.4	2.5	818128	4	US-09-949-016-14554	Sequence 14554, A
c 432	41.6	2.5	10877	4	US-09-674-311-1	Sequence 1, Appli	c 505	41.4	2.5	818128	4	US-09-949-016-14555	Sequence 14555, A
c 433	41.6	2.5	18107	4	US-09-949-016-13674	Sequence 13674, A	c 506	41.4	2.5	818128	4	US-09-949-016-14556	Sequence 14556, A
434	41.6	2.5	20721	4	US-09-949-016-16257	Sequence 16257, A	c 507	41.4	2.5	818128	4	US-09-949-016-14557	Sequence 14557, A
435	41.6	2.5	26684	4	US-09-949-016-15109	Sequence 15109, A	c 508	41.4	2.5	818128	4	US-09-949-016-14558	Sequence 14558, A
436	41.6	2.5	26684	4	US-09-949-016-15110	Sequence 15110, A	c 509	41.4	2.5	818128	4	US-09-949-016-14559	Sequence 14559, A
437	41.6	2.5	26684	4	US-09-949-016-17409	Sequence 17409, A	c 510	41.4	2.5	818128	4	US-09-949-016-14560	Sequence 14560, A
438	41.6	2.5	26684	4	US-09-949-016-17410	Sequence 17410, A	c 511	41.4	2.5	818128	4	US-09-949-016-14561	Sequence 14561, A
439	41.6	2.5	46823	4	US-09-949-016-12723	Sequence 12723, A	c 512	41.4	2.5	818128	4	US-09-949-016-14562	Sequence 14562, A
440	41.6	2.5	46940	4	US-09-949-016-16252	Sequence 16252, A	c 513	41.4	2.5	818128	4	US-09-949-016-14564	Sequence 14564, A
c 441	41.6	2.5	53332	4	US-09-801-861-3	Sequence 3, Appli	c 514	41.4	2.5	818128	4	US-09-949-016-14565	Sequence 14565, A
c 442	41.6	2.5	53332	4	US-10-224-562-3	Sequence 3, Appli	c 515	41.4	2.5	818128	4	US-09-949-016-14566	Sequence 14566, A
c 443	41.6	2.5	151088	4	US-09-949-016-16240	Sequence 16240, A	c 516	41.4	2.5	818128	4	US-09-949-016-14567	Sequence 14567, A
444	41.4	2.5	111	3	US-09-297-535-23	Sequence 23, Appl	517	41.2	2.5	250	4	US-09-621-976-11744	Sequence 11744, A
445	41.4	2.5	111	4	US-09-621-976-14677	Sequence 14677, A	518	41.2	2.5	250	4	US-09-621-976-17371	Sequence 17371, A
446	41.4	2.5	351	4	US-09-621-976-15134	Sequence 15134, A	519	41.2	2.5	333	3	US-09-018-584A-27	Sequence 27, Appl
447	41.4	2.5	510	4	US-09-248-796A-13735	Sequence 13735, A	520	41.2	2.5	333	4	US-09-784-423-27	Sequence 27, Appl
c 448	41.4	2.5	601	4	US-09-949-016-149677	Sequence 149677, A	521	41.2	2.5	396	4	US-09-640-173-10	Sequence 10, Appl
c 449	41.4	2.5	601	4	US-09-949-016-186673	Sequence 186673, A	522	41.2	2.5	396	4	US-09-713-550-10	Sequence 10, Appl
c 450	41.4	2.5	601	4	US-09-949-016-186674	Sequence 186674, A	c 523	41.2	2.5	396	4	US-09-825-294-10	Sequence 10, Appl
c 451	41.4	2.5	601	4	US-09-949-016-186675	Sequence 186675, A	c 524	41.2	2.5	396	4	US-09-970-966-10	Sequence 10, Appl
c 452	41.4	2.5	844	4	US-09-690-942-3	Sequence 3, Appli	c 525	41.2	2.5	1335	4	US-09-270-767-13052	Sequence 13052, A
453	41.4	2.5	890	4	US-09-621-976-2725	Sequence 2725, Ap	526	41.2	2.5	1508	3	US-09-039-046-1	Sequence 1, Appli
454	41.4	2.5	2239	3	US-09-196-390-1	Sequence 1, Appli	527	41.2	2.5	1544	4	US-09-187-999-14	Sequence 14, Appli
455	41.4	2.5	2239	4	US-09-952-677-1	Sequence 1, Appli	528	41.2	2.5	1835	3	US-09-485-549-1	Sequence 1, Appli
456	41.4	2.5	3410	3	US-09-020-956-110	Sequence 110, App	529	41.2	2.5	2599	4	US-09-949-016-4676	Sequence 4676, Ap
457	41.4	2.5	3410	3	US-09-030-607-110	Sequence 110, App	530	41.2	2.5	2633	4	US-09-023-655-90	Sequence 950, App
458	41.4	2.5	3410	3	US-09-439-313-110	Sequence 110, App	531	41.2	2.5	2852	3	US-09-027-137-2	Sequence 2, Appli
459	41.4	2.5	3410	3	US-09-352-616A-110	Sequence 110, App	532	41.2	2.5	2852	3	US-09-344-441-2	Sequence 2, Appli
460	41.4	2.5	3410	3	US-09-602-877A-100	Sequence 100, App	533	41.2	2.5	5807	3	US-09-976-594-245	Sequence 245, App
461	41.4	2.5	3410	3	US-09-232-149A-110	Sequence 110, App	c 534	41.2	2.5	23222	4	US-09-949-016-15949	Sequence 15949, A
462	41.4	2.5	3410	4	US-09-159-812-110	Sequence 110, App	c 535	41.2	2.5	25922	4	US-09-949-016-11874	Sequence 11874, A
463	41.4	2.5	3410	4	US-09-636-215-110	Sequence 110, App	536	41.2	2.5	72604	3	US-09-268-392-7	Sequence 7, Appli
464	41.4	2.5	3410	4	US-09-685-166A-110	Sequence 110, App	537	41.2	2.5	72604	3	US-09-657-474-7	Sequence 7, Appli
465	41.4	2.5	3410	4	US-09-115-453-110	Sequence 110, App	c 538	41.2	2.5	87780	4	US-09-949-016-17011	Sequence 17011, A



C 539	41.2	2.5	90428	4	US-09-949-016-12564	Sequence 13564, A	612	40.6	2.4	2718	4	US-09-667-135-1	Sequence 1, Appli
C 540	41.2	2.5	145928	4	US-09-949-016-15444	Sequence 15444, A	613	40.6	2.4	2989	6	5378464-1	Patent No. 5378464
C 541	41.2	2.5	251672	4	US-09-949-016-17296	Sequence 17296, A	614	40.6	2.4	2989	6	5378464-1	Sequence 1, Appli
C 542	41.2	2.5	251682	4	US-09-949-016-11973	Sequence 11973, A	615	40.6	2.4	8353	3	US-08-611-587-1	Sequence 6, Appli
C 543	41	2.4	163	4	US-09-621-976-9608	Sequence 9608, Ap	C 616	40.6	2.4	8638	4	US-10-029-907-6	Sequence 4, Appli
C 544	41	2.4	257	2	US-08-520-678A-24	Sequence 24, Appl	C 617	40.6	2.4	8638	4	US-10-029-907-6	Sequence 3, Appli
C 545	41	2.4	257	3	US-08-897-136-24	Sequence 24, Appl	C 618	40.6	2.4	13146	2	US-08-724-354D-3	Sequence 3, Appli
C 546	41	2.4	601	4	US-09-949-016-193621	Sequence 193621,	C 619	40.6	2.4	13146	2	US-09-270-984A-3	Sequence 3, Appli
C 547	41	2.4	985	4	US-09-322-409-27	Sequence 27, Appl	620	40.6	2.4	15108	4	US-09-949-016-11786	Sequence 1786, A
C 548	41	2.4	985	4	US-09-322-409-27	Sequence 27, Appl	621	40.6	2.4	15108	4	US-09-949-016-11786	Sequence 17205, A
C 549	41	2.4	985	4	US-09-451-527-25	Sequence 25, Appl	622	40.6	2.4	15661	4	US-09-949-016-13161	Sequence 13161, A
C 550	41	2.4	985	4	US-09-451-527-25	Sequence 25, Appl	623	40.6	2.4	15661	4	US-09-949-016-13161	Sequence 14257, A
C 551	41	2.4	1406	4	US-10-000-489-81	Sequence 81, Appl	624	40.6	2.4	29321	4	US-09-949-016-14258	Sequence 14258, A
C 552	41	2.4	1493	1	US-08-340-820-24	Sequence 24, Appl	625	40.6	2.4	50000	3	US-09-146-053-3	Sequence 3, Appli
C 553	41	2.4	1493	1	US-08-593-535-24	Sequence 24, Appl	626	40.6	2.4	55298	4	US-09-491-356C-1	Sequence 1, Appli
C 554	41	2.4	2311	4	US-09-800-729-66	Sequence 66, Appl	627	40.6	2.4	82178	4	US-09-949-016-13394	Sequence 13394, A
C 555	41	2.4	2311	4	US-09-720-317A-19	Sequence 19, Appl	628	40.6	2.4	83708	4	US-09-949-016-17207	Sequence 17207, A
C 556	41	2.4	2320	3	US-09-202-904A-13	Sequence 13, Appl	C 629	40.6	2.4	87752	4	US-09-949-016-16807	Sequence 16807, A
C 557	41	2.4	2406	4	US-09-594-506-37	Sequence 37, Appl	C 630	40.6	2.4	175265	4	US-09-949-016-16089	Sequence 16089, A
C 558	41	2.4	6200	3	US-09-439-923-1	Sequence 1, Appli	631	40.6	2.4	268449	4	US-09-949-016-17244	Sequence 17244, A
C 559	41	2.4	6200	4	US-09-711-205A-1	Sequence 1, Appli	632	40.6	2.4	390416	4	US-09-949-016-17244	Sequence 16923, A
C 560	41	2.4	6200	4	US-09-711-205A-1	Sequence 1, Appli	633	40.4	2.4	124	6	5185243-1	Patent No. 5185243
C 561	41	2.4	7286	3	US-09-331-581-3	Sequence 3, Appli	C 634	40.4	2.4	124	6	5185243-1	Patent No. 5185243
C 562	41	2.4	7938	3	US-09-331-581-14	Sequence 14, Appl	635	40.4	2.4	190	4	US-09-621-976-16784	Sequence 16784, A
C 563	41	2.4	54033	4	US-09-949-016-12091	Sequence 12091, A	636	40.4	2.4	326	4	US-09-621-976-16034	Sequence 16034, A
C 564	41	2.4	54033	4	US-09-949-016-14325	Sequence 14325, A	637	40.4	2.4	334	4	US-09-621-976-16044	Sequence 16044, A
C 565	41	2.4	68283	4	US-09-949-016-12261	Sequence 12261, A	638	40.4	2.4	335	4	US-09-621-976-16044	Sequence 16061, A
C 566	41	2.4	113701	4	US-09-949-016-13214	Sequence 13214, A	639	40.4	2.4	336	4	US-09-621-976-16013	Sequence 16013, A
C 567	41	2.4	124264	4	US-09-949-016-16396	Sequence 16396, A	640	40.4	2.4	336	4	US-09-621-976-16013	Sequence 16051, A
C 568	41	2.4	128175	4	US-09-949-016-16268	Sequence 16268, A	641	40.4	2.4	338	4	US-09-621-976-16041	Sequence 16041, A
C 569	40.8	2.4	84	4	US-09-621-976-14571	Sequence 14571, A	C 642	40.4	2.4	389	4	US-09-513-999C-420	Sequence 420, App
C 570	40.8	2.4	102	4	US-09-621-976-14804	Sequence 14804, A	643	40.4	2.4	593	4	US-09-904-615-59	Sequence 59, Appl
C 571	40.8	2.4	179	4	US-09-621-976-9575	Sequence 9575, Ap	644	40.4	2.4	601	4	US-09-949-016-189988	Sequence 189988,
C 572	40.8	2.4	188	4	US-09-621-976-9575	Sequence 10364, A	645	40.4	2.4	1052	4	US-09-949-016-189988	Sequence 23, Appl
C 573	40.8	2.4	273	4	US-09-809-545A-31	Sequence 31, Appl	646	40.4	2.4	1503	4	US-09-907-794A-220	Sequence 220, App
C 574	40.8	2.4	283	4	US-09-621-976-16989	Sequence 16989, A	647	40.4	2.4	1503	4	US-09-905-125A-220	Sequence 220, App
C 575	40.8	2.4	1129	3	US-09-227-357-40	Sequence 40, Appl	648	40.4	2.4	1503	4	US-09-902-775A-220	Sequence 220, App
C 576	40.8	2.4	1214	4	US-09-780-717-28	Sequence 28, Appl	649	40.4	2.4	1503	4	US-09-906-700-220	Sequence 220, App
C 577	40.8	2.4	1683	3	US-09-347-803-11	Sequence 11, Appl	650	40.4	2.4	1503	4	US-09-903-603A-220	Sequence 220, App
C 578	40.8	2.4	2488	4	US-09-816-093-1	Sequence 1, Appli	651	40.4	2.4	1503	4	US-09-904-920A-220	Sequence 220, App
C 579	40.8	2.4	3124	3	US-09-734-030-1	Sequence 1, Appli	652	40.4	2.4	1503	4	US-09-909-064-220	Sequence 220, App
C 580	40.8	2.4	3124	4	US-10-153-921-1	Sequence 1, Appli	653	40.4	2.4	1503	4	US-09-905-381A-220	Sequence 220, App
C 581	40.8	2.4	3124	4	US-10-669-689-1	Sequence 1, Appli	654	40.4	2.4	1503	4	US-09-906-618-220	Sequence 220, App
C 582	40.8	2.4	15722	4	US-09-949-016-16709	Sequence 16709, A	655	40.4	2.4	1512	2	US-08-909-965C-8	Sequence 8, Appli
C 583	40.8	2.4	61124	4	US-09-949-016-11914	Sequence 11914, A	656	40.4	2.4	1542	4	US-09-205-258-123	Sequence 123, App
C 584	40.8	2.4	61140	4	US-09-949-016-15771	Sequence 15771, A	657	40.4	2.4	1685	4	US-09-907-794A-83	Sequence 83, Appl
C 585	40.8	2.4	65744	4	US-09-949-016-12591	Sequence 12591, A	658	40.4	2.4	1685	4	US-09-905-125A-83	Sequence 83, Appl
C 586	40.8	2.4	65745	4	US-09-949-016-15871	Sequence 15871, A	659	40.4	2.4	1685	4	US-09-902-775A-83	Sequence 83, Appl
C 587	40.8	2.4	76269	4	US-09-949-016-14603	Sequence 14603, A	660	40.4	2.4	1685	4	US-09-906-700-83	Sequence 83, Appl
C 588	40.8	2.4	100836	4	US-09-949-016-12871	Sequence 12871, A	661	40.4	2.4	1685	4	US-09-903-603A-83	Sequence 83, Appl
C 589	40.8	2.4	100837	4	US-09-949-016-17063	Sequence 17063, A	662	40.4	2.4	1685	4	US-09-904-920A-83	Sequence 83, Appl
C 590	40.8	2.4	321022	4	US-09-949-016-11852	Sequence 11852, A	663	40.4	2.4	1685	4	US-09-909-064-83	Sequence 83, Appl
C 591	40.8	2.4	321022	4	US-09-949-016-14166	Sequence 14166, A	664	40.4	2.4	1685	4	US-09-905-381A-83	Sequence 83, Appl
C 592	40.8	2.4	1684976	4	US-08-916-421B-1	Sequence 1, Appli	665	40.4	2.4	1685	4	US-09-906-618-83	Sequence 83, Appl
C 593	40.8	2.4	1684976	4	US-09-692-570-1	Sequence 1, Appli	666	40.4	2.4	1718	4	US-09-778-510-5	Sequence 5, Appli
C 594	40.6	2.4	147	4	US-09-621-976-8551	Sequence 8551, Ap	667	40.4	2.4	1820	4	US-09-778-510-1	Sequence 1, Appli
C 595	40.6	2.4	189	4	US-09-621-976-14761	Sequence 14761, A	668	40.4	2.4	2233	4	US-09-248-796A-409	Sequence 4, Appli
C 596	40.6	2.4	376	2	US-08-623-906A-18	Sequence 18, Appl	669	40.4	2.4	2820	1	US-08-257-073-4	Sequence 4, Appli
C 597	40.6	2.4	601	4	US-09-949-016-47249	Sequence 47249, A	670	40.4	2.4	3200	1	US-08-444-405-1	Sequence 1, Appli
C 598	40.6	2.4	601	4	US-09-949-016-47327	Sequence 47327, A	671	40.4	2.4	3200	1	US-08-384-850-1	Sequence 1, Appli
C 599	40.6	2.4	601	4	US-09-949-016-57131	Sequence 57131, A	672	40.4	2.4	192700	4	US-09-949-016-11820	Sequence 11820, A
C 600	40.6	2.4	601	4	US-09-949-016-57132	Sequence 57132, A	673	40.4	2.4	192704	4	US-09-949-016-17182	Sequence 17182, A
C 601	40.6	2.4	601	4	US-09-949-016-57133	Sequence 57133, A	674	40.4	2.4	202001	4	US-09-734-674-3	Sequence 3, Appli
C 602	40.6	2.4	601	4	US-09-949-016-88560	Sequence 88560, A	C 675	40.4	2.4	422592	4	US-09-949-016-14182	Sequence 14182, A
C 603	40.6	2.4	601	4	US-09-949-016-88565	Sequence 88565, A	676	40.2	2.4	454	2	US-08-623-906A-6	Sequence 6, Appli
C 604	40.6	2.4	601	4	US-09-949-016-193622	Sequence 193622,	677	40.2	2.4	572	3	US-09-342-653-5	Sequence 5, Appli
C 605	40.6	2.4	601	4	US-09-949-016-193623	Sequence 193623,	678	40.2	2.4	601	4	US-09-949-016-17855	Sequence 17855, A
C 606	40.6	2.4	601	4	US-09-949-016-193624	Sequence 193624,	679	40.2	2.4	601	4	US-09-949-016-41735	Sequence 41735, A
C 607	40.6	2.4	795	4	US-09-270-767-14068	Sequence 14068, A	680	40.2	2.4	601	4	US-09-949-016-56224	Sequence 56224, A
C 608	40.6	2.4	1147	1	US-08-665-716-1	Sequence 1, Appli	C 681	40.2	2.4	601	4	US-09-949-016-84943	Sequence 84943, A
C 609	40.6	2.4	1198	3	US-09-248-335-27	Sequence 27, Appl	682	40.2	2.4	601	4	US-09-949-016-162251	Sequence 162251,
C 610	40.6	2.4	1878	3	US-09-465-558-39	Sequence 39, Appl	683	40.2	2.4	601	4	US-09-949-016-162252	Sequence 162252,
C 611	40.6	2.4	2458	3	US-08-611-587-6	Sequence 6, Appli	C 684	40.2	2.4	601	4	US-09-949-016-204750	Sequence 204750,

685	40.2	2.4	753	4	US-09-902-331B-9	Sequence 9, Appli	758	39.8	2.4	332	4	US-09-621-976-16050	Sequence 16050, A
686	40.2	2.4	958	2	US-08-757-046A-5	Sequence 5, Appli	759	39.8	2.4	332	4	US-09-621-976-16053	Sequence 16053, A
687	40.2	2.4	958	3	US-09-447-208-5	Sequence 5, Appli	760	39.8	2.4	443	4	US-09-621-976-17631	Sequence 17631, A
688	40.2	2.4	958	3	US-09-135-988-5	Sequence 5, Appli	761	39.8	2.4	588	4	US-09-205-258-64	Sequence 64, Appli
689	40.2	2.4	958	3	US-08-277-716-5	Sequence 5, Appli	762	39.8	2.4	601	4	US-09-949-016-29142	Sequence 29142, A
690	40.2	2.4	958	3	US-09-597-274A-5	Sequence 5, Appli	763	39.8	2.4	601	4	US-09-949-016-29143	Sequence 29143, A
691	40.2	2.4	958	3	US-08-908-909-5	Sequence 5, Appli	764	39.8	2.4	601	4	US-09-949-016-29144	Sequence 29144, A
692	40.2	2.4	958	3	US-09-609-161B-5	Sequence 5, Appli	765	39.8	2.4	601	4	US-09-949-016-29145	Sequence 29145, A
693	40.2	2.4	958	3	US-08-990-103-5	Sequence 5, Appli	766	39.8	2.4	601	4	US-09-949-016-41097	Sequence 41097, A
694	40.2	2.4	958	3	US-08-946-485A-5	Sequence 5, Appli	767	39.8	2.4	601	4	US-09-949-016-41098	Sequence 41098, A
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696	40.2	2.4	958	4	US-10-126-798-5	Sequence 5, Appli	769	39.8	2.4	601	4	US-09-949-016-41100	Sequence 41100, A
697	40.2	2.4	958	4	US-10-126-777-5	Sequence 5, Appli	770	39.8	2.4	601	4	US-09-949-016-161232	Sequence 161232, A
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700	40.2	2.4	1359	3	US-09-387-574-11	Sequence 11, Appli	773	39.8	2.4	1046	1	US-08-361-467B-4	Sequence 4, Appli
701	40.2	2.4	1359	3	US-09-668-096-11	Sequence 11, Appli	774	39.8	2.4	1046	1	US-08-484-332C-4	Sequence 4, Appli
702	40.2	2.4	1606	4	US-09-820-004-1	Sequence 1, Appli	775	39.8	2.4	1172	1	US-07-945-288-9	Sequence 9, Appli
703	40.2	2.4	1895	3	US-09-444-336-7	Sequence 7, Appli	776	39.8	2.4	1172	1	US-08-462-831-9	Sequence 9, Appli
704	40.2	2.4	2065	2	US-08-968-751-1	Sequence 1, Appli	777	39.8	2.4	1172	1	US-08-461-809-9	Sequence 9, Appli
705	40.2	2.4	5506	4	US-09-976-594-530	Sequence 530, App	778	39.8	2.4	1172	1	US-08-461-441-9	Sequence 9, Appli
706	40.2	2.4	5083	4	US-09-943-016-17600	Sequence 17600, A	779	39.8	2.4	1172	5	PCT-US93-08518-9	Sequence 9, Appli
c 707	40.2	2.4	53769	4	US-09-949-016-17527	Sequence 17527, A	780	39.8	2.4	1602	1	US-08-530-950-3	Sequence 3, Appli
c 708	40.2	2.4	86639	4	US-09-949-016-17397	Sequence 17397, A	781	39.8	2.4	1602	3	US-08-888-429A-3	Sequence 3, Appli
c 709	40.2	2.4	89240	4	US-09-949-016-16279	Sequence 16279, A	782	39.8	2.4	1602	3	US-09-149-879-3	Sequence 3, Appli
710	40.2	2.4	89843	4	US-09-949-016-12346	Sequence 12346, A	783	39.8	2.4	1602	4	US-09-057-009-3	Sequence 3, Appli
711	40.2	2.4	89844	4	US-09-949-016-13656	Sequence 13656, A	784	39.8	2.4	1602	4	US-09-593-653-3	Sequence 3, Appli
c 712	40.2	2.4	93398	4	US-09-949-016-14167	Sequence 14167, A	785	39.8	2.4	1692	4	US-09-821-803A-5	Sequence 5, Appli
c 713	40.2	2.4	144158	4	US-09-949-016-11755	Sequence 11755, A	786	39.8	2.4	1725	4	US-09-668-097A-21	Sequence 21, Appli
c 714	40.2	2.4	144158	4	US-09-949-016-12936	Sequence 12936, A	787	39.8	2.4	2239	4	US-10-380-105-7	Sequence 7, Appli
c 715	40.2	2.4	256287	4	US-09-949-016-14608	Sequence 14608, A	788	39.8	2.4	4860	4	US-09-949-016-195763	Sequence 296, App
716	40.2	2.4	92	4	US-09-621-976-13620	Sequence 13620, A	789	39.8	2.4	5173	1	US-08-242-677-1	Sequence 1, Appli
717	40.2	2.4	146	4	US-09-621-976-8550	Sequence 8550, Ap	790	39.8	2.4	10502	4	US-09-949-016-16708	Sequence 16708, A
718	40.2	2.4	160	4	US-09-621-976-8550	Sequence 8550, Ap	791	39.8	2.4	16073	4	US-09-949-016-12312	Sequence 12312, A
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721	40.2	2.4	293	4	US-09-621-976-16965	Sequence 16965, A	794	39.8	2.4	25175	4	US-09-949-016-16247	Sequence 16247, A
722	40.2	2.4	333	4	US-09-621-976-16032	Sequence 16032, A	795	39.8	2.4	25175	4	US-09-949-016-16248	Sequence 16248, A
723	40.2	2.4	333	4	US-09-621-976-16045	Sequence 16045, A	796	39.8	2.4	25175	4	US-09-949-016-16273	Sequence 16273, A
724	40.2	2.4	601	4	US-09-949-016-40844	Sequence 40844, A	c 797	39.8	2.4	36159	3	US-09-749-588-3	Sequence 3, Appli
725	40.2	2.4	601	4	US-09-949-016-40845	Sequence 40845, A	c 798	39.8	2.4	36159	4	US-10-135-687-3	Sequence 3, Appli
726	40.2	2.4	601	4	US-09-949-016-40846	Sequence 40846, A	799	39.8	2.4	38772	4	US-09-949-016-12382	Sequence 12382, A
727	40.2	2.4	1578	3	US-09-416-050A-1	Sequence 1, Appli	800	39.8	2.4	38772	4	US-09-949-016-12729	Sequence 12729, A
728	40.2	2.4	1578	3	US-09-664-800-1	Sequence 1, Appli	c 801	39.8	2.4	83178	4	US-09-949-016-14606	Sequence 14606, A
729	40.2	2.4	1578	3	US-09-665-309-1	Sequence 1, Appli	802	39.8	2.4	83894	4	US-09-949-016-13629	Sequence 13629, A
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732	40.2	2.4	2628	1	US-08-143-219-1	Sequence 1, Appli	805	39.6	2.4	109	4	US-09-621-976-14592	Sequence 14592, A
733	40.2	2.4	5225	4	US-09-949-016-16351	Sequence 16351, A	806	39.6	2.4	316	4	US-09-513-999C-838	Sequence 838, App
734	40.2	2.4	6243	2	US-09-056-075-1	Sequence 1, Appli	807	39.6	2.4	339	4	US-09-621-976-16015	Sequence 16015, A
735	40.2	2.4	7224	4	US-08-486-049-1	Sequence 1, Appli	c 808	39.6	2.4	516	3	US-09-018-584A-24	Sequence 24, Appli
736	40.2	2.4	8100	4	US-09-554-337-4	Sequence 4, Appli	c 809	39.6	2.4	516	4	US-09-784-423-24	Sequence 24, Appli
737	40.2	2.4	1538	4	US-09-949-016-13046	Sequence 1, Appli	c 810	39.6	2.4	593	3	US-09-385-982-262	Sequence 262, App
c 738	40.2	2.4	28555	4	US-09-949-016-12778	Sequence 12778, A	c 811	39.6	2.4	601	4	US-09-949-016-160808	Sequence 160808, A
c 739	40.2	2.4	35064	4	US-09-949-016-13196	Sequence 13196, A	812	39.6	2.4	633	4	US-09-270-767-6288	Sequence 6288, Ap
c 740	40.2	2.4	35065	4	US-09-949-016-13196	Sequence 13196, A	813	39.6	2.4	633	4	US-09-270-767-21570	Sequence 21570, A
c 741	40.2	2.4	43323	4	US-09-949-016-16142	Sequence 16142, A	814	39.6	2.4	711	4	US-09-621-976-17854	Sequence 17854, A
c 742	40.2	2.4	43323	4	US-09-949-016-16142	Sequence 16142, A	815	39.6	2.4	796	1	US-08-104-073-2	Sequence 2, Appli
c 743	40.2	2.4	43323	4	US-09-949-016-16142	Sequence 16142, A	816	39.6	2.4	1210	3	US-09-443-041A-29	Sequence 29, Appli
c 744	40.2	2.4	137046	4	US-09-949-016-12427	Sequence 12427, A	817	39.6	2.4	1332	2	US-09-057-762-1	Sequence 1, Appli
c 745	40.2	2.4	137048	4	US-09-949-016-13438	Sequence 13438, A	818	39.6	2.4	1332	3	US-08-326-119A-1	Sequence 1, Appli
c 746	40.2	2.4	462589	4	US-09-949-016-12900	Sequence 12900, A	819	39.6	2.4	1559	4	US-09-489-847-42	Sequence 42, Appli
c 747	40.2	2.4	476044	4	US-09-949-016-12412	Sequence 12412, A	820	39.6	2.4	1740	4	US-09-709-103-45	Sequence 45, Appli
748	39.8	2.4	786431	4	US-09-751-389-3	Sequence 3, Appli	821	39.6	2.4	1740	4	US-09-439-410A-45	Sequence 45, Appli
749	39.8	2.4	92	4	US-09-621-976-14689	Sequence 14689, A	822	39.6	2.4	2445	4	US-09-949-016-781	Sequence 781, App
750	39.8	2.4	97	4	US-09-621-976-12430	Sequence 12430, A	823	39.6	2.4	2539	4	US-10-144-198-21	Sequence 21, Appli
751	39.8	2.4	98	1	US-08-088-658-42	Sequence 42, Appli	824	39.6	2.4	2550	6	5258287-23	Patent No. 5258287
752	39.8	2.4	98	2	US-08-471-907A-42	Sequence 42, Appli	825	39.6	2.4	2550	6	5258287-23	Patent No. 5258287
753	39.8	2.4	98	4	US-09-621-976-12160	Sequence 12160, A	826	39.6	2.4	3366	4	US-09-596-141C-6	Sequence 6, Appli
754	39.8	2.4	98	4	US-09-621-976-15091	Sequence 15091, A	827	39.6	2.4	3366	4	US-09-595-526C-6	Sequence 6, Appli
755	39.8	2.4	159	4	US-09-621-976-17448	Sequence 17448, A	828	39.6	2.4	4239	4	US-09-815-048-1	Sequence 1, Appli
c 756	39.8	2.4	179	4	US-09-621-976-18054	Sequence 18054, A	829	39.6	2.4	10442	4	US-09-596-141C-1	Sequence 1, Appli
757	39.8	2.4	200	3	US-09-014-416-64	Sequence 64, Appli	830	39.6	2.4	10442	4	US-09-595-526C-1	Sequence 1, Appli

831	39.6	2.4	10474	4	US-09-596-141C-7	Sequence 7, Appli	904	39.2	2.3	3080	4	US-09-865-364-25	Sequence 25, Appli
832	39.6	2.4	10474	4	US-09-596-141C-7	Sequence 9, Appli	c 905	39.2	2.3	5852	1	US-07-867-106-2	Sequence 2, Appli
833	39.6	2.4	10474	4	US-09-595-526C-9	Sequence 7, Appli	c 906	39.2	2.3	6370	3	US-09-306-595C-2	Sequence 2, Appli
834	39.6	2.4	10474	3	US-09-595-526C-9	Sequence 9, Appli	c 907	39.2	2.3	6370	4	US-09-925-388-2	Sequence 2, Appli
835	39.6	2.4	16595	3	US-09-146-053-7	Sequence 7, Appli	c 908	39.2	2.3	16549	4	US-09-949-016-16456	Sequence 5, Appli
836	39.6	2.4	23193	4	US-09-949-016-17215	Sequence 17215, A	c 909	39.2	2.3	44453	3	US-09-146-053-5	Sequence 5, Appli
837	39.6	2.4	80246	3	US-09-078-294-3	Sequence 4, Appli	c 910	39.2	2.3	46698	4	US-09-949-016-17323	Sequence 17323, A
838	39.6	2.4	80595	3	US-09-078-294-3	Sequence 3, Appli	c 911	39.2	2.3	54382	4	US-09-949-016-12139	Sequence 12139, A
839	39.6	2.4	83369	4	US-09-949-016-12171	Sequence 12171, A	c 912	39.2	2.3	61913	4	US-09-949-016-15338	Sequence 15338, A
840	39.6	2.4	117001	4	US-09-949-016-15684	Sequence 15684, A	c 913	39.2	2.3	61922	4	US-09-949-016-11772	Sequence 11772, A
841	39.6	2.4	250958	4	US-09-949-016-16061	Sequence 16061, A	c 914	39.2	2.3	68580	4	US-09-949-016-15844	Sequence 15844, A
842	39.6	2.4	312474	4	US-09-949-016-17434	Sequence 17434, A	c 915	39.2	2.3	73519	4	US-09-949-016-16344	Sequence 16344, A
843	39.4	2.3	169	4	US-09-621-976-11249	Sequence 11249, A	c 916	39.2	2.3	105919	4	US-09-949-016-11769	Sequence 11769, A
844	39.4	2.3	196	4	US-09-270-767-23394	Sequence 23394, A	c 917	39.2	2.3	112219	4	US-09-949-016-12453	Sequence 12453, A
845	39.4	2.3	601	4	US-09-949-016-120672	Sequence 120672, A	c 918	39.2	2.3	112222	4	US-09-949-016-14324	Sequence 14324, A
846	39.4	2.3	621	4	US-09-949-016-175160	Sequence 175160, A	c 919	39.2	2.3	113186	4	US-09-949-016-17572	Sequence 17572, A
847	39.4	2.3	624	4	US-09-270-767-13424	Sequence 13424, A	c 920	39.2	2.3	113701	4	US-09-949-016-13214	Sequence 13214, A
848	39.4	2.3	647	4	US-09-495-050A-54	Sequence 54, Appli	c 921	39.2	2.3	158841	4	US-09-949-016-16192	Sequence 16192, A
849	39.4	2.3	1509	3	US-09-149-476-179	Sequence 179, App	c 922	39.2	2.3	187595	4	US-09-949-016-15546	Sequence 15546, A
850	39.4	2.3	12703	4	US-09-949-016-16685	Sequence 16685, A	c 923	39.2	2.3	260286	4	US-09-949-016-17037	Sequence 17037, A
851	39.4	2.3	19601	4	US-09-949-016-15629	Sequence 15629, A	c 924	39.2	2.3	260293	4	US-09-949-016-12106	Sequence 12106, A
852	39.4	2.3	24645	4	US-09-949-016-14062	Sequence 14062, A	c 925	39.2	2.3	392000	4	US-10-027-983-11	Sequence 11, Appli
853	39.4	2.3	25659	4	US-09-949-016-15052	Sequence 15052, A	c 926	39	2.3	127	3	US-09-014-416-59	Sequence 59, Appli
854	39.4	2.3	29927	4	US-09-949-016-11814	Sequence 11814, A	c 927	39	2.3	176	3	US-09-014-416-60	Sequence 60, Appli
855	39.4	2.3	29927	4	US-09-949-016-17474	Sequence 17474, A	c 928	39	2.3	183	3	US-09-014-416-60	Sequence 60, Appli
856	39.4	2.3	29927	4	US-09-949-016-17475	Sequence 17475, A	c 929	39	2.3	185	4	US-09-621-976-16779	Sequence 16779, A
857	39.4	2.3	3111	4	US-09-949-016-15628	Sequence 15628, A	c 930	39	2.3	204	4	US-09-621-976-1323	Sequence 1323, Ap
858	39.4	2.3	34372	4	US-09-949-016-13098	Sequence 13098, A	c 931	39	2.3	266	4	US-09-621-976-16813	Sequence 16813, A
859	39.4	2.3	34875	4	US-09-949-016-13099	Sequence 13099, A	c 932	39	2.3	299	4	US-09-621-976-16226	Sequence 16226, A
860	39.4	2.3	37802	4	US-09-949-016-12639	Sequence 12639, A	c 933	39	2.3	321	2	US-08-520-678A-23	Sequence 23, Appli
861	39.4	2.3	44393	4	US-09-949-016-14944	Sequence 14944, A	c 934	39	2.3	321	3	US-08-897-126-23	Sequence 23, Appli
862	39.4	2.3	44393	4	US-09-949-016-14945	Sequence 14945, A	c 935	39	2.3	348	2	US-09-621-976-16031	Sequence 16031, A
863	39.4	2.3	44393	4	US-09-949-016-14946	Sequence 14946, A	c 936	39	2.3	536	1	US-08-623-906A-14	Sequence 14, Appli
864	39.4	2.3	44393	4	US-09-949-016-16911	Sequence 16911, A	c 937	39	2.3	536	2	US-08-341-568-1	Sequence 1, Appli
865	39.4	2.3	55841	4	US-09-949-016-16602	Sequence 16602, A	c 938	39	2.3	599	3	US-08-911-020-1	Sequence 1, Appli
866	39.4	2.3	67888	4	US-09-949-016-13670	Sequence 37, Appli	c 939	39	2.3	601	4	US-09-328-111-147	Sequence 147, App
867	39.4	2.3	83851	4	US-09-949-016-13847	Sequence 13847, A	c 940	39	2.3	601	4	US-09-949-016-19754	Sequence 19754, A
868	39.4	2.3	86936	4	US-09-949-016-17314	Sequence 17314, A	c 941	39	2.3	601	4	US-09-949-016-43955	Sequence 43955, A
869	39.4	2.3	94877	4	US-09-949-016-16114	Sequence 16114, A	c 942	39	2.3	601	4	US-09-949-016-71483	Sequence 71483, A
870	39.4	2.3	116452	4	US-09-818-512-3	Sequence 11809, A	c 943	39	2.3	601	4	US-09-949-016-80449	Sequence 80449, A
871	39.4	2.3	137949	4	US-09-818-512-3	Sequence 3, Appli	c 944	39	2.3	601	4	US-09-949-016-80451	Sequence 80451, A
872	39.4	2.3	137949	4	US-09-949-016-12196	Sequence 12196, A	c 945	39	2.3	601	4	US-09-949-016-81973	Sequence 81973, A
873	39.4	2.3	137949	4	US-09-949-016-12196	Sequence 12196, A	c 946	39	2.3	601	4	US-09-949-016-152093	Sequence 152093, A
874	39.4	2.3	236341	4	US-09-949-016-13760	Sequence 13760, A	c 947	39	2.3	601	4	US-09-949-016-152166	Sequence 152166, A
875	39.4	2.3	253345	4	US-09-949-016-12656	Sequence 13978, A	c 948	39	2.3	601	4	US-09-949-016-152239	Sequence 152239, A
876	39.4	2.3	253364	4	US-09-949-016-13639	Sequence 13639, A	c 949	39	2.3	601	4	US-09-949-016-152312	Sequence 152312, A
877	39.2	2.3	85	4	US-09-621-976-13395	Sequence 13395, A	c 950	39	2.3	601	4	US-09-949-016-159398	Sequence 159398, A
878	39.2	2.3	85	4	US-09-621-976-14949	Sequence 14949, A	c 951	39	2.3	601	4	US-09-949-016-159471	Sequence 159471, A
879	39.2	2.3	89	4	US-09-621-976-14974	Sequence 14974, A	c 952	39	2.3	601	4	US-09-949-016-159544	Sequence 159544, A
880	39.2	2.3	89	4	US-09-621-976-14974	Sequence 14974, A	c 953	39	2.3	601	4	US-09-949-016-159617	Sequence 159617, A
881	39.2	2.3	91	4	US-09-621-976-12161	Sequence 12161, A	c 954	39	2.3	601	4	US-09-949-016-160807	Sequence 160807, A
882	39.2	2.3	208	1	US-08-686-878A-37	Sequence 37, Appli	c 955	39	2.3	601	4	US-09-949-016-161983	Sequence 161983, A
883	39.2	2.3	208	3	US-09-175-928-37	Sequence 37, Appli	c 956	39	2.3	1069	3	US-09-372-422A-7	Sequence 7, Appli
884	39.2	2.3	271	4	US-09-621-976-10380	Sequence 10380, A	c 957	39	2.3	1133	4	US-09-916-204-1	Sequence 1, Appli
885	39.2	2.3	505	4	US-09-621-976-15639	Sequence 15639, A	c 958	39	2.3	1133	4	US-10-282-048-1	Sequence 1, Appli
886	39.2	2.3	601	4	US-09-949-016-126414	Sequence 126414, A	c 959	39	2.3	1249	4	US-09-461-325-128	Sequence 128, App
887	39.2	2.3	601	4	US-09-949-016-126417	Sequence 126417, A	c 960	39	2.3	1249	4	US-10-012-542-128	Sequence 128, App
888	39.2	2.3	601	4	US-09-949-016-145250	Sequence 145250, A	c 961	39	2.3	1249	4	US-10-115-123-128	Sequence 128, App
889	39.2	2.3	601	4	US-09-949-016-145251	Sequence 145251, A	c 962	39	2.3	1260	4	US-09-461-325-93	Sequence 93, Appli
890	39.2	2.3	601	4	US-09-949-016-145251	Sequence 145251, A	c 963	39	2.3	1260	4	US-10-012-542-93	Sequence 93, Appli
891	39.2	2.3	756	4	US-09-614-912-93	Sequence 93, Appli	c 964	39	2.3	1260	4	US-10-115-123-93	Sequence 93, Appli
892	39.2	2.3	803	3	US-09-270-767-28941	Sequence 28941, A	c 965	39	2.3	1785	4	US-09-248-796A-928	Sequence 928, App
893	39.2	2.3	960	3	US-09-248-335-57	Sequence 57, Appli	c 966	39	2.3	1798	2	US-08-557-128-12	Sequence 12, Appli
894	39.2	2.3	1476	4	US-09-248-796A-5437	Sequence 5437, Ap	c 967	39	2.3	2378	3	US-08-802-805D-20	Sequence 20, Appli
895	39.2	2.3	1700	2	US-08-897-340-4	Sequence 4, Appli	c 968	39	2.3	2378	4	US-08-860-370-1	Sequence 1, Appli
896	39.2	2.3	1700	3	US-09-252-329-4	Sequence 4, Appli	c 969	39	2.3	2485	4	US-09-889-463A-9	Sequence 9, Appli
897	39.2	2.3	2045	3	US-09-150-060-22	Sequence 22, Appli	c 970	39	2.3	2744	3	US-09-071-101-1	Sequence 1, Appli
898	39.2	2.3	2291	4	US-09-220-132-114	Sequence 114, App	c 971	39	2.3	2744	3	US-09-369-618-1	Sequence 1, Appli
899	39.2	2.3	2291	4	US-09-814-915A-95	Sequence 95, Appli	c 972	39	2.3	2744	3	US-09-369-617-1	Sequence 1, Appli
900	39.2	2.3	3080	3	US-09-099-041A-25	Sequence 25, Appli	c 973	39	2.3	3450	4	US-09-902-540-9001	Sequence 9001, Ap
901	39.2	2.3	3080	3	US-09-245-281-25	Sequence 25, Appli	c 974	39	2.3	3527	2	US-08-909-965C-7	Sequence 7, Appli
902	39.2	2.3	3080	3	US-09-207-359B-25	Sequence 25, Appli	c 975	39	2.3	4137	3	US-09-499-964-2	Sequence 2, Appli
903	39.2	2.3	3080	4	US-09-340-620A-25	Sequence 25, Appli	c 976	39	2.3	7305	4	US-09-902-540-961	Sequence 961, App

c 977	39	2.3	7989	4	US-09-539-601-10	Sequence 10, Appl	1050	38.8	2.3	225	4	US-09-248-796A-10883	Sequence 10883, A
c 978	39	2.3	8001	4	US-09-539-601-7	Sequence 7, Appl	1051	38.8	2.3	259	4	US-09-621-976-16294	Sequence 16294, A
c 979	39	2.3	8001	4	US-09-539-601-16	Sequence 16, Appl	1052	38.8	2.3	371	4	US-09-621-976-19223	Sequence 19223, A
c 980	39	2.3	8001	4	US-09-539-601-22	Sequence 22, Appl	c1053	38.8	2.3	599	4	US-09-270-767-13708	Sequence 13708, A
c 981	39	2.3	8001	4	US-09-539-601-28	Sequence 28, Appl	1054	38.8	2.3	601	4	US-09-949-016-67114	Sequence 67114, A
c 982	39	2.3	8637	4	US-09-539-601-4	Sequence 4, Appl	1055	38.8	2.3	601	4	US-09-949-016-67115	Sequence 67115, A
c 983	39	2.3	8638	4	US-10-029-907-7	Sequence 7, Appl	1056	38.8	2.3	601	4	US-09-949-016-76961	Sequence 76961, A
c 984	39	2.3	8638	4	US-10-029-907-24	Sequence 24, Appl	1057	38.8	2.3	601	4	US-09-949-016-76962	Sequence 76962, A
c 985	39	2.3	8638	4	US-10-029-907-25	Sequence 25, Appl	1058	38.8	2.3	601	4	US-09-949-016-76963	Sequence 76963, A
c 986	39	2.3	8639	4	US-10-029-907-1	Sequence 1, Appl	1059	38.8	2.3	601	4	US-09-949-016-76964	Sequence 76964, A
c 987	39	2.3	8649	4	US-09-539-601-13	Sequence 13, Appl	1060	38.8	2.3	601	4	US-09-949-016-109665	Sequence 109665, A
c 988	39	2.3	8905	4	US-09-949-016-11761	Sequence 1761, A	1061	38.8	2.3	601	4	US-09-949-016-113694	Sequence 113694, A
c 989	39	2.3	8907	4	US-09-949-016-16261	Sequence 16261, A	1062	38.8	2.3	601	4	US-09-949-016-113695	Sequence 113695, A
c 990	39	2.3	9595	3	US-09-014-416-4	Sequence 4, Appl	c1063	38.8	2.3	601	4	US-09-949-016-126415	Sequence 126415, A
c 991	39	2.3	9599	3	US-09-014-416-2	Sequence 2, Appl	c1064	38.8	2.3	601	4	US-09-949-016-127893	Sequence 127893, A
c 992	39	2.3	9599	3	US-09-014-416-6	Sequence 6, Appl	c1065	38.8	2.3	601	4	US-09-949-016-128230	Sequence 128230, A
c 993	39	2.3	9740	4	US-09-949-016-15833	Sequence 15833, A	c1066	38.8	2.3	601	4	US-09-949-016-145252	Sequence 145252, A
c 994	39	2.3	11076	4	US-09-539-601-1	Sequence 1, Appl	1067	38.8	2.3	601	4	US-09-949-016-201489	Sequence 201489, A
c 995	39	2.3	11076	4	US-09-539-601-19	Sequence 19, Appl	1068	38.8	2.3	1492	4	US-09-369-247-23	Sequence 23, Appl
c 996	39	2.3	11076	4	US-09-539-601-25	Sequence 25, Appl	1069	38.8	2.3	1843	4	US-09-328-925-49	Sequence 49, Appl
c 997	39	2.3	11076	4	US-09-539-601-31	Sequence 31, Appl	1070	38.8	2.3	1843	4	US-09-949-016-50	Sequence 50, Appl
c 998	39	2.3	11517	1	US-07-920-281C-1	Sequence 1, Appl	1071	38.8	2.3	1844	4	US-10-003-392-7	Sequence 7, Appl
c 999	39	2.3	11517	3	US-08-466-277-1	Sequence 1, Appl	1072	38.8	2.3	4773	4	US-09-270-767-14129	Sequence 14129, A
c1000	39	2.3	11517	4	US-09-688-842-1	Sequence 1, Appl	1073	38.8	2.3	5009	1	US-08-487-890A-3	Sequence 3, Appl
c1001	39	2.3	11641	4	US-09-949-016-11906	Sequence 11906, A	1074	38.8	2.3	5009	2	US-08-478-435-3	Sequence 3, Appl
c1002	39	2.3	11643	4	US-09-949-016-14931	Sequence 14931, A	1075	38.8	2.3	5009	2	US-08-337-483-3	Sequence 3, Appl
c1003	39	2.3	17879	4	US-09-949-016-12992	Sequence 12992, A	1076	38.8	2.3	5009	2	US-08-478-373-3	Sequence 3, Appl
c1004	39	2.3	23319	4	US-09-949-016-14407	Sequence 14407, A	1077	38.8	2.3	5009	3	US-08-474-671-3	Sequence 3, Appl
c1005	39	2.3	28431	4	US-09-949-016-12334	Sequence 12334, A	1078	38.8	2.3	5009	3	US-08-483-577A-3	Sequence 3, Appl
c1006	39	2.3	37215	4	US-09-949-016-15526	Sequence 15526, A	1079	38.8	2.3	5009	3	US-08-897-438-3	Sequence 3, Appl
c1007	39	2.3	45427	4	US-09-949-016-16243	Sequence 16243, A	1080	38.8	2.3	5009	3	US-08-637-654-3	Sequence 3, Appl
c1008	39	2.3	45467	3	US-09-146-053-6	Sequence 6, Appl	1081	38.8	2.3	5009	3	US-08-649-518-3	Sequence 3, Appl
c1009	39	2.3	50383	4	US-09-949-016-17600	Sequence 17600, A	1082	38.8	2.3	5033	1	US-08-487-890A-2	Sequence 2, Appl
c1010	39	2.3	51698	4	US-09-949-016-12671	Sequence 12671, A	1083	38.8	2.3	5033	2	US-08-478-435-2	Sequence 2, Appl
c1011	39	2.3	78846	4	US-09-949-016-12396	Sequence 12396, A	1084	38.8	2.3	5033	2	US-08-337-483-2	Sequence 2, Appl
c1012	39	2.3	78846	4	US-09-949-016-12791	Sequence 12791, A	1085	38.8	2.3	5033	2	US-08-478-373-2	Sequence 2, Appl
c1013	39	2.3	78846	4	US-09-949-016-12792	Sequence 12792, A	1086	38.8	2.3	5033	3	US-08-474-671-2	Sequence 2, Appl
c1014	39	2.3	78846	4	US-09-949-016-12793	Sequence 12793, A	1087	38.8	2.3	5033	3	US-08-483-577A-2	Sequence 2, Appl
c1015	39	2.3	78850	4	US-09-949-016-16013	Sequence 16013, A	1088	38.8	2.3	5033	3	US-08-897-438-2	Sequence 2, Appl
c1016	39	2.3	78850	4	US-09-949-016-16014	Sequence 16014, A	1089	38.8	2.3	5033	3	US-08-637-654-2	Sequence 2, Appl
c1017	39	2.3	78850	4	US-09-949-016-16015	Sequence 16015, A	1090	38.8	2.3	5033	3	US-08-649-518-2	Sequence 2, Appl
c1018	39	2.3	78850	4	US-09-949-016-16016	Sequence 16016, A	1091	38.8	2.3	20445	4	US-09-949-016-14875	Sequence 14875, A
c1019	39	2.3	78850	4	US-09-949-016-16201	Sequence 16201, A	c1092	38.8	2.3	20852	4	US-09-949-016-14974	Sequence 14974, A
c1020	39	2.3	78850	4	US-09-949-016-16202	Sequence 16202, A	1093	38.8	2.3	13469	4	US-09-949-016-13722	Sequence 13722, A
c1021	39	2.3	78850	4	US-09-949-016-16203	Sequence 16203, A	c1094	38.8	2.3	41454	4	US-09-949-016-17107	Sequence 17107, A
c1022	39	2.3	78850	4	US-09-949-016-16204	Sequence 16204, A	1095	38.8	2.3	45469	4	US-09-949-016-13398	Sequence 13398, A
c1023	39	2.3	118382	4	US-09-949-016-15996	Sequence 15996, A	c1096	38.8	2.3	55195	4	US-09-949-016-15854	Sequence 15854, A
c1024	39	2.3	118382	4	US-09-949-016-15997	Sequence 15997, A	c1097	38.8	2.3	65990	4	US-09-949-016-11830	Sequence 11830, A
c1025	39	2.3	134140	4	US-09-949-016-12672	Sequence 12672, A	1098	38.8	2.3	74177	4	US-09-949-016-11988	Sequence 11988, A
c1026	39	2.3	134241	4	US-09-949-016-12424	Sequence 12424, A	1099	38.8	2.3	74177	4	US-09-949-016-17388	Sequence 17388, A
c1027	39	2.3	134242	4	US-09-949-016-15813	Sequence 15813, A	c1100	38.8	2.3	118067	4	US-09-497-855A-32	Sequence 32, Appl
c1028	39	2.3	134242	4	US-09-949-016-15814	Sequence 15814, A	c1101	38.8	2.3	133559	4	US-09-949-016-15845	Sequence 15845, A
c1029	39	2.3	134242	4	US-09-949-016-15815	Sequence 15815, A	1102	38.6	2.3	83	4	US-09-621-976-12087	Sequence 12087, A
c1030	39	2.3	177797	4	US-09-949-016-14125	Sequence 14125, A	1103	38.6	2.3	83	4	US-09-621-976-12175	Sequence 12175, A
c1031	39	2.3	186595	4	US-09-949-016-13125	Sequence 13125, A	1104	38.6	2.3	83	4	US-09-621-976-12429	Sequence 12429, A
c1032	39	2.3	192506	4	US-09-949-016-15830	Sequence 15830, A	1105	38.6	2.3	83	4	US-09-621-976-12450	Sequence 12450, A
c1033	39	2.3	227979	4	US-09-949-016-11842	Sequence 11842, A	1106	38.6	2.3	84	1	US-08-664-596B-3	Sequence 3, Appl
c1034	39	2.3	235064	4	US-09-949-016-15390	Sequence 15390, A	1107	38.6	2.3	84	1	US-08-738-367-3	Sequence 3, Appl
c1035	39	2.3	238815	4	US-09-949-016-16274	Sequence 16274, A	1108	38.6	2.3	91	4	US-09-621-976-14925	Sequence 14925, A
c1036	39	2.3	258775	4	US-09-949-016-16435	Sequence 16435, A	1109	38.6	2.3	102	4	US-09-621-976-11436	Sequence 11436, A
c1037	39	2.3	421491	4	US-09-949-016-12805	Sequence 12805, A	1110	38.6	2.3	299	4	US-09-621-976-10211	Sequence 10211, A
c1038	39	2.3	421494	4	US-09-949-016-14060	Sequence 14060, A	1111	38.6	2.3	300	4	US-09-621-976-16227	Sequence 16227, A
c1039	38.8	2.3	84	4	US-09-621-976-14577	Sequence 14577, A	1112	38.6	2.3	327	4	US-09-621-976-16018	Sequence 16018, A
c1040	38.8	2.3	91	3	US-09-404-879A-201	Sequence 201, App	1113	38.6	2.3	344	2	US-08-623-906A-8	Sequence 8, Appl
c1041	38.8	2.3	91	4	US-09-338-933-201	Sequence 201, App	1114	38.6	2.3	443	3	US-09-936-885A-1	Sequence 1, Appl
c1042	38.8	2.3	91	4	US-09-215-681-201	Sequence 201, App	c1115	38.6	2.3	500	4	US-09-270-767-3118	Sequence 3118, Ap
c1043	38.8	2.3	91	4	US-09-216-003A-201	Sequence 201, App	c1116	38.6	2.3	500	4	US-09-270-767-18400	Sequence 18400, A
c1044	38.8	2.3	91	4	US-09-667-857-201	Sequence 201, App	1117	38.6	2.3	601	4	US-09-949-016-59330	Sequence 59330, A
c1045	38.8	2.3	101	3	US-09-404-879A-293	Sequence 293, App	1118	38.6	2.3	601	4	US-09-949-016-126899	Sequence 126899, A
c1046	38.8	2.3	101	4	US-09-338-933-293	Sequence 293, App	1119	38.6	2.3	601	4	US-09-949-016-180024	Sequence 180024, A
c1047	38.8	2.3	101	4	US-09-215-681-293	Sequence 293, App	1120	38.6	2.3	700	3	US-09-152-060-26	Sequence 26, Appl
c1048	38.8	2.3	101	4	US-09-216-003A-293	Sequence 293, App	c1121	38.6	2.3	986	4	US-09-328-475C-141	Sequence 141, Appl
c1049	38.8	2.3	101	4	US-09-667-857-293	Sequence 293, App	1122	38.6	2.3	1027	3	US-09-465-558-57	Sequence 57, Appl

1123	38.6	2.3	1279	3	US-09-248-335-25	Sequence 25, Appl	1196	38.4	2.3	7119	4	US-09-949-016-15358	Sequence 15358, A
c1124	38.6	2.3	1447	4	US-09-976-594-338	Sequence 338, App	c1197	38.4	2.3	78630	4	US-09-949-016-16790	Sequence 16790, A
1125	38.6	2.3	2031	4	US-09-417-251A-9	Sequence 9, Appl	c1198	38.4	2.3	129415	4	US-09-949-016-16937	Sequence 16937, A
c1126	38.6	2.3	5021	4	US-09-949-016-786	Sequence 786, App	c1199	38.4	2.3	137394	4	US-09-949-016-13872	Sequence 13872, A
c1127	38.6	2.3	23569	4	US-09-949-016-12153	Sequence 12153, A	c1200	38.4	2.3	137743	4	US-09-949-016-12178	Sequence 12178, A
c1128	38.6	2.3	23574	4	US-09-949-016-15351	Sequence 15351, A	c1201	38.4	2.3	150780	4	US-09-949-016-14711	Sequence 14711, A
1129	38.6	2.3	2843	4	US-09-949-016-17208	Sequence 17208, A	c1202	38.4	2.3	176373	3	US-09-128-155-17	Sequence 17, Appl
c1130	38.6	2.3	3292	4	US-09-949-016-15382	Sequence 15382, A	c1203	38.4	2.3	181429	4	US-09-949-016-12372	Sequence 12372, A
1131	38.6	2.3	43255	4	US-09-949-016-11909	Sequence 11909, A	c1204	38.4	2.3	211049	4	US-09-949-016-15772	Sequence 15772, A
1132	38.6	2.3	43507	4	US-09-949-016-13297	Sequence 13297, A	c1205	38.4	2.3	211769	4	US-09-949-016-13185	Sequence 13185, A
1133	38.6	2.3	46841	4	US-09-949-016-13466	Sequence 13466, A	c1206	38.4	2.3	251769	4	US-09-949-016-13185	Sequence 13185, A
c1134	38.6	2.3	51259	4	US-08-781-891-209	Sequence 209, App	c1207	38.4	2.3	251769	4	US-09-949-016-13185	Sequence 13185, A
c1135	38.6	2.3	51259	4	US-09-618-166-209	Sequence 209, App	c1208	38.4	2.3	256748	4	US-09-949-016-13187	Sequence 13187, A
c1136	38.6	2.3	56326	4	US-09-949-016-16468	Sequence 16468, A	c1209	38.4	2.3	266748	4	US-09-949-016-13188	Sequence 13188, A
c1137	38.6	2.3	95648	4	US-09-949-016-13139	Sequence 13139, A	c1210	38.4	2.3	784019	4	US-09-949-016-14033	Sequence 14033, A
1138	38.6	2.3	152331	3	US-09-128-155-16	Sequence 16, Appl	c1211	38.4	2.3	828152	4	US-09-949-016-12777	Sequence 12777, A
c1139	38.6	2.3	173992	4	US-09-949-016-13379	Sequence 13379, A	c1212	38.2	2.3	83	4	US-09-621-976-12799	Sequence 12799, A
1140	38.4	2.3	80	1	US-07-920-281C-25	Sequence 25, Appl	c1213	38.2	2.3	83	4	US-09-621-976-12799	Sequence 12799, A
1141	38.4	2.3	80	3	US-08-466-277-25	Sequence 25, Appl	c1214	38.2	2.3	83	4	US-09-621-976-12799	Sequence 12799, A
1142	38.4	2.3	80	4	US-09-688-842-25	Sequence 25, Appl	c1215	38.2	2.3	138	4	US-09-621-976-12799	Sequence 12799, A
1143	38.4	2.3	106	4	US-09-621-976-12079	Sequence 12079, A	c1216	38.2	2.3	232	4	US-09-621-976-12799	Sequence 12799, A
c1144	38.4	2.3	141	3	US-08-737-078A-1	Sequence 1, Appl	c1217	38.2	2.3	253	4	US-09-621-976-12799	Sequence 12799, A
c1145	38.4	2.3	141	5	PCT-US94-04706-1	Sequence 1, Appl	c1218	38.2	2.3	271	2	US-08-731-272A-29	Sequence 29, Appl
1146	38.4	2.3	234	4	US-09-621-976-16557	Sequence 16557, A	c1219	38.2	2.3	333	4	US-09-248-796A-11241	Sequence 11241, A
1147	38.4	2.3	250	4	US-09-621-976-18363	Sequence 18363, A	c1220	38.2	2.3	388	2	US-08-623-906A-13	Sequence 13, Appl
1148	38.4	2.3	366	4	US-09-252-991A-620	Sequence 620, App	c1221	38.2	2.3	601	4	US-09-949-016-32559	Sequence 32559, A
1149	38.4	2.3	366	4	US-09-134-000C-11	Sequence 11, Appl	c1222	38.2	2.3	601	4	US-09-949-016-32561	Sequence 32561, A
1150	38.4	2.3	591	1	US-09-134-000C-11	Sequence 11, Appl	c1223	38.2	2.3	601	4	US-09-949-016-66245	Sequence 66245, A
1151	38.4	2.3	601	4	US-09-949-016-48846	Sequence 48846, A	c1224	38.2	2.3	601	4	US-09-949-016-80104	Sequence 80104, A
1152	38.4	2.3	601	4	US-09-949-016-49018	Sequence 49018, A	c1225	38.2	2.3	601	4	US-09-949-016-94321	Sequence 94321, A
1153	38.4	2.3	601	4	US-09-949-016-49190	Sequence 49190, A	c1226	38.2	2.3	601	4	US-09-949-016-126059	Sequence 126059, A
c1154	38.4	2.3	601	4	US-09-949-016-49366	Sequence 49366, A	c1227	38.2	2.3	601	4	US-09-949-016-132201	Sequence 132201, A
c1155	38.4	2.3	601	4	US-09-949-016-127053	Sequence 127053, A	c1228	38.2	2.3	601	4	US-09-949-016-133406	Sequence 133406, A
c1156	38.4	2.3	601	4	US-09-949-016-127054	Sequence 127054, A	c1229	38.2	2.3	601	4	US-09-949-016-140018	Sequence 140018, A
c1157	38.4	2.3	601	4	US-09-949-016-127055	Sequence 127055, A	c1230	38.2	2.3	601	4	US-09-949-016-155055	Sequence 155055, A
c1158	38.4	2.3	601	4	US-09-949-016-127056	Sequence 127056, A	c1231	38.2	2.3	601	4	US-09-949-016-155362	Sequence 155362, A
c1159	38.4	2.3	601	4	US-09-949-016-127058	Sequence 127058, A	c1232	38.2	2.3	601	4	US-09-949-016-155364	Sequence 155364, A
c1160	38.4	2.3	601	4	US-09-949-016-127059	Sequence 127059, A	c1233	38.2	2.3	601	4	US-09-949-016-173108	Sequence 173108, A
c1161	38.4	2.3	601	4	US-09-949-016-127060	Sequence 127060, A	c1234	38.2	2.3	601	4	US-09-949-016-173109	Sequence 173109, A
c1162	38.4	2.3	601	4	US-09-949-016-127061	Sequence 127061, A	c1235	38.2	2.3	601	4	US-09-949-016-179952	Sequence 179952, A
1163	38.4	2.3	601	4	US-09-949-016-161233	Sequence 161233, A	c1236	38.2	2.3	832	4	US-09-621-976-2813	Sequence 2813, App
1164	38.4	2.3	601	4	US-09-949-016-205887	Sequence 205887, A	c1237	38.2	2.3	1074	3	US-09-248-335-67	Sequence 67, Appl
c1165	38.4	2.3	730	4	US-09-270-767-14600	Sequence 14600, A	c1238	38.2	2.3	1100	3	US-07-861-458C-4	Sequence 4, Appl
c1166	38.4	2.3	912	4	US-09-252-991A-774	Sequence 774, App	c1239	38.2	2.3	1325	1	US-08-306-691B-51	Sequence 51, Appl
1167	38.4	2.3	948	4	US-09-252-991A-643	Sequence 643, App	c1240	38.2	2.3	1325	2	US-08-464-517-1	Sequence 1, Appl
c1168	38.4	2.3	997	4	US-09-907-794A-376	Sequence 376, App	c1241	38.2	2.3	1325	2	US-08-246-361A-1	Sequence 1, Appl
c1169	38.4	2.3	997	4	US-09-905-125A-376	Sequence 376, App	c1242	38.2	2.3	1325	3	US-08-463-772-1	Sequence 1, Appl
1170	38.4	2.3	997	4	US-09-902-775A-376	Sequence 376, App	c1243	38.2	2.3	1325	5	PCT-US93-05000-1	Sequence 1, Appl
1171	38.4	2.3	997	4	US-09-906-700-376	Sequence 376, App	c1244	38.2	2.3	1663	4	US-09-464-535-43	Sequence 43, Appl
1172	38.4	2.3	997	4	US-09-903-603A-376	Sequence 376, App	c1245	38.2	2.3	1872	3	US-09-291-922-27	Sequence 27, Appl
1173	38.4	2.3	997	4	US-09-904-920A-376	Sequence 376, App	c1246	38.2	2.3	2445	6	5215909-9	Patent No. 5215909
1174	38.4	2.3	997	4	US-09-905-064-376	Sequence 376, App	c1247	38.2	2.3	2460	6	5215909-9	Patent No. 5215909
1175	38.4	2.3	997	4	US-09-905-381A-376	Sequence 376, App	c1248	38.2	2.3	2460	6	5215909-9	Patent No. 5215909
1176	38.4	2.3	997	4	US-09-906-618-376	Sequence 376, App	c1249	38.2	2.3	9157	4	US-09-949-016-16185	Sequence 16185, A
1177	38.4	2.3	1518	4	US-09-614-912-191	Sequence 191, App	c1250	38.2	2.3	9558	4	US-09-949-016-13026	Sequence 13026, A
1178	38.4	2.3	1810	4	US-09-800-729-77	Sequence 73, Appl	c1251	38.2	2.3	10451	4	US-09-949-016-12192	Sequence 12192, A
c1179	38.4	2.3	1811	4	US-09-800-729-77	Sequence 77, Appl	c1252	38.2	2.3	12047	3	US-09-022-461-1	Sequence 1, Appl
1180	38.4	2.3	1972	4	US-09-403-861A-1	Sequence 1, Appl	c1253	38.2	2.3	12047	3	US-09-033-556-3	Sequence 3, Appl
1181	38.4	2.3	3243	4	US-09-949-016-12186	Sequence 12186, A	c1254	38.2	2.3	12047	4	US-09-474-699-11	Sequence 11, Appl
1182	38.4	2.3	4890	4	US-09-677-046A-3	Sequence 3, Appl	c1255	38.2	2.3	12047	4	US-09-151-376-3	Sequence 3, Appl
1183	38.4	2.3	4943	4	US-09-677-046A-7	Sequence 7, Appl	c1256	38.2	2.3	12047	4	US-09-814-351-11	Sequence 11, Appl
1184	38.4	2.3	5170	4	US-09-677-046A-5	Sequence 5, Appl	c1257	38.2	2.3	15575	4	US-09-949-016-16568	Sequence 16568, A
1185	38.4	2.3	6124	3	US-08-213-419B-3	Sequence 3, Appl	c1258	38.2	2.3	15575	4	US-09-949-016-16568	Sequence 16568, A
c1186	38.4	2.3	8642	4	US-10-029-907-2	Sequence 2, Appl	c1259	38.2	2.3	20229	4	US-09-949-016-16649	Sequence 16649, A
c1187	38.4	2.3	17656	3	US-09-433-579-3	Sequence 3, Appl	c1260	38.2	2.3	20805	4	US-09-949-016-13772	Sequence 13772, A
c1188	38.4	2.3	36171	4	US-09-943-016-13876	Sequence 13876, A	c1261	38.2	2.3	23907	4	US-09-949-016-15329	Sequence 15329, A
c1189	38.4	2.3	36274	4	US-09-949-016-12369	Sequence 12369, A	c1262	38.2	2.3	32327	4	US-09-949-016-14108	Sequence 14108, A
c1190	38.4	2.3	38009	4	US-09-949-016-13617	Sequence 13617, A	c1263	38.2	2.3	33099	4	US-09-949-016-16094	Sequence 16094, A
1191	38.4	2.3	41708	3	US-09-470-512A-3	Sequence 3, Appl	c1264	38.2	2.3	38983	4	US-09-949-016-15700	Sequence 15700, A
1192	38.4	2.3	41708	3	US-09-676-519-18	Sequence 18, Appl	c1265	38.2	2.3	41639	4	US-09-949-016-15471	Sequence 15471, A
1193	38.4	2.3	41798	4	US-09-949-016-16058	Sequence 16058, A	c1266	38.2	2.3	53336	4	US-09-949-016-12500	Sequence 12500, A
c1194	38.4	2.3	42348	4	US-09-949-016-17157	Sequence 17157, A	c1267	38.2	2.3	53337	4	US-09-949-016-16092	Sequence 16092, A
1195	38.4	2.3	67479	4	US-09-949-016-11804	Sequence 11804, A	c1268	38.2	2.3	58397	4	US-09-949-016-14469	Sequence 14469, A

c1269	38.2	2.3	59076	4	US-09-949-016-15097	Sequence 15097, A	c1342	38	2.3	84587	4	US-09-949-016-15733	Sequence 15733, A
c1270	38.2	2.3	62072	4	US-09-949-016-15076	Sequence 16076, A	c1343	38	2.3	117838	4	US-09-949-016-17595	Sequence 17595, A
c1271	38.2	2.3	82000	4	US-09-949-016-15595	Sequence 15595, A	c1344	38	2.3	124110	4	US-09-949-016-13353	Sequence 13353, A
c1272	38.2	2.3	89689	4	US-09-949-016-13089	Sequence 13089, A	c1345	38	2.3	145812	4	US-09-949-016-15698	Sequence 15698, A
c1273	38.2	2.3	101356	4	US-09-949-016-12364	Sequence 12364, A	c1346	38	2.3	152070	4	US-09-949-016-15402	Sequence 15402, A
c1274	38.2	2.3	101357	4	US-09-949-016-16924	Sequence 16924, A	c1347	38	2.3	152486	4	US-09-949-016-12869	Sequence 12869, A
c1275	38.2	2.3	106746	4	US-09-326-402C-1	Sequence 1, Appl	c1348	38	2.3	192700	4	US-09-949-016-11820	Sequence 11820, A
c1276	38.2	2.3	106746	4	US-09-326-402C-12	Sequence 12, Appl	c1349	38	2.3	192704	4	US-09-949-016-17182	Sequence 17182, A
c1277	38.2	2.3	107980	4	US-09-949-016-14370	Sequence 14370, A	c1350	38	2.3	205044	4	US-09-949-016-15851	Sequence 15851, A
c1278	38.2	2.3	113876	4	US-09-949-016-14828	Sequence 14828, A	c1351	38	2.3	205044	4	US-09-949-016-15852	Sequence 15852, A
c1279	38.2	2.3	113876	4	US-09-949-016-14828	Sequence 14828, A	c1352	38	2.3	205044	4	US-09-949-016-15853	Sequence 15853, A
c1280	38.2	2.3	115508	4	US-09-949-016-11800	Sequence 11800, A	c1353	38	2.3	223471	4	US-09-949-016-12387	Sequence 12387, A
c1281	38.2	2.3	115508	4	US-09-949-016-14826	Sequence 14826, A	c1354	38	2.3	223471	4	US-09-949-016-12724	Sequence 12724, A
c1282	38.2	2.3	115508	4	US-09-949-016-14827	Sequence 14827, A	c1355	38	2.3	223471	4	US-09-949-016-12725	Sequence 12725, A
c1283	38.2	2.3	142508	4	US-09-949-016-13693	Sequence 13693, A	c1356	38	2.3	300598	4	US-09-949-016-11868	Sequence 11868, A
c1284	38.2	2.3	142506	4	US-09-949-016-12474	Sequence 12474, A	c1357	38	2.3	302604	4	US-09-949-016-14588	Sequence 14588, A
c1285	38.2	2.3	149971	4	US-09-949-016-13590	Sequence 13590, A	c1358	38	2.3	302604	4	US-09-949-016-14589	Sequence 14589, A
c1286	38.2	2.3	157822	4	US-09-949-016-16723	Sequence 16723, A	c1359	38	2.3	308362	4	US-09-949-016-17119	Sequence 17119, A
c1287	38.2	2.3	161124	4	US-09-949-016-11760	Sequence 11760, A	c1360	38	2.3	389504	4	US-09-949-016-11774	Sequence 11774, A
c1288	38.2	2.3	183770	4	US-09-949-016-15494	Sequence 15494, A	c1361	37.8	2.3	165	4	US-09-621-976-8127	Sequence 8127, Ap
c1289	38.2	2.3	191433	4	US-09-949-016-16144	Sequence 16144, A	c1362	37.8	2.3	233	4	US-09-621-976-16559	Sequence 16559, A
c1290	38.2	2.3	232024	4	US-09-949-016-13477	Sequence 13477, A	c1363	37.8	2.3	235	4	US-09-621-976-16550	Sequence 16550, A
c1291	38.2	2.3	232452	4	US-09-949-016-13675	Sequence 13675, A	c1364	37.8	2.3	258	4	US-09-621-976-15353	Sequence 15353, A
c1292	38.2	2.3	300402	4	US-09-949-016-13632	Sequence 13632, A	c1365	37.8	2.3	278	2	US-08-332-766A-42	Sequence 42, Appl
c1293	38.2	2.3	312470	4	US-09-949-016-14043	Sequence 14043, A	c1366	37.8	2.3	279	2	US-08-332-766A-3	Sequence 3, Appl
c1294	38.2	2.3	336024	4	US-09-949-016-12373	Sequence 12373, A	c1367	37.8	2.3	334	2	US-08-623-906A-9	Sequence 9, Appl
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; Sequence 1, Application US/09700397  
; Patent No. 6664383  
; GENERAL INFORMATION:  
; APPLICANT: Ono Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of t  
; FILE REFERENCE: Q61459  
; CURRENT APPLICATION NUMBER: US/09/700.397  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: JP 10-131815  
; PRIOR FILING DATE: 1998-05-14  
; PRIOR APPLICATION NUMBER: PCT/JP99/02485  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1032  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-700-397-1

Query Match 61.5%; Score 1032; DB 4; Length 1032;  
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Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
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US-09-700-397-5
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; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
;
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:
;
; US-09-135-080-3

Query Match 20.4%; Score 343; DB 3; Length 1238;
Best Local Similarity 62.0%; Pred. No. 9.5e-84;
Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

Qy 205 TCTCTTCCAGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCAAAGCTATG3ACAA 264
Db 121 TCTTCCCAAGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCAAAGCTATG3ACAA 174
Qy 265 CGTGACGCTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGGTCA 324
Db 175 CATCAGCTGAGGAGGGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGGTCA 234
Qy 325 CCGGTTGGCTCGCTTAACCCGAGCAGCACCCTCTATCTGGGAATGACAAAGTGGTGC 384
Db 235 GAAAGTGGCTGGTTGAACCGCTCTGGCATCATCTCGTGACACGACAGTGGTCTCT 294
Qy 385 GGATCTCGCTGGTCTCTTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
Db 295 GGACCTCGGTTGAGCTGGAGAAACGCGCATGCTTGGAAATACAGCCTCCGAATCCAG 354
Qy 445 CGTGAGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACACACACCCCAA 504
Db 355 GGTGATGTCTATGATGAAGATCTTACAGATGCTCAGTTCAGACACAGCATGAGCCCA 414
Qy 505 GACCTCTAGGCTCCACCTCATTTGCAAGTATCTCCCAAAATTTGAGAGTTCTTCAGA 564
Db 415 GACCTCTCAAGTTACTTGTATGATGATGTTCCACCAAGATCTCCAAATCTCTCGGA 474
Qy 565 TATCTCCATTAATGAGGGAACAATATATGAGCTCAGCTGATAGGAACTGGTAGACCA 624
Db 475 TGTCACTGTGAATGAGGCGCAATATGTAACCTGCTGCTGATGGCCAAATGGGCGCC 534
Qy 625 GCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGCA 684
Db 535 ACCTGTTATCACTTGGAGACACCTTACACCACTTGGAAAGAAATTTGAAGGAGAAGA 594
Qy 685 ATACTTTGAAATTCAGGCGATCACCCGCGGAGCAGTTCAGGAGCTACAGAGTGCAGT 744
Db 595 ATATCTGGAGATCTTAGGCATCACAGGGAACAGTCCAGCAATATGATGCAAGGTGC 654
Qy 745 CAATGACGTGGCGCGCCGCTGGTACGAGAGTAAAGGTACCGGTACCGTAACTATCC 804
Db 655 CAACGAGGTCTCTCCGCGGATGTCAAAACAGTCAAGGTCACTGTGAATATCCACCCAC 714
Qy 805 CATTTCCAGAACCGGATGACAGGTGTCCTCGTGGGACAAAGGGGACACTGCAAGTGA 864
Db 715 CATCACAGAGTCTAAGAGCAATGAAGCCACACAGGAGCAAGCTTCCCTCAATGTGA 774
Qy 865 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAAAGACTGATTGA 924
Db 775 AGCCTCAGCGGTGCTGACCTGACTTGTGATGGTACCGGGATGACACCGAG---GATA 831
Qy 925 AGGAAAGAAAGGGTGAAGTGGAAACACAGACCTTTTCTCTCAAAACTCATCTTTTCAA 984
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Db 832 CAGTGCAAACGGCCTTGAGATTAAAGAGCACTGAGGCGCAGTCTCTCCCTGACGGTGACCAA 891
Qy 985 TGTCTCTGAACATGACTATGGAACATACACTTGGTGGCCCTCCAAACAAAGCTGGGCGCACAC 1044
Db 892 CGTCACTGAGAAACACTACGCAACTATCTCTGTGTGCTGCCAAACAGCTCGGCGTCAC 951
Qy 1045 CAATGCCAGCATCATGCTATTGTTGTCAGGCGCGTGCAGGAGGTGAGCAACCGGACGTC 1104
Db 952 CAATGCCAGCTAGTCTCTTTTTCAGACCCGGTGGTGAG---AGGAATCAACGGATCCAT 1008
Qy 1105 GAGGAGGCGAGGCTGCTGCTGGCTGCTCTCTTCTGCTTGGTTCACCTGCTTCTCAAAAT 1164
Db 1009 CAGTCTGGCGGTACCACTGTGCTGCTGGCAGCGTCCCTGTCTGCTTCTCAGCAAAATG 1068
Qy 1165 TTGAT 1169
Db 1069 TTAAT 1073

RESULT 6
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE OF INVENTION: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 403
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CBI
;
; US-09-976-594-403

Query Match 20.3%; Score 341.6; DB 4; Length 1195;
Best Local Similarity 60.1%; Pred. No. 2.3e-83;
Matches 626; Conservative 0; Mismatches 404; Indels 12; Gaps 3;

Qy 205 TCTCTTCCAAAGGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCAAAGCTATG3ACAA 264
Db 66 TCTTCCCAAGGAGTGCCTGCTGGCAGCGTGGAT-----TTTAAACGAGGACCGGACAA 119
Qy 265 CGTGACGCTCCGCGAGGGGAGCGCCACCTCAGGTGCACTATTTCACACCGGGTCA 324
Db 120 CATCAGCTGAGGCGAGGGGAGCACAGCCATCTCCTCAGGTGCGTTCTAGAAGACAAGAACTC 179
Qy 325 CCGGTTGGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGGTGCCT 384
Db 180 AAGGTGGCTGGTTGAACCGGTTCTGCGCATCATTTTTTCTGGACATGCAAGTGGTCTCT 239
Qy 385 GGATCTCGGCTGGTCTCTCTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
Db 240 GGACCCACGGTTGAGCTGGAGAAACGCCATTTCTTGGAAATACAGCCTCCGAAATCCAGAA 299
Qy 445 CGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAGACACACCCCAA 504
Db 300 GGTGGATGTCTATGATGAGGGTTCTTACACTTGTCTAGTTCCAGATGAGGCCCAA 359
Qy 505 GACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGA 564
Db 360 GACCTCCCAAGTTTACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 419
Qy 565 TATCTCCATTAATGAAGGGAAACAATATTAAGCTTCACTGCTGCAATAGCAACTGGTAGACCA 624
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QY 865 AGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGGATGACAAAAGACTGATGA 924  
DB 699 GGCCTCGGAGTGCCTGACACCTGACTTTGAGTGGTACCGGATGACACTAG---GATAAA 755  
QY 925 AGGAAAGAAAGGGTGAAAGTGGAAACAGACCTTCTCTCAAAACTCATCTTCTTCAA 984  
DB 756 TAGTCCCAATGGCCCTTGAGATTAAAGAGCAGGAGGGCCAGTCTTCCCTTGACGGTGACCAA 815  
QY 985 TGTCTCTGAACATGACTATGGAACTACACTTGGCGTCCCAACAAAGCTGGGCCACAC 1044  
DB 816 CTTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCGCAACAAGCTGGGGTGCAC 875  
QY 1045 CAATGCCAGCATCATGCTATTGTTGGTCCAGGGCCCTCAGCG 1085  
DB 876 CAATGCCAGCTAGTCCCTTTTCAGACCTGGGTGGTGAGAG 916

## RESULT 8

US-08-414-657D-1

; Sequence 1, Application US/08414657D  
; Patent No. 5861283  
; GENERAL INFORMATION:  
; APPLICANT: Levitt, Pat  
; APPLICANT: Pimenta, Aurea  
; APPLICANT: Fischer, Itzhak  
; APPLICANT: Zhukareva, Victoria  
; TITLE OF INVENTION: Limbic System-Associated Membrane  
; TITLE OF INVENTION: Protein and DNA  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,657D  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 317743-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 977 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 2...976  
; OTHER INFORMATION:  
; US-08-414-657D-1

Query Match 20.3%; Score 340.6; DB 2; Length 977;  
Best Local Similarity 63.3%; Pred. No. 3.8e-83;  
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

QY 205 TCTCTTCCAAAGAGTGGCCCGTGGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264  
DB 46 TCTTCCACACAGACTGCTGTTTCGACGCTGAT-----TTTAAACCGAGGCAACGACAA 99  
QY 265 CGTCAAGCTCGGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAAACCGGGTGCAC 324  
DB 100 CATCACCGTGGAGCGAGGGGACACAGGCCATCCTCAGGTGGCTTTAGAAAGACAAGAACTC 159  
QY 325 CCGGGTGGCCCTGGCTAAACCCGACAGCACCCTCTATGCTGGGAATGACAAAGTGGTGCCT 384  
DB 160 AAAGTGGCCCTGGTGGAAACCGTCTTGGCATCATTTTTTCTGGACATGACAAAGTGGTCTCT 219  
QY 385 GGATCTCTGGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATCGAGATCGAGAA 444  
DB 220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGNAATACAGCCTCCGAAATCCAGAA 279  
QY 445 CGTGGATGTGTATCAGCAGGGGCCCTTACACCTGCTCGGTGCGAGACAGCAACCCACCAA 504  
DB 280 GGTGGATGTCTATGATGAGGGTTCTTACACTTGTCTAGTTCAGACACAGCATGAGCCCAA 339  
QY 505 GACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTTCAGA 564  
DB 340 GACCTCCCAAGTTTACTTGTATCGTACAAAGTCCCAACAAAGATCTCCAATATCTCTCTCGA 399  
QY 565 TATCTCCATTAAATGAAGGGAACAAATATTTAGCCTCACCTGCAATAGCAACTGGTAGACCA 624  
DB 400 TGTCACTGTGAATGAGGGCAGCAACGGTGACTCTGCTGTGATGGCCAAATGSCCGTCTCTGA 459  
QY 625 GCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684  
DB 460 ACCTGTTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAGAAGA 519  
QY 685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTC 744  
DB 520 ATATCTGGAGATCCTTGGCATCACCGGAGCAGTCAAGGCAAAATATGAGTGCAAAGCTGC 579  
QY 745 CAATGACGTGGCCCGCCCGTGGTACGGAGAGTAAAGGTCAACCGTGAATATCCACCCATA 804  
DB 580 CAACGAGGTCTCTCTCGGGGATGTCAAAACAAGTCAAGGTCACTGTGAATCTCTCCCCAC 639  
QY 805 CATTTGAGAAGCCAAAGGTACAGGTGTCCTCGGTGGGACAAAGGGGACACTGTCAGTGTGA 864  
DB 640 TATCACAGAATCCAAAGAGCAATGAAGCCACCCACAGGACGACAAAGCTTCACTCAAAATGTA 699  
QY 865 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTGTACAAAGGATGACAAAGACTGATTGA 924  
DB 700 GGCCTCGGAGTGCCTGCACCTGACTTTGAGTGGTACCGGATGACACTAG---GATAAA 756  
QY 925 AGGAAAGAAAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAA 984  
DB 757 TAGTGCCAATGGCCCTTGAGATTAAAGACACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 816  
QY 985 TGTCTCTGAACATGACTATGGGAACTACACTTGGGTGGCCCTCCAAAGCTGGGCGCACAC 1044  
DB 817 CGTCACTGAGGAGCACTACGCGCAACTACCTGTGTGGTGGTCCCAACAAAGCTGGGGGTGCAC 876  
QY 1045 CAATGCCAGCATCATGCTATTGTTGGTCCAGGGCCCTCAGCG 1085  
DB 877 CAATGCCAGCTAGTCCCTTTTCAGACCTGGGTGGTGAGAG 917

## RESULT 9

US-09-135-080-1

; Sequence 1, Application US/09135080  
; Patent No. 6423827  
; GENERAL INFORMATION:  
; APPLICANT: Levitt, Pat R.  
; APPLICANT: Pimenta, Aurea  
; APPLICANT: Fischer, Itzhak  
; APPLICANT: Zhukareva, Victoria  
; TITLE OF INVENTION: Limbic System-Associated Membrane  
; TITLE OF INVENTION: Protein and DNA  
; NUMBER OF SEQUENCES: 29



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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
; US-08-414-657D-5

Query Match      20.3%; Score 340.6; DB 2; Length 1014;
Best Local Similarity 61.9%; Pred. No. 3.9e-83;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

Qy 205 TCTCTTCCAAAGAGTGCCGTCGGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAA 264
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TCTTCCCAACAGAGTCCCGTTCGACGGTGGAT-----TTTAAACGAGGACGGACAA 119
Qy 265 CGTGACGGTCCGGCAGGCGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGGTCAC 324
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 CATCACCGTGAGCGAGGGGGACCGGCATCCTCAGGTGTGTGTGAGAGAACAGAACTC 179
Qy 325 CCGGTGCGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGTGCT 384
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
180 GAAAGTGGCTGTTGAACCGCTCTGGCATCATCTTCTGTCGACACGCAAGTGTCTCT 239
Qy 385 GGATCCTCGCTGGTCTTCTTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 GGACCTCGGTGAGCTGGAGAAACGCGCATGCTCTGGAATACAGCCTCCGAAATCCAGAA 299
Qy 445 CGTGGATGTATGACGAGGCGCTTACACCTGCTCGGTGCGAGACAGACACCCCAAA 504
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
300 GGTGGATGCTATGATGAAGATCCTACACATGCTCAGTTTCAGACACAGCATGAGCCCA 359
Qy 505 GACCTCTAGGTCACACCTATTGTGCAAGTATCTCCCAAAATGTAGAGATTTCTTCAGA 564
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
360 GACCTCTCAAGTTACTTGTGTGATGATGTTCCACCAAGATCTCCACATCTCTCGGA 419
Qy 565 TATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACTGCTAGACCGA 624
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
420 TGTCACTGTAATGAGGCGAGCAATGTAACCTGTCTGCTGCAATGGCGCCCTGA 479
Qy 625 GCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTCGCTTGTGAGTGAAGACGA 684
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
480 ACCTGTTATCACTGGAGACACCTTACACCACTTGGAAAGAAATTTGAAGGAGAAAGA 539
Qy 685 ATACTTGAATTCAGGGCATCACCCGGGAGCAGTCAGGCGACTACAGTGCAGTGCCTC 744
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
540 ATATCTGGAGATCTAGGCATCACCGGGAACAGTCAGGCAATATGATGCAAGGTGC 599
Qy 745 CAATGACGTGCGCGCCGTCGGTACGGAGAGTAAAGGTCAACGTCACCGTGAATCCACCATA 804
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
600 CAACGAGGTCTCTCCGCGGATGTCAAAACAAGTCAAGGTCACTGTGAACATATCCACCCAC 659
Qy 805 CATTTCAAGAACCAAGGTACAGGTGTCCTCGTGGGACAAAGGGGACACTGCAGTGTGA 864
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
660 CATCACAGAGTCTAAGACCAATGAAGCCACACAGGACGCAAGCTTCCCTCAAAATGTGA 719
Qy 865 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAAAAGACTGATTGA 924
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
720 AGCCTCAGCGGTGCTGCACTGACTTTGAGTGGTACCGGATGACACCAG---GATAAA 776
Qy 925 AGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAA 984
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
777 CAGTGCAAAACGGCTTGAGATTAAAGAGCACTGAGGGCCAGTCTCTCCCTGACGGTGACCAA 836
Qy 985 TGTCTCTGAACATGACTATGGAACTACACTTGGTGGCTCCAAACAGCTGGGCGACAC 1044
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
837 CGTCACTAGGAACAACACTACGGCAACTATACCTGTGTGGCTGCCAACAGCTCGGCGTCA 896
Qy 1045 CAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGAGCAACGCGCATGC 1104
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
897 CAATGCCAGCCTAGTCTCTTTTCAGAACCCGGGTGCGGTGAG---AGGAATCAACCGGATCCAT 953
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Qy 1105 GAGAGGGCAGGCTGCTCTGGTGTGCTCTTCTGGTCTTGACCTGTCTTCAAATT 1164
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
954 CAGTCTGCGGTACCACTGTGGTGTGCTGGCAGCGTCCCTTCTGCTTCTCAGCAAATG 1013
Qy 1165 T 1165
Db 1014 T 1014

RESULT 11
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
; US-09-135-080-7

Query Match      20.3%; Score 340.6; DB 3; Length 1014;
Best Local Similarity 61.9%; Pred. No. 3.9e-83;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

Qy 205 TCTTTTCCAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAA 264
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TCTTCCCAACAGAGTCCCGTTCGACGGTGGAT-----TTTAAACGAGGACGGACAA 119
Qy 265 CGTGACGGTCCGGCAGGCGGAGAGCGCCACCTCAGGTGCACTATTGACAAACCGGGTCAC 324
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 CATCACCGTGAGCGAGGGGACCGGCATCCTCAGGTGTGTGTGAGAGAACAGAACTC 179
Qy 325 CCGGTGCGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGTGCT 384
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180 GAAAGTGGCCCTGGTTGAACCGCTCTGGCATCATCTTGGTCGACAGCAAGTGTCTCT 239
385 GGATCTCGCTGGTCTCTTCTGAGCAACACCAACGAGTACAGCATCGAGATCCAGAA 444
240 GGACCCCTGGGTGAGCTGGAGAAACGCGCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299
445 CGTGATGTGTATGACGAGGCGCTTACACCTGCTCGGTGCGAGACAGCAACACCCAAA 504
300 GGTGATGTCTATGATGAAGGATCTTACATATGCTCAGTTTCTGAGACAGCATGAGCCCA 359
505 GACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTCAGA 564
360 GACCTCTCAAGTTTACTTTGATTGTACAGTTTCCACCAAGATCTCCAAATCTCTCCGGA 419
565 TATCTCCATTAATGAGGGAACAATATTAGGCTACCTGCTACCTGCAATGGAATCTGTAGACCA 624
420 TGTCACTGTGAATGAGGCGAGCAATGTAAACCTGTGCTGCAATGGCCCAATGGGCGCCCTGA 479
625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
480 ACCTGTTATACCTTGGAGACACCTTACACCACTTGGAAAGAAATTTGAGGAGAGAAAGA 539
685 ATACTTGGAAATTTAGGGCATCACCCGGGAGCAGTTCAGGGACTACGAGTGCAGTGCCTC 744
540 ATATCTGGAGATCTTAGGCATCACCGAGGAACAGTCAAGCAATATGAGTCAAGGCTGC 599
745 CAATGACGTGGCGGCGGCGCTGTGAGGAGAGTAAAGTCAACCGTGAACATATCCACCAATA 804
600 CAACGAGGTCTCTCCGCGGATGTCAAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659
805 CATTTTCAGAACCAAGGTCACAGGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGA 864
660 CATCACAGAGTCTAAGACAAATGAAGCCACACAGGACGACAGCTTCCCTCAATGTGA 719
865 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAAAGGATGACAAAGAGACTGATTGA 924
720 AGCCTCAGCGGTGCTGCACCTGACTTTGAGTGTGTACCGGGATGACACCCAG--GATAAA 776
925 AGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAATCATCTCTTCAAA 984
777 CAGTGCAAACGGCTTGAGATTTAAGAGCACTGAGGGCCAGTCTCTCCCTGACGGTGACCAA 836
985 TGTCTCTGAACATGACTATGGAACTACACTTGGCTGGCTCCCAACAGCTGGGCCACAC 1044
837 CGTCACTGAGGAACACTAGGCACTATACCTGTGTGGCTGCTGCAACAAAGCTCGGGGTGAC 896
1045 CAATGCCAGCATCATGCTATTGTTGTCAGGGCGCGTCAAGGAGGTGAGCAACGGCACGTC 1104
897 CAATGCCAGCTTAGTCTCTTTTTCAGACCCCGGTGCGTGAG---AGGAATCAACGGATCCAT 953
1105 GAGGAGGCGAGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
954 CAGTCTGGCCGCTACCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013
1165 T 1165
. 1014 T 1014
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RESULT 12
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...861
; OTHER INFORMATION:
US-08-414-657D-9
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Query Match      20.2%; Score 338.6; DB 2; Length 861;
Best Local Similarity 63.7%; Pred. No. 1.2e-82;
Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
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QY 253 AGCTATATGACAACTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACATTTGA 312
DB 24 AGGCACGGAACAATCACCGTGAAGCGAGGGGAGACAGCCATCTCAGGTGGTCTTAGA 83
QY 313 CAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGACACCATCTCTATGTGGAATGA 372
DB 84 AGACAAGAACTCAAAAGGTGGCTGGTTGAACCGTTCTGGCATCATTTTGTGGACATGA 143
QY 373 CAAGTGTGCTGGATCCTCGGTGGTCTTCTGAGCAACACCCAAACGCGAGTACAGAT 432
DB 144 CAAGTGTGCTTGGACCCACCGGTTGAGCTGGAGAAACGCCATCTCTGGAATACAGCT 203
QY 433 CGAGATCCAGAACCTGGATGTGTATGACAGGGGCCCTTTACACCTGCTCGGTGCGAGACA 492
DB 204 CCGAATCCAGAAAGTGGATGTCTATGATAGGGTTCCTACACTTGTCTCAGTTCAGACACA 263
QY 493 CAACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGA 552
DB 264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGTATCGTACAGTCCCAAGATCTCCAA 323
QY 553 GATTTCTTCAGATATCTCCATTAAATGAGGAAACAATATTAGCTCTACCTCATAGCAAC 612
DB 324 TATCTCTCGGATGTCTGTAATGAGGAGCAACCGTGAATCTGCTGCTGATGCGCCAA 383
QY 613 TGGTAGACACGAGCTAGCGTTACTTTGAGACACATCTCTCCCAAGCGGTGGCTTTGT 672
DB 384 TGGCGGTCTTGAACCTGTTATCACTCTGGAGACACCTTACACCACTGGAAGGAATTTGA 443
QY 673 GAGTGAAGACCAATCTTTGGAATTCAGGGCATCACCCGGGAGCAGTCAAGGAGACTAGA 732
DB 444 AGGAGAAGAGAATATCTGGAGATCTTGGCATCACCCAGGGAGCAGTCAAGGCAATATGA 503
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QY 733 GTGCAGTCCCTCCATGACGTGGCGCGCCCGTGTACGGAGAGTAAGGTACCGGTGAA 792  
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QY 793 CTATCCACCATATTTTCAGAGCCNAGGTACAGGTGTCCCGTGGGACAAAAGGGGAC 852  
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QY 853 ACTGCACTGTAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAA 912  
DB 624 ACTCAATGTGAGCCTCGGAGTGCCTGACCTGACTTTGAGTGGTACCGGGATGACAC 683  
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DB 684 TAG---GATAAATAGTGCCAAATGGCCTTGAGATTAAAGACACGGAGGGCCAGTCTTCCT 740  
QY 973 CATCTTCTCAATGCTCTGAACATGACTATGGNACTACACTTGGCGCTCCAAACAA 1032  
DB 741 GACGGTGACCAACGCTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAAACAA 800  
QY 1033 GCTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGCGCGCTCAGCG 1085  
DB 801 GCTGGGGTCAACCAATGCCAGCTAGTCTCTTTTCAGACCTGGGTGGTGAGAG 853

## RESULT 13

US-08-414-657D-6  
; Sequence 6, Application US/08414657D  
; Patent No. 5861283  
; GENERAL INFORMATION:  
; APPLICANT: Levitt, Pat  
; APPLICANT: Pimenta, Aurea  
; APPLICANT: Fischer, Itzhak  
; APPLICANT: Zhukareva, Victoria  
; TITLE OF INVENTION: Limbic System-Associated Membrane  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,657D  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 317743-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 912 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence

; LOCATION: 1...912  
; OTHER INFORMATION:  
US-08-414-657D-6

Query Match 20.28; Score 338.6; DB 2; Length 912;  
Best Local Similarity 63.7%; Pred. No. 1.3e-82;  
Matches 531; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 253 AGCTATATGACAAACGTGACGGTCCGGCAGAGGGGAGAGCCACCTCAGGTGCACATTTGA 312  
DB 24 AGGCACGACAAACATACACCGTGGAGCGAGGGGACACAGCCATCTCAGGTGGTCTAGA 83  
QY 313 CAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA 372  
DB 84 AGACAAGAACTCAAAAGGTGGCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGA 143  
QY 373 CAAGTGTGCTGTGATCCTCGCGTGTCTCTGAGCAACACCCAAACGAGTACAGCAT 432  
DB 144 CAAGTGTCTCTGACCCACCGGTTGAGCTGGAGAAACGCCATTTCTCTGGAAATACAGCT 203  
QY 433 CGAGATCCAGAACGCTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGACA 492  
DB 204 CCGAATCCAGAGGTGATGTCTATGATGAGGGTCTCTACACTTCTCAGTTCAGACACA 263  
QY 493 CAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTA 552  
DB 264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGTATCGTACAGTCCCAACCAAGATCTCCA 323  
QY 553 GATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCTCCTCAGTCATAGCAAC 612  
DB 324 TATCTCTCGGATGTCACTGTGAATGAGGGGACGACGTTGACTCTGGTCTCATGGCCAA 383  
QY 613 TGGTAGACACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGT 672  
DB 384 TGGCGCTCTGAACCTGTATCACTTGGAGACACTTTACACCAACTGGAAGGAATTTGA 443  
QY 673 GAGTGAAGACGAATPACTTGGAAATTCAGGGCATCACCGGAGCAGTCAGGGGACTAGA 732  
DB 444 AGGAGAAGAAAGAAATATCTGGAGATCTTTGGCATCACCGAGGAGCAGTCAGGCAAAATGA 503  
QY 733 GTGCAGTGCCTCCCAATGACGTGGCGCGCGCTGTACGGAGAGTAAGGTACCGGTGAA 792  
DB 504 GTGCAAGCTGCCCAACGAGGTCTCTCGCGGATGTCAAAACAGTCAAGGTCACTGTGAA 563  
QY 793 CTATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGAC 852  
DB 564 CTATCTCTCCCACTATCACAGATCCAGAGCAATGAAGCCACACACAGCAGCAAGCTTC 623  
QY 853 ACTGCACTGTAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAA 912  
DB 624 ACTCAATGTGAGGCTCGGAGTGCCTGACCTGACTTTGAGTGGTACCGGGATGACAC 683  
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DB 684 TAG---GATAAATAGTGCCAAATGGCCTTGAGATTAAAGACACGGAGGGCCAGTCTTCCT 740  
QY 973 CATCTTCTCAATGCTCTGAACATGACTATGGAACTTACACTTGGTGGGCTCCAAACAA 1032  
DB 741 GACGGTGACCAACGCTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGTGGCAACAA 800  
QY 1033 GCTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGGCGCGTCAAGCG 1085  
DB 801 GCTGGGGTCAACCAATGCCAGCTAGTCTCTTTTCAGACCTGGGTGGTGAGAG 853

## RESULT 14

US-08-414-657D-8  
; Sequence 8, Application US/08414657D  
; Patent No. 5861283  
; GENERAL INFORMATION:  
; APPLICANT: Levitt, Pat  
; APPLICANT: Pimenta, Aurea  
; APPLICANT: Fischer, Itzhak



Search completed: October 30, 2005, 11:29:30  
Job time : 403 secs

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; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
US-08-414-657D-10

Query Match      19.9%; Score 333.8; DB 2; Length 861;
Best Local Similarity 63.4%; Pred. No. 2.6e-81;
Matches 528; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

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144 CAAGTGGTCTCTGGACCTCGGGTTGAGCTGGAGAAACGCCCATGCTCTGGAATACAGCT 203
Qy 433 CGAGATCCAGAACGTGGATGTATGACGAGGGCCCTTTACACCTGCTCGGTGCAGACAGA 492
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Qy 493 CAACCAACCAAGAGCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGA 552
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324 CATCTCTCGGATGTCACTGTGAATGAGGCGAGCAATGTAACTTGGTCTGCATGGCCAA 383
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
384 TGGGCGCCCTGAACCTGTATATCAGCTGGAGACACCTTACACCACTTGGAGAGAAATTTGA 443
Qy 673 GAGTGAAGACCAATACCTTGGAAATTCAGGGCATCACCGGGAGCAGTCCAGGGACTAGA 732
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
444 AGGAGAAGAGAATATCTGGAGATCTTAGGCATCACAGGGAAACAGTCAGGCAAAATATGA 503
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504 GTGCAAGGCTGCCAACGAGGTCTCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563
Qy 793 CTATCCACCATACATTTTCAAGCAAGCGGTPACAGGTGTCCCGTGGGACAAAAGGGGAC 852
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564 CTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACACAGGACGACAAGCTTC 623
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624 CCTCAAATGTGAAGCTCAGCGGTGCTGACCTGACCTTTGAGTGGTACCGGGATGACAC 683
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684 CAG---GATAACAGTGCANACGGCTTGAGATTAAAGCACTGAGGGCCAGTCTCTCCCT 740
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741 GACGGTGACCAACGCTCACTGAGGAACACTACGGCAACTATATACCTGTGTGGCTGCCAACAA 800
Qy 1033 GCTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGCGCGCTCAGCG 1085
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
801 GCTCGGGGTCAACCAATGCCAGCTAGTCTCTTTTTCAGACCCCGGTCGGTGAGAG 853
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 30, 2005, 07:42:46 ; Search time 5171 Seconds  
(without alignments)  
3223.476 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKHNSISWAIPTGL.....RRAGCVWLLPLVLHLLK 344

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

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Database :

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2: gb.htg:\*  
3: gb.in:\*  
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5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1806	100.0	1032	6	AR439648 Sequence
2	1806	100.0	1679	6	CQ768055 Sequence
3	1806	100.0	1679	6	AR528639 Sequence
4	1806	100.0	1679	6	AX358872 Sequence

5	1806	100.0	1679	6	AX362365 Sequence
6	1806	100.0	1679	6	AX403748 Sequence
7	1806	100.0	1679	6	AX454470 Sequence
8	1806	100.0	1679	6	AX464242 Sequence
9	1806	100.0	1679	6	AX490948 Sequence
10	1806	100.0	1679	9	AY358331 Homo sapi
11	1806	100.0	1693	6	AR439649 Sequence
12	1665.5	92.2	1839	6	AX665342 Sequence
13	1665.5	92.2	1839	9	AF126426 Homo sapi
14	1650	91.4	1068	6	AX665344 Sequence
15	1647.5	91.2	1615	10	BC023307 Mus muscu
16	1644	90.9	1104	6	AX665346 Sequence
17	1642	90.9	939	6	AR439650 Sequence
18	1639.5	90.8	2040	10	RNU16845
19	1638	90.7	1140	6	AX665348 Sequence
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22	1500.5	83.1	1325	9	BC050716 Homo sapi
23	1477.5	81.8	1257	5	GGCEPUI
24	1428	79.1	1058	5	AF292935 Gallus ga
25	1427.5	79.0	1035	5	AB011810 Gallus ga
26	1393	77.1	1638	12	AF271233 Synthetic
27	1357.5	75.2	1013	5	AF292936 Gallus ga
28	1307	72.4	6005	10	BC076581 Mus muscu
29	1306.5	72.3	3216	5	GGCEPUS
30	1306	72.3	1533	5	FFNINH55A
31	1296.5	71.8	6380	9	BSM805672
32	1286.5	71.2	3069	10	RATCALMA
33	1276.5	70.7	1370	5	BC074283
34	1275.5	70.6	1556	5	AF292934
35	1271.5	70.4	2935	12	AF271618
36	1270.5	70.3	1108	9	BC074742 Homo sapi
37	1268	70.2	1111	9	BC074773 Homo sapi
38	1268	70.2	1478	9	HUMOBICAM
39	1268	70.2	3110	6	AX665340 Sequence
40	1267	70.2	2593	4	BT0BCAM
41	1259	69.7	2179	10	RATCALMB
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43	993.5	55.0	2055	5	BC081685
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46	938.5	52.0	1158	5	GGLAMPG19
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61	908	50.3	924	6	AR030579 Sequence
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68	859	47.6	503	5	CQ768057 Sequence
69	842	46.6	1059	5	GGAI32999
70	823	45.6	1196	6	AX662341 Sequence
71	823	45.6	1327	6	AX704747 Sequence
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73	823	45.6	4834	6	AX362241 Sequence
74	823	45.6	4834	6	AX403774 Sequence
75	823	45.6	5582	9	BSM806161
76	822	45.5	1119	6	AX675563 Sequence
77	820	45.4	2383	6	AX747470 Sequence

78	820	45.4	2383	9	AK092307	AK092307 Homo sapi	151	297.5	16.5	84246	3	AC002512	AC002512 Drosophil
79	819	45.3	1165	6	AX662343	AX662343 Sequence	c 152	297.5	16.5	110000	3	AE001572_2	Continuation (3 of
80	815	45.1	1809	10	AB017139	AB017139 Rattus no	153	297.5	16.5	170801	3	AC095014	AC095014 Drosophil
81	815	45.1	2840	9	AX358132	AX358132 Homo sapi	154	297.5	16.5	298020	3	AE003674	AE003674 Drosophil
82	814	44.1	1179	10	MMU487032	AJ487032 Mus muscu	c 155	293	16.2	157263	2	EX957285	EX957285 Danio rer
83	796.5	44.1	756	6	AR030589	AR030589 Sequence	156	290.5	16.1	8546	6	AX828406	AX828406 Sequence
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85	768.5	42.6	5605	9	BC036771	BC036771 Homo sapi	158	230.5	16.1	18207	6	AX828384	AX828384 Sequence
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92	721	39.9	1169	6	AX644999	AX644999 Sequence	165	282.5	15.6	2544	10	BC011310	BC011310 Mus muscu
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c 94	670	37.1	197553	2	AC146103	AC146103 Pan trogl	167	279	15.4	237376	2	AC124949	AC124949 Rattus no
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98	599	33.2	786	5	GCN13298	GCN13298 Gallus Ga	171	277.5	15.4	3170	10	RNNCAM14	X06564 Rat mrNA fo
99	578	32.0	452	6	AX079423	AX079423 Sequence	172	277.5	15.4	3720	5	XELNCAM	M25696 X.laevis ne
100	545	30.2	333	6	AX907426	AX907426 Sequence	173	277.5	15.4	4454	5	BC081181	BC081181 Xenopus l
101	545	30.2	333	6	BD042959	BD042959 Sequence	174	276.5	15.3	2256	5	BC057517	BC057517 Danio rer
102	509.5	28.2	531	6	C0719449	C0719449 Sequence	175	276	15.3	2799	9	HSNCAME	X16841 Human mrNA
103	490.5	27.2	585	6	AX079674	AX079674 Sequence	176	276	15.3	2960	6	AX658287	AX658287 Sequence
104	466.5	25.8	793	5	BX932289	BX932289 Gallus ga	177	276	15.3	2960	9	S71824	S71824 N-CAMs-145 k
105	430	23.8	504	6	CQ715694	CQ715694 Sequence	178	276	15.3	3266	6	CQ728451	CQ728451 Sequence
106	429.5	23.8	20731	9	AP004721	AP004721 Homo sapi	179	276	15.3	3309	6	AX714869	AX714869 Sequence
107	429.5	23.8	43087	9	AP005155	AP005155 Homo sapi	180	276	15.3	3309	9	AK057509	AK057509 Homo sapi
108	424.5	23.5	168745	2	AC119552	AC119552 Rattus no	181	276	15.3	8513	6	AX207284	AX207284 Sequence
109	424.5	23.5	248329	2	AC109989	AC109989 Rattus no	182	275.5	15.3	3574	4	BTADCYC	X16451 Bovine mrNA
c 110	421	23.3	110000	2	AC102028_1	Continuation (2 of	183	275	15.2	2633	6	AR380405	AR380405 Sequence
c 111	400.5	22.2	408	6	AX684132	AX684132 Sequence	184	275	15.2	2633	9	HSU63041	US3041 Human neur
112	391.5	21.7	540	6	AX665354	AX665354 Sequence	185	274	15.2	5807	6	AR447664	AR447664 Sequence
113	391.5	21.7	116069	2	AP000784	AP000784 Homo sapi	186	273.5	15.1	2118	6	AR506699	AR506699 Sequence
c 114	391.5	21.7	123320	9	AP000863	AP000863 Homo sapi	187	273.5	15.1	2178	5	AB008163	AB008163 Xenopus l
115	391.5	21.7	176676	2	AC012334	AC012334 Homo sapi	188	273.5	15.1	7097	6	AX921114	AX921114 Sequence
116	391.5	21.7	177102	2	AP002808	AP002808 Homo sapi	c 189	273	15.1	184716	2	AC018368	AC018368 Homo sapi
117	382	21.2	642	6	CQ732119	CQ732119 Sequence	190	273	15.1	191071	9	AP004248	AP004248 Homo sapi
c 118	382	21.2	184012	10	AC116523	AC116523 Mus muscu	191	272.5	15.1	2879	5	BC075300	BC075300 Xenopus t
c 119	382	21.2	242565	2	AC094728	AC094728 Rattus no	192	272.5	15.1	3971	5	CHKCONNE	D16541 Gallus gall
120	382	21.2	251570	2	AC094463	AC094463 Rattus no	193	272	15.1	131490	10	AC122207	AC122207 Mus muscu
121	378	20.9	371	6	CQ731074	CQ731074 Sequence	194	272	15.1	177251	10	AC124565	AC124565 Mus muscu
122	350.5	19.4	3847	3	BT010243	BT010243 Drosophil	195	271.5	15.0	4321	6	AX921112	AX921112 Sequence
123	349.5	19.4	3460	3	BT011190	BT011190 Drosophil	c 196	271.5	15.0	169582	2	AC102190	AC102190 Mus muscu
124	348	19.3	3590	3	BT003528	BT003528 Drosophil	197	271	15.0	4050	9	BC047244	BC047244 Homo sapi
125	344	19.0	352	6	AX886912	AX886912 Sequence	198	270.5	15.0	3814	5	XELNCAMA	M76710 Xenopus lae
126	344	19.0	352	6	BD026522	BD026522 Sequence	199	270	15.0	2190	6	CQ604731	CQ604731 Sequence
127	339	18.8	187203	2	AP000832	AP000832 Homo sapi	c 200	270	15.0	110000	2	AC102028_0	AC102028 Mus muscu
c 128	339	18.8	191204	9	AP000843	AP000843 Homo sapi	c 201	270	15.0	186110	2	AC102204	AC102204 Mus muscu
129	338.5	18.7	1242	6	CQ607488	CQ607488 Sequence	202	269.5	14.9	1912	3	SAREGALPT	X93601 S.americana
130	338.5	18.7	3106	3	AY060653	AY060653 Drosophil	c 203	269	14.9	142000	9	AC078813	AC078813 Homo sapi
131	336	18.6	292	6	CQ716587	CQ716587 Sequence	204	268.5	14.9	4491	6	CQ848038	CQ848038 Sequence
132	333	18.4	411	6	CQ731080	CQ731080 Sequence	205	268.5	14.9	4491	6	CQ848044	CQ848044 Sequence
133	333	18.4	948	6	CQ595959	CQ595959 Sequence	206	268.5	14.9	5510	6	AX409111	AX409111 Sequence
134	308.5	17.1	3927	3	DMU78177	U78177 Drosophila	207	268.5	14.9	5510	9	D86983	D86983 Human mrNA
135	306.5	17.0	2010	6	CQ586755	CQ586755 Sequence	208	268.5	14.9	6847	9	AF200348	AF200348 Homo sapi
136	306.5	17.0	4052	3	AY060363	AY060363 Drosophil	209	268.5	14.9	6939	6	AX780120	AX780120 Sequence
137	303.5	16.8	950	3	AY052162	AY052162 Drosophil	210	268.5	14.9	6939	6	AX780121	AX780121 Sequence
138	303.5	16.8	950	3	AY052163	AY052163 Drosophil	c 211	267	14.8	3060	6	CQ595958	CQ595958 Sequence
139	302.5	16.7	913	6	AR542162	AR542162 Sequence	212	267	14.8	64674	3	AC004247	AC004247 Drosophil
140	300.5	16.6	950	3	AY052156	AY052156 Drosophil	c 213	267	14.8	110526	2	AC019598	AC019598 Drosophil
141	300.5	16.6	950	3	AY052160	AY052160 Drosophil	c 214	267	14.8	174376	3	AC092230	AC092230 Drosophil
142	297.5	16.5	950	3	AY052157	AY052157 Drosophil	c 215	267	14.8	259718	4	AE003614	AE003614 Drosophil
143	297.5	16.5	950	3	AY052158	AY052158 Drosophil	216	266	14.7	268	4	AF271984	AF271984 Bos tauru
144	297.5	16.5	950	3	AY052159	AY052159 Drosophil	217	266	14.7	110000	2	AC110642_3	Continuation (4 of
145	297.5	16.5	950	3	AY052161	AY052161 Drosophil	218	265.5	14.7	6332	10	AK122223	AK122223 Mus muscu
146	297.5	16.5	1110	6	CQ575874	CQ575874 Sequence	219	265	14.7	8035	3	AF254867	AF254867 Drosophil
147	297.5	16.5	1563	3	AY051911	AY051911 Drosophil	c 220	264	14.6	110000	2	AC110642_2	Continuation (3 of
148	297.5	16.5	2135	3	DROAMA	M23561 D.melanogas	221	263.5	14.6	6814	6	AR220825	AR220825 Sequence
c 149	297.5	16.5	3426	6	CQ575873	CQ575873 Sequence	222	263	14.6	11850	4	AY136513	AY136513 Canis fam
c 150	297.5	16.5	6228	2	AC020270	AC020270 Drosophil	223	262	14.5	3738	5	AY029401	AY029401 Danio rer

224	262	14.5	134184	2	AC150028	Canis fam
225	261.5	14.5	1314	9	AF538973	Homo sapi
226	261.5	14.5	4619	5	GGF11	XI4877 Gallus gall
227	261.5	14.5	4991	5	GGCONTAC	Y00813 Chicken mRN
228	261.5	14.5	18848	4	OCY14852	Y14852 Oryctolagus
229	261	14.5	863	5	EX935847	EX935847 Gallus ga
230	261	14.5	4188	6	BD085986	BD085986 Method of
231	261	14.5	6440	3	AF040989	AF040989 Drosophil
232	261	14.5	10232	10	AF525411	AF525411 Rattus no
233	260.5	14.4	1956	3	AF134113	AF134113 Drosophil
234	260.5	14.4	2050	3	AY047524	AY047524 Drosophil
235	260.5	14.4	2113	6	CY585189	CY585189 Sequence
236	260	14.4	4290	9	BC014205	BC014205 Homo sapi
237	260	14.4	4355	6	CQ603804	CQ603804 Sequence
238	259.5	14.4	89623	6	CQ730839	CQ730839 Sequence
239	259	14.3	23887	9	HSTI11NN2	X90569 H. sapiens m
240	259	14.3	93801	6	BD186121	BD186121 Preventio
241	259	14.3	93805	6	CQ730837	CQ730837 Sequence
242	259	14.3	103053	6	CQ848088	CQ848088 Sequence
243	258.5	14.3	4272	6	CQ715893	CQ715893 Sequence
244	258.5	14.3	4833	9	AK125056	AK125056 Homo sapi
245	258	14.3	169206	10	AC123550	AC123550 Mus muscu
246	258	14.3	277603	2	AC079543	AC079543 Mus muscu
247	257	14.2	4221	5	BC045307	BC045307 Danio rer
248	256	14.2	2110	3	DR0LACH	LI3255 Fruitfly la
249	256	14.2	2131	6	CQ590793	CQ590793 Sequence
250	256	14.2	2157	3	AY051829	AY051829 Drosophil
251	255.5	14.1	2726	5	AY029402	AY029402 Danio rer
252	255.5	14.1	202505	2	AP000912	AP000912 Homo sapi
253	254.5	14.1	15597	3	AF074901	AF074901 Caenorhab
254	253.5	14.0	2116	6	AX058616	AX058616 Sequence
255	252.5	14.0	175963	3	AC148913	AC148913 Sus scrof
256	252	14.0	187746	2	AC087123	AC087123 Mus muscu
257	251.5	13.9	3485	10	AF016619	AF016619 Mus muscu
258	251.5	13.9	3488	10	AF001287	AF001287 Mus muscu
259	251.5	13.9	4496	6	CQ715482	CQ715482 Sequence
260	251.5	13.9	4821	10	AF001286	AF001286 Mus muscu
261	251	13.9	219713	2	AC112456	AC112456 Rattus no
262	251	13.9	234283	2	AC114113	AC114113 Rattus no
263	251	13.9	250355	2	AC127766	AC127766 Rattus no
264	251	13.9	263661	2	AC106603	AC106603 Rattus no
265	251	13.9	319104	2	AC106602	AC106602 Rattus no
266	250.5	13.9	2658	6	CQ583539	CQ583539 Sequence
267	250.5	13.9	4306	3	AF312580	AF312580 Drosophil
268	250.5	13.9	5514	3	BT015246	BT015246 Grasehopper
269	250	13.8	2007	3	SCALACH	LI3256 Grasehopper
270	250	13.8	2895	5	AY029403	AY029403 Danio rer
271	250	13.8	8907	9	AF478693	AF478693 Homo sapi
272	249.5	13.8	3588	6	CQ870412	CQ870412 Sequence
273	249.5	13.8	4306	9	AK124736	AK124736 Homo sapi
274	249.5	13.8	4479	9	HSTAG1	X68274 Homo sapien
275	249.5	13.8	4548	6	AR453309	AR453309 Sequence
276	249.5	13.8	4548	6	AR305052	AR305052 Sequence
277	249.5	13.8	6137	6	CQ870414	CQ870414 Sequence
278	249.5	13.8	6137	6	CQ870414	CQ870414 Sequence
279	249.5	13.8	195993	2	AC134953	AC134953 Pan trogl
280	248.5	13.8	295	6	CQ732164	CQ732164 Sequence
281	248.5	13.8	1880	6	AX714170	AX714170 Sequence
282	248.5	13.8	1880	9	AK056336	AK056336 Homo sapi
283	248	13.7	1404	6	CQ605679	CQ605679 Sequence
284	248	13.7	2229	6	CQ729908	CQ729908 Sequence
285	248	13.7	74368	9	AL391239	AL391239 Human DNA
286	248	13.7	131457	9	AL356600	AL356600 Human DNA
287	248	13.7	153852	2	AC009694	AC009694 Homo sapi
288	248	13.7	219424	10	AC125214	AC125214 Mus muscu
289	248	13.7	315761	2	AL158079	AL158079 Homo sapi
290	247	13.7	172146	2	AC130272	AC130272 Papio anu
291	246.5	13.6	2988	9	BC036569	BC036569 Homo s
292	246.5	13.6	3314	6	AX556980	AX556980 Sequence
293	246.5	13.6	3314	6	HSU07819	HSU07819 Human conta
294	246.5	13.6	3319	6	CQ727274	CQ727274 Sequence
295	246.5	13.6	3335	9	HSU07820	HSU07820 Human conta

297	246.5	13.6	3360	6	AR001474	AR001474 Sequence
298	246.5	13.6	3360	6	CQ776853	CQ776853 Sequence
299	246.5	13.6	3360	6	I74665	I74665 Sequence 5
300	246.5	13.6	3360	6	I93559	I93559 Sequence 5
301	246.5	13.6	3360	6	AX331543	AX331543 Sequence
302	246.5	13.6	3360	6	AX331937	AX331937 Sequence
303	246.5	13.6	3360	6	AX556979	AX556979 Sequence
304	246.5	13.6	3360	9	HSCNTCTNA	221488 H. sapiens c
305	246.5	13.6	3412	10	AY495696	AY495696 Rattus no
306	246.5	13.6	4249	10	AY495695	AY495695 Rattus no
307	246	13.6	3366	9	AK123606	AK123606 Homo sapi
308	246	13.6	4015	6	CQ726266	CQ726266 Sequence
309	246	13.6	4015	6	AB018349	AB018349 Homo sapi
310	246	13.6	168861	2	AC130786	AC130786 Papio anu
311	245	13.6	5095	5	BC072368	BC072368 Xenopus 1
312	245	13.6	212752	9	AC063977	AC063977 Homo sapi
313	244.5	13.5	830	5	EX933439	EX933439 Gallus ga
314	244.5	13.5	163120	5	EX296535	EX296535 Zebrafish
315	244.5	13.5	180842	2	CR536619	CR536619 Danio rer
316	243.5	13.5	2962	9	AY358125	AY358125 Homo sapi
317	243.5	13.5	3214	10	RATP3A	D38492 Rat mRNA fo
318	243.5	13.5	3362	10	AY371925	AY371925 Mus muscu
319	243.5	13.5	3619	9	BC052946	BC052946 Homo sapi
320	243.5	13.5	3648	9	AY369208	AY369208 Homo sapi
321	243.5	13.5	3967	5	GDAXONIN	YG3101 G.domesticu
322	242.5	13.4	3355	10	AY371924	AY371924 Rattus no
323	242.5	13.4	3897	10	BC066864	BC066864 Mus muscu
324	241.5	13.4	3412	4	BOVF3F11C	D32135 Bovine mRNA
325	241.5	13.4	3843	6	CQ777685	CQ777685 Sequence
326	241.5	13.4	3843	10	MMF3	X14943 Mouse mRNA
327	241.5	13.4	3870	6	AX714318	AX714318 Sequence
328	241.5	13.4	3870	9	AK056557	AK056557 Homo sapi
329	241.5	13.4	4723	9	HSU75330	U75330 Human neutra
330	241	13.3	229330	2	AC137057	AC137057 Rattus no
331	241	13.3	238070	2	AC134313	AC134313 Rattus no
332	241	13.3	242260	2	AC094567	AC094567 Rattus no
333	241	13.3	255120	2	AC127219	AC127219 Rattus no
334	240	13.2	12667	10	MUSPERPA	M77174 Mouse parle
335	239	13.2	1174	5	BC078550	BC078550 Xenopus 1
336	239	13.2	2884	5	CR386716	CR386716 Gallus ga
337	238.5	13.2	2766	6	AX114541	AX114541 Sequence
338	238.5	13.2	2771	6	AX114540	AX114540 Sequence
339	238.5	13.2	2771	6	AX114542	AX114542 Sequence
340	238.5	13.2	3060	6	AX114539	AX114539 Sequence
341	238.5	13.2	3065	6	AX114544	AX114544 Sequence
342	237.5	13.2	5975	10	AK173030	AK173030 Mus muscu
343	237	13.1	219	6	AR030583	AR030583 Sequence
344	237	13.1	219	6	AR030584	AR030584 Sequence
345	237	13.1	2611	3	HMU92814	U92814 Hirudo medi
346	236.5	13.1	2451	6	CQ850834	CQ850834 Sequence
347	236	13.1	2451	9	AK128020	AK128020 Homo sapi
348	236	13.1	2451	9	AK128020	AK128020 Homo sapi
349	235.5	13.0	3373	5	AF461120	AF461120 Danio rer
350	235.5	13.0	4086	6	CQ850958	CQ850958 Sequence
351	235.5	13.0	4086	9	AK128160	AK128160 Homo sapi
352	235.5	13.0	4233	5	AGA309935	AG309935 Gallus ga
353	235.5	13.0	7872	9	AY273815	AY273815 Homo sapi
354	234.5	13.0	1198	5	EX935151	EX935151 Gallus ga
355	234.5	13.0	4053	3	AF103899	AF103899 Manduca s
356	234.5	13.0	5040	10	RATTAG1	M1725 Rat axonal
357	234.5	13.0	5626	3	AF103900	AF103900 Manduca s
358	234.5	13.0	39130	3	CBRG42E21	CBRG42E21 Caenorhab
359	234	13.0	2420	6	AX746808	AX746808 Sequence
360	234	13.0	2420	9	AK091149	AK091149 Homo sapi
361	233.5	12.9	1427	6	AX454490	AX454490 Sequence
362	233.5	12.9	1427	6	AX490968	AX490968 Sequence
363	233.5	12.9	3682	9	AB013803	AB013803 Homo sapi
364	233.5	12.9	3904	6	CQ875308	CQ875308 Sequence
365	233.5	12.9	3904	6	AB013802	AB013802 Homo sapi
366	233.5	12.9	8410	6	CQ603803	CQ603803 Sequence
367	233.5	12.9	16652	2	AC014298	AC014298 Drosophil
368	233.5	12.9	169534	3	AC008350	AC008350 Drosophil
369	233.5	12.9	302225	3	AE003458	AE003458 Drosophil

370	233	12.9	3413	10	D87248	D87248 Rattus norv	443	224.5	12.4	7642	9	AF002246	Homo sapi
371	233	12.9	4956	5	BC044084	BC044084 Xenopus l	444	224.5	12.4	7647	6	AR454602	Sequence
372	232.5	12.9	1073	5	DRU63292	U63292 Danio rerio	445	224	12.4	2436	9	AL833710	Homo sapi
373	232.5	12.9	2611	10	AF115400	AF115400 Mus muscu	446	224	12.4	2500	6	CQ783752	Sequence
374	232.5	12.9	36859	3	U800022	U80022 Caenorhabdi	447	224	12.4	2500	6	BD127814	Primer fo
c 375	232.5	12.9	126899	3	AY130758	AY130758 Caenorhab	448	224	12.4	2500	9	AK074921	Homo sapi
376	232	12.8	7876	6	AX592082	AX592082 Sequence	449	224	12.4	3662	6	BD172466	Secreted
377	232	12.8	8270	6	AX592092	AX592092 Sequence	450	224	12.4	3662	6	BD172785	Secreted
378	232	12.8	152686	2	AC018913	AC018913 Homo sapi	451	224	12.4	3662	6	BD173104	Secreted
379	231.5	12.8	3218	5	D86505	D86505 Xenopus lae	452	224	12.4	3662	6	BD173423	Secreted
380	231.5	12.8	3821	10	MUSLRAM	L02844 Mus musculu	453	224	12.4	3662	6	BD175457	Secretory
381	231.5	12.8	173270	9	AC024886	AC024886 Homo sapi	454	224	12.4	3662	6	AR410836	Sequence
382	231	12.8	3087	10	AB032602	AB032602 Mus muscu	455	224	12.4	3662	6	AR439200	Sequence
383	231	12.8	3346	6	C0728965	C0728965 Sequence	456	224	12.4	3662	6	AR473220	Sequence
384	231	12.8	3442	6	BD190857	BD190857 Secreted	457	224	12.4	3662	6	AR527206	Sequence
385	231	12.8	3530	9	AB003592	AB003592 Homo sapi	458	224	12.4	3662	6	AR566239	Sequence
386	231	12.8	4189	10	AF317839	AF317839 Mus muscu	459	224	12.4	3662	6	AX098383	Sequence
387	230.5	12.8	1766	6	CQ731700	CQ731700 Sequence	460	224	12.4	3662	6	AX697698	Sequence
388	230.5	12.8	2855	10	RNU34985	U34985 Rattus norv	461	224	12.4	3662	6	BD075606	Secretory
389	230.5	12.8	2869	6	A72401	A72401 Sequence 2	462	224	12.4	3662	9	AY358295	Homo sapi
390	230.5	12.8	2869	6	AR043363	AR043363 Sequence	463	224	12.4	3810	10	AF531873	Mus muscu
391	230.5	12.8	2869	6	I60497	I60497 Sequence 2	464	224	12.4	3864	9	AY505340	Homo sapi
392	230.5	12.8	2869	6	AR217165	AR217165 Sequence	465	224	12.4	4053	6	BD172468	Secreted
393	230.5	12.8	4988	5	BC066766	BC066766 Danio rer	466	224	12.4	4053	6	BD172787	Secreted
394	230.5	12.8	5868	10	BC066106	BC066106 Mus muscu	467	224	12.4	4053	6	BD173106	Secreted
395	230.5	12.8	8455	6	C0870409	C0870409 Sequence	468	224	12.4	4053	6	BD173425	Secreted
396	230.5	12.8	10976	6	C0869763	C0869763 Sequence	469	224	12.4	4053	6	BD175459	Secretory
397	230	12.7	2610	6	AR043379	AR043379 Sequence	470	224	12.4	4053	6	AR410838	Sequence
398	230	12.7	2610	6	C0847968	C0847968 Sequence	471	224	12.4	4053	6	AR439202	Sequence
399	230	12.7	2610	6	I60505	I60505 Sequence 17	472	224	12.4	4053	6	AR473222	Sequence
400	230	12.7	2610	6	AR217181	AR217181 Sequence	473	224	12.4	4053	6	AR527208	Sequence
401	230	12.7	2659	10	AK129481	AK129481 Mus muscu	474	224	12.4	4053	6	AR528627	Sequence
402	230	12.7	2666	9	AF006464	AF006464 Homo sapi	475	224	12.4	4053	6	AR566241	Sequence
403	230	12.7	2692	9	AY358128	AY358128 Homo sapi	476	224	12.4	4053	6	AX056647	Sequence
404	230	12.7	13793	9	HSEHSP	X62515 H. sapiens m	477	224	12.4	4053	6	AX098387	Sequence
405	229.5	12.7	2004	6	AK034890	AK034890 Sequence	478	224	12.4	4053	6	AX464218	Sequence
406	229.5	12.7	2004	9	AK097578	AK097578 Homo sapi	479	224	12.4	4053	6	AX697702	Sequence
407	229	12.7	5396	5	AF388036	AF388036 Xenopus l	480	224	12.4	4053	6	BD075608	Secretory
408	228.5	12.7	3707	10	BC065142	BC065142 Mus muscu	481	224	12.4	4053	9	AY358288	Homo sapi
409	228.5	12.7	3893	10	AY053341	AY053341 Mus muscu	482	224	12.4	4256	10	BC076578	Mus muscu
410	228.5	12.7	3980	5	AF064799	AF064799 Danio rer	483	223	12.3	1254	10	AB183401	Mus muscu
411	228	12.6	3613	10	BC076594	BC076594 Mus muscu	484	223	12.3	1254	10	AY351388	Mus muscu
412	227.5	12.6	1954	10	AB114443	AB114443 Rattus no	485	223	12.3	1674	9	BC047021	Homo sapi
413	227.5	12.6	3341	10	D87212	D87212 Rattus norv	486	223	12.3	184716	2	AC018368	Homo sapi
414	227.5	12.6	3788	5	CHKKGG	M63437 Chicken KLG	c 487	223	12.3	213331	2	AC125960	Rattus no
c 415	227.5	12.6	21829	10	AL645854	AL645854 Mouse DNA	488	222.5	12.3	3795	10	MUSCD22A	Mus musculu
416	227	12.6	4009	6	AX405987	AX405987 Sequence	489	222.5	12.3	95745	9	AL359510	Human DNA
417	227	12.6	4036	9	AB037776	AB037776 Homo sapi	490	222	12.3	4783	6	E34509	Novel rpoA.
418	227	12.6	4230	10	BC040281	BC040281 Mus muscu	491	222	12.3	4783	6	E34511	Novel rpoA.
419	227	12.6	4542	6	C0718773	C0718773 Sequence	492	222	12.3	4783	6	E34513	Novel utili
420	227	12.6	13149	6	C0728817	C0728817 Sequence	493	222	12.3	4783	6	E34515	Human LIG-1
421	227	12.6	186110	2	AC102204	AC102204 Mus muscu	c 494	222	12.3	7171	6	CQ604730	Sequence
422	226.5	12.5	1801	10	BC078966	BC078966 Rattus no	495	222	12.3	10002	2	AC020372	Drosophil
423	226.5	12.5	3870	10	BC036291	BC036291 Mus muscu	c 496	222	12.3	149801	2	CR382301	Danio rer
424	226	12.5	5171	5	BC060500	BC060500 Xenopus l	497	222	12.3	156022	2	BX324195	Danio rer
425	226	12.5	46638	3	CBU33058	CBU33058 Caenorhabdi	498	222	12.3	157314	2	CR352289	Danio rer
426	226	12.5	46996	3	U88310	U88310 Caenorhabdi	499	222	12.3	168601	3	CR352289	Danio rer
427	226	12.5	56649	3	AR003131	AR003131 Caenorhab	c 500	222	12.3	180916	2	CR381704	Danio rer
428	226	12.5	294136	2	AC006901	AC006901 Caenorhab	501	222	12.3	201070	5	EX004830	Sequence
429	226	12.5	299719	2	AC006858	AC006858 Caenorhab	502	222	12.3	271696	3	AB003835	Drosophil
430	225.5	12.5	3328	10	NMU37708	U37708 Mus musculu	503	221.5	12.3	1112	9	AB094146	Homo sapi
431	225.5	12.5	3352	10	NMU37709	U37709 Mus musculu	504	221.5	12.3	1112	10	AB092414	Mus muscu
432	225	12.5	2607	6	AX179390	AX179390 Sequence	505	221.5	12.3	5314	5	BC074401	Xenopus l
433	225	12.5	2607	6	AX259864	AX259864 Sequence	506	221	12.2	1308	3	AF456362	Caenorhab
434	225	12.5	5586	6	CQ729937	CQ729937 Sequence	507	221	12.2	4525	9	AF456362	Caenorhab
435	225	12.5	14327	9	HOMHSPGB	M85289 Human hepar	508	221	12.2	5374	9	AF289030	Homo sapi
c 436	225	12.5	39158	3	CBRG19K24	AC087734 Caenorhab	509	221	12.2	5387	9	CQ731799	Sequence
437	224.5	12.4	2404	6	CQ728038	CQ728038 Sequence	510	221	12.2	6110	9	AF023449	Homo sapi
438	224.5	12.4	2611	10	AF115401	AF115401 Mus muscu	511	221	12.2	6435	9	AF023450	Homo sapi
439	224.5	12.4	3960	6	CQ849821	CQ849821 Sequence	512	221	12.2	6435	9	AF461119	Xenopus l
440	224.5	12.4	3960	6	AK126878	AK126878 Homo sapi	513	221	12.2	6649	9	AF217525	Homo sapi
441	224.5	12.4	7642	6	CQ776627	CQ776627 Sequence	514	220.5	12.2	1011	10	AB183402	Mus muscu
442	224.5	12.4	7642	6	AX818174	AX818174 Sequence	515	220.5	12.2	1287	10	AB183400	Mus muscu



516	220.5	12.2	1329	6	BD261770	BD261770 12 human	589	218	12.1	6656	10	AF334385	AF334385 Rattus no
517	220.5	12.2	1329	9	CR457157	CR457157 Homo sapi	590	218	12.1	6829	10	AY005483	AY005483 Mus muscu
518	220.5	12.2	1338	10	AB103339	AB103339 Mus muscu	591	218	12.1	146352	2	CR548641	CR548641 Danio rer
519	220.5	12.2	1413	6	BD140567	BD140567 Polypepti	592	218	12.1	186279	5	BX950870	BX950870 Zebrafish
520	220.5	12.2	1413	6	AR429086	AR429086 Sequence	593	218	12.1	191779	2	CR376789	CR376789 Danio rer
521	220.5	12.2	1413	6	AR534977	AR534977 Sequence	594	217	12.0	3429	4	SSC459296	AJ459296 Sus scrof
522	220.5	12.2	1413	6	AX375966	AX375966 Sequence	595	217	12.0	4410	3	AY118274	AY118274 Drosophil
523	220.5	12.2	1413	9	AX358334	AX358334 Homo sapi	596	217	12.0	41345	3	CEFI15G9	Z47068 Caenorhabdi
524	220.5	12.2	1448	9	BC035930	BC035930 Homo sapi	597	216.5	12.0	3057	6	Q8442487	Q8442487 Sequence
525	220.5	12.2	1450	10	AB064265	AB064265 Mus muscu	598	216.5	12.0	3057	9	AK125460	AK125460 Homo sapi
526	220.5	12.2	1508	6	BD261716	BD261716 12 human	599	216.5	12.0	4054	3	MSU50719	U50719 Manduca sex
527	220.5	12.2	1520	6	BD261709	BD261709 12 human	600	216.5	12.0	4430	10	BC062892	BC062892 Mus muscu
528	220.5	12.2	1548	6	AX136299	AX136299 Sequence	601	216	12.0	260998	2	AC099089	AC099089 Rattus no
529	220.5	12.2	1548	6	BD123602	BD123602 Secretary	602	215.5	11.9	2957	6	CO591957	CO591957 Sequence
530	220.5	12.2	1548	9	AK075502	AK075502 Homo sapi	603	215.5	11.9	3264	3	AY119465	AY119465 Drosophil
531	220.5	12.2	1598	6	BD247472	BD247472 Molecules	604	215.5	11.9	3397	6	AX780431	AX780431 Sequence
532	220.5	12.2	1598	6	AR278813	AR278813 Sequence	605	215.5	11.9	3397	9	AF312678	AF312678 Homo sapi
533	220.5	12.2	1817	10	AF539424	AF539424 Mus muscu	606	215.5	11.9	3498	10	RNU81035	U81035 Rattus norv
534	220.5	12.2	1862	6	AX399846	AX399846 Sequence	607	215.5	11.9	3853	3	DRONRGAA	M28231 Drosophila
535	220.5	12.2	1935	6	BD247473	BD247473 Molecules	608	215.5	11.9	4041	6	CO573942	CO573942 Sequence
536	220.5	12.2	1935	6	AR278814	AR278814 Sequence	609	215.5	11.9	4044	9	BC002377	BC002377 Homo sapi
537	220.5	12.2	1958	10	BC057125	BC057125 Mus muscu	610	215.5	11.9	4044	9	BC014626	BC014626 Homo sapi
538	220.5	12.2	2024	10	AB052293	AB052293 Mus muscu	611	215.5	11.9	4433	3	AY058284	AY058284 Drosophil
539	220.5	12.2	2940	6	Q8700000	Q8700000 Sequence	612	215.5	11.9	5026	3	CO591956	CO591956 Sequence
540	220.5	12.2	4444	10	AF434663	AF434663 Mus muscu	613	215.5	11.9	8574	3	DMNRG2	AF050085 Drosophil
541	220	12.2	2845	6	Q0716675	Q0716675 Sequence	614	215.5	11.9	8883	10	AY273816	AY273816 Rattus no
542	220	12.2	4717	6	AX463544	AX463544 Sequence	615	215.5	11.9	20510	6	CO573941	CO573941 Sequence
543	220	12.2	4759	6	AX463530	AX463530 Sequence	616	215.5	11.9	62442	2	AC018325	AC018325 Drosophil
544	220	12.2	5287	9	AB050468	AB050468 Homo sapi	617	215.5	11.9	71320	2	AC020124	AC020124 Drosophil
545	220	12.2	5719	6	Q869705	Q869705 Sequence	618	215.5	11.9	165512	3	AC099010	AC099010 Drosophil
546	219.5	12.2	991	5	AF364047	AF364047 Gallus ga	619	215.5	11.9	174287	3	AC007977	AC007977 Drosophil
547	219.5	12.2	1247	5	BC078527	BC078527 Xenopus l	620	215.5	11.9	174367	3	AC023696	AC023696 Drosophil
548	219.5	12.2	1258	9	AF0005070	AF0005070 Homo sapi	621	215.5	11.9	185405	3	AC023743	AC023743 Drosophil
549	219.5	12.2	2259	6	BD204924	BD204924 Novel mol	622	215.5	11.9	270766	3	AE003615	AE003615 Drosophil
550	219.5	12.2	3512	9	AF132811	AF132811 Homo sapi	623	215.5	11.9	29686	3	AE003444	AE003444 Drosophil
551	219.5	12.2	3534	9	AF027658	AF027658 Homo sapi	624	215	11.9	1332	3	AF456363	AF456363 Caenorhab
552	219.5	12.2	4002	9	BC075829	BC075829 Homo sapi	625	215	11.9	3213	6	CO847970	CO847970 Sequence
553	219.5	12.2	4277	6	AX4576372	AX4576372 Sequence	626	215	11.9	4236	9	HSU33635	U33635 Human col
554	219.5	12.2	4277	6	AX454572	AX454572 Sequence	627	215	11.9	5067	5	AF304131	AF304131 Danio rer
555	219.5	12.2	4277	6	AX491050	AX491050 Sequence	628	214.5	11.9	4956	10	AF041082	AF041082 Rattus no
556	219.5	12.2	4277	6	AX696989	AX696989 Sequence	629	214	11.8	77635	2	DMBR40010	AL122024 Drosophil
557	219.5	12.2	4277	9	AX358328	AX358328 Homo sapi	630	213.5	11.8	1121	6	CO727036	CO727036 Sequence
558	219.5	12.2	4279	6	BD204923	BD204923 Novel mol	631	213.5	11.8	1242	9	AY046418	AY046418 Homo sapi
559	219.5	12.2	6789	9	HSU0071	Z95705 Human DNA s	632	213.5	11.8	1614	6	BD177640	BD177640 MBGP1 pol
560	219	12.1	756	6	CO729341	CO729341 Sequence	633	213.5	11.8	1614	6	E37854	E37854 MBGP1 polyp
561	219	12.1	2638	6	AX833755	AX833755 Sequence	634	213.5	11.8	1614	6	AX003003	AX003003 Sequence
562	219	12.1	2638	9	AK095729	AK095729 Homo sapi	635	213.5	11.8	1680	9	BC033819	BC033819 Homo sapi
563	219	12.1	3210	5	AB015205	AB015205 Xenopus l	636	213.5	11.8	1685	6	BD172296	BD172296 Secreted
564	219	12.1	3690	9	AF549455	AF549455 Homo sapi	637	213.5	11.8	1685	6	BD172615	BD172615 Secreted
565	219	12.1	4129	6	Q849703	Q849703 Sequence	638	213.5	11.8	1685	6	BD172934	BD172934 Secreted
566	219	12.1	4129	9	AK126745	AK126745 Homo sapi	639	213.5	11.8	1685	6	BD173253	BD173253 Secreted
567	219	12.1	4762	9	AF381545	AF381545 Homo sapi	640	213.5	11.8	1685	6	BD175287	BD175287 Secretary
568	219	12.1	4805	9	AF730707	AF730707 Homo sapi	641	213.5	11.8	1685	6	AR410665	AR410665 Sequence
569	219	12.1	4822	6	E12950	E12950 cDNA GA3-43	642	213.5	11.8	1685	6	AR439029	AR439029 Sequence
570	219	12.1	4822	10	D78572	D78572 Mus musculus	643	213.5	11.8	1685	6	AR473049	AR473049 Sequence
571	219	12.1	4832	10	Q869702	Q869702 Sequence	644	213.5	11.8	1685	6	AR527035	AR527035 Sequence
572	219	12.1	5035	5	AY090737	AY090737 Homo sapi	645	213.5	11.8	1685	6	AR528625	AR528625 Sequence
573	219	12.1	12255	5	AY584653	AY584653 Gallus ga	646	213.5	11.8	1685	6	AR566068	AR566068 Sequence
574	218.5	12.1	1425	6	CO725721	CO725721 Sequence	647	213.5	11.8	1685	6	AX454458	AX454458 Sequence
575	218.5	12.1	4015	9	BC030141	BC030141 Homo sapi	648	213.5	11.8	1685	6	AX464214	AX464214 Sequence
576	218.5	12.1	4020	6	Q8070598	Q8070598 Sequence	649	213.5	11.8	1685	6	AX490936	AX490936 Sequence
577	218.5	12.1	6922	10	NMU17793	Y17793 Mus musculu	650	213.5	11.8	1685	6	AX697492	AX697492 Sequence
578	218.5	12.1	152686	2	AC018913	AC018913 Homo sapi	651	213.5	11.8	1685	6	BD075436	BD075436 Secretary
579	218	12.1	1689	9	AB056375	AB056375 Macaca fa	652	213.5	11.8	1685	9	AX358332	AX358332 Homo sapi
580	218	12.1	1884	6	CO734341	CO734341 Sequence	653	213.5	11.8	1718	6	BD247477	BD247477 Molecules
581	218	12.1	2350	6	Q8078954	Q8078954 Sequence	654	213.5	11.8	1718	6	AR278800	AR278800 Sequence
582	218	12.1	3958	9	AF531872	AF531872 Homo sapi	655	213.5	11.8	2496	6	BD191411	BD191411 Secreted
583	218	12.1	4191	6	CO789354	CO789354 Sequence	656	213.5	11.8	3557	9	AF363367	AF363367 Homo sapi
584	218	12.1	4191	9	AF531868	AF531868 Homo sapi	657	213.5	11.8	4155	6	AX704746	AX704746 Sequence
585	218	12.1	4191	9	HSU40271	U40271 Homo sapien	658	213.5	11.8	4594	9	AB040929	AB040929 Homo sapi
586	218	12.1	4193	6	CO715771	CO715771 Sequence	659	213.5	11.8	5384	5	AF337036	AF337036 Danio rer
587	218	12.1	4238	9	BC071557	BC071557 Homo sapi	660	213	11.8	177	6	AR030585	AR030585 Sequence
588	218	12.1	6267	10	AF315558	AF315558 Mus muscu	661	213	11.8	851	5	BX932255	BX932255 Gallus ga

589	218	12.1	6656	10	AF334385	AF334385 Rattus no
590	218	12.1	6829	10	AY005483	AY005483 Mus muscu
591	218	12.1	146352	2	CR548641	CR548641 Danio rer
592	218	12.1	186279	5	BX950870	BX950870 Zebrafish
593	218	12.1	191779	2	CR376789	CR376789 Danio rer
594	217	12.0	3429	4	SSC459296	AJ459296 Sus scrof
595	217	12.0	4410	3	AY118274	AY118274 Drosophil
596	217	12.0	41345	3	CEFI15G9	Z47068 Caenorhabdi
597	216.5	12.0	3057	6	Q8442487	Q8442487 Sequence
598	216.5	12.0	3057	9	AK125460	AK125460 Homo sapi
599	216.5	12.0	4054	3	MSU50719	U50719 Manduca sex
600	216.5	12.0	4430	10	BC062892	BC062892 Mus muscu
601	216	12.0	260998	2	AC099089	AC099089 Rattus no
602	215.5	11.9	2957	6	CO591957	CO591957 Sequence
603	215.5	11.9	3264	3	AY119465	AY119465 Drosophil
604	215.5	11.9	3397	6	AX780431	AX780431 Sequence
605	215.5	11.9	3397	9	AF312678	AF312678 Homo sapi
606	215.5	11.9	3498	10	RNU81035	U81035 Rattus norv
607	215.5	11.9	3853	3	DRONRGAA	M28231 Drosophila
608	215.5	11.9	4041	6	CO573942	CO573942 Sequence
609	215.5	11.9	4044	9	BC002377	BC002377 Homo sapi
610	215.5	11.9	4044	9	BC014626	BC014626 Homo sapi
611	215.5	11.9	4433	3	AY058284	AY058284 Drosophil
612	215.5	11.9	5026	3	CO591956	CO591956 Sequence
613	215.5	11.9	8574	3	DMNRG2	AF050085 Drosophil
614	215.5	11.9	8883	10	AY273816	AY273816 Rattus no
615	215.5	11.9	20510	6	CO573941	CO573941 Sequence
616	215.5	11.9	62442	2	AC018325	AC018325 Drosophil</

662	213	11.8	1605	6	CQ59856	Sequence	735	209	11.6	3402	6	AX080803	Sequence
663	213	11.8	1892	5	AB117614	Xenopus 1	736	209	11.6	3402	6	AX191426	Sequence
664	213	11.8	2043	6	C0717926	Sequence	737	209	11.6	3402	6	AX401321	Sequence
665	213	11.8	4381	10	AK173340	Mus muscu	738	209	11.6	3402	9	AY358303	Homo sapi
666	213	11.8	4479	5	AF538326	AF538326	739	208.5	11.5	2811	10	AF487347	Mus muscu
667	212.5	11.8	2650	10	AF102134	Mus muscu	740	208.5	11.5	3448	10	MUSNGP	101991 Mus muscu
668	212.5	11.8	2732	10	NMBTG2A	X99043 M.musculus	741	208.5	11.5	3678	3	BT014656	BT014656 Drosophi
669	212.5	11.8	4071	9	AF531869	Homo sapi	742	208.5	11.5	4956	6	BD085989	BD085989 Method of
670	212.5	11.8	4631	9	HSU72391	Human neoge	743	208.5	11.5	4956	9	AF040990	AF040990 Homo sapi
671	212.5	11.8	5021	6	C0729613	Sequence	744	208.5	11.5	5667	6	CQ606753	CQ606753 Sequence
672	212	11.7	177	6	AR030586	Sequence	745	208	11.5	6592	6	CQ598305	Sequence
673	212	11.7	3752	10	AY061639	Rattus no	746	208	11.5	152024	2	CR407703	CR407703 Danio rer
674	212	11.7	4609	10	RNU35371	U35371 Rattus norv	747	207.5	11.5	2220	6	AX748214	AX748214 Sequence
675	211.5	11.7	2818	3	DROFAS2A	MT7165 D.melanogas	748	207.5	11.5	2220	9	AK093583	AK093583 Homo sapi
676	211.5	11.7	2901	3	BT014661	BT014661 Drosophi	749	207.5	11.5	188751	10	AC122038	AC122038 Mus muscu
677	211.5	11.7	3070	3	DROFAS2B	MT7165 D.melanogas	750	207.5	11.5	247498	10	AC135238	AC135238 Mus muscu
678	211.5	11.7	3132	10	MNNSK22	X86445 M.musculus	751	207	11.5	2735	6	CQ728959	Sequence
679	211.5	11.7	3257	10	MMNSK21	X86444 M.musculus	752	207	11.5	2846	6	AX834922	AX834922 Sequence
680	211.5	11.7	3414	6	CQ579258	CQ579258 Sequence	753	207	11.5	2846	9	AK097633	Homo sapi
681	211.5	11.7	3798	10	AF398037	AF398037 Mus muscu	754	207	11.5	5175	6	CQ585188	Sequence
682	211.5	11.7	4376	10	BC078631	BC078631 Mus muscu	755	207	11.5	36654	2	AC017551	AC017551 Drosophi
683	211.5	11.7	4460	2	AC020249	AC020249 Drosophi	756	207	11.5	177736	3	AC005714	AC005714 Drosophi
684	211.5	11.7	5297	6	AX587800	AX587800 Sequence	757	207	11.5	151467	3	AC008348	AC008348 Drosophi
685	211.5	11.7	5297	6	AX771417	AX771417 Sequence	758	207	11.5	307323	3	AE003457	AE003457 Drosophi
686	211.5	11.7	5297	9	HSU61262	U61262 Human neoge	759	206.5	11.4	980	9	BC013797	BC013797 Homo sapi
687	211.5	11.7	5506	6	AR447897	AR447897 Sequence	760	206	11.4	3762	3	AF456361	AF456361 Caenorhab
688	211.5	11.7	6168	3	DMSEGD007	AL033125 Drosophi	761	205.5	11.4	708	5	CR385737	CR385737 Gallus ga
689	211.5	11.7	165928	3	AC023725	AC023725 Drosophi	762	205.5	11.4	1542	6	BD193028	BD193028 207 human
690	211.5	11.7	172784	3	AC105352	AC105352 Drosophi	763	205.5	11.4	1542	6	CQ822024	Sequence
691	211.5	11.7	295177	3	AE003430	AE003430 Drosophi	764	205.5	11.4	2067	10	AY210400	AY210400 Mus muscu
692	211	11.7	1273	6	AR278799	AR278799 Sequence	765	205.5	11.4	2539	6	CQ782770	Sequence
693	211	11.7	2377	10	AF195662	AF195662 Mus muscu	766	205.5	11.4	2539	6	BD127305	BD127305 Primer fo
694	211	11.7	3366	10	AY059393	AY059393 Mus muscu	767	205.5	11.4	2539	9	AK074825	AK074825 Homo sapi
695	211	11.7	5563	9	AF068603	AF068603 Homo sapi	768	205.5	11.4	4128	10	RNU11031	U11031 Rattus norv
696	211	11.7	5719	9	AF069601	AF069601 Homo sapi	769	205.5	11.4	4465	10	MMU543322	MMU543322 Mus muscu
697	211	11.7	20435	9	HSAGJ2535	HSAGJ2535 Homo sapi	770	205.5	11.4	5071	10	AK129207	AK129207 Mus muscu
698	210.5	11.7	1837	6	CQ869997	CQ869997 Sequence	771	205.5	11.4	53424	3	AB055861	AB055861 Procambar
699	210.5	11.7	3231	6	CQ724644	CQ724644 Sequence	772	205	11.4	1299	6	CQ728323	CQ728323 Sequence
700	210.5	11.7	5913	6	CQ869760	CQ869760 Sequence	773	205	11.4	1820	6	BD247476	BD247476 Molecules
701	210	11.6	577	6	AR496051	AR496051 Sequence	774	205	11.4	1820	6	AR278798	AR278798 Sequence
702	210	11.6	4078	6	AR511333	AR511333 Sequence	775	205	11.4	2540	9	AF062733	AF062733 Homo sapi
703	210	11.6	4078	6	AR270557	AR270557 Sequence	776	204.5	11.3	2096	6	CQ579750	Sequence
704	210	11.6	5193	4	AF509585	Sus scrofa	777	204.5	11.3	2111	5	AF035677	AF035677 Gallus ga
705	210	11.6	5193	4	AF598036	AF598036 Sequence	778	204.5	11.3	4641	10	RNU68726	U68726 Rattus norv
706	210	11.6	5193	6	AF598038	AF598038 Sequence	779	204.5	11.3	6860	5	AF304130	AF304130 Danio rer
707	210	11.6	5745	9	AF339601	AF339601 Homo sapi	780	204.5	11.3	83495	5	BC087076	BC087076 Caenorhab
708	210	11.6	5770	9	AF069602	AF069602 Homo sapi	781	204	11.3	1038	5	BC083011	BC083011 Xenopus 1
709	210	11.6	5896	9	BC064695	BC064695 Homo sapi	782	204	11.3	4517	10	MMDCCTSG	X85788 M.musculus
710	210	11.6	5926	6	AR482482	AR482482 Sequence	783	204	11.3	4784	5	GDU07644	GDU07644 Gallus gall
711	210	11.6	5926	6	AX329738	AX329738 Sequence	784	204	11.3	5211	6	CQ870291	Sequence
712	210	11.6	5926	6	AX330278	AX330278 Sequence	785	204	11.3	5892	6	CQ588164	Sequence
713	210	11.6	5926	6	AX333040	AX333040 Sequence	786	204	11.3	20686	2	AC017508	AC017508 Drosophi
714	210	11.6	5926	6	AX337264	AX337264 Sequence	787	204	11.3	149752	2	AC004616	AC004616 Homo sapi
715	210	11.6	5926	6	AX375038	AX375038 Sequence	788	204	11.3	174920	3	AC010701	AC010701 Drosophi
716	210	11.6	5926	6	AX410725	AX410725 Sequence	789	204	11.3	294272	3	AE003595	AE003595 Drosophi
717	210	11.6	5926	6	HSU48959	U48959 Homo sapien	790	203.5	11.3	4435	5	AF388035	AF388035 Xenopus 1
718	210	11.6	5992	10	BC058610	BC058610 Mus muscu	791	203.5	11.3	5824	6	AR338581	AR338581 Sequence
719	209.5	11.6	7644	6	CQ727360	CQ727360 Sequence	792	203.5	11.3	6811	9	AF334384	AF334384 Homo sapi
720	209.5	11.6	17193	6	CQ583538	CQ583538 Sequence	793	203.5	11.3	6834	9	AB032958	AB032958 Homo sapi
721	209.5	11.6	58651	2	AC017558	AC017558 Drosophi	794	203.5	11.3	6899	9	AF491813	AF491813 Homo sapi
722	209.5	11.6	69992	3	AC005421	AC005421 Drosophi	795	203	11.2	2749	5	DRE574916	DRE574916 Danio rer
723	209.5	11.6	189315	3	AC008319	AC008319 Drosophi	796	203	11.2	2774	5	BC053245	BC053245 Danio rer
724	209.5	11.6	306696	3	AE003586	AE003586 Drosophi	797	203	11.2	4248	6	AX054979	AX054979 Sequence
725	209	11.6	1248	6	CQ725953	CQ725953 Sequence	798	203	11.2	4775	3	CEU70618	U70618 Caenorhabdi
726	209	11.6	1450	6	AX287596	AX287596 Sequence	799	203	11.2	6021	10	AY237726	AY237726 Mus muscu
727	209	11.6	1489	9	AK172829	AK172829 Homo sapi	800	203	11.2	18524	6	CQ730656	CQ730656 Sequence
728	209	11.6	1565	9	AF279689	AF279689 Homo sapi	801	202.5	11.2	2697	6	CQ728585	Sequence
729	209	11.6	3080	6	AX287610	AX287610 Sequence	802	202.5	11.2	3801	9	AF531870	AF531870 Homo sapi
730	209	11.6	3080	9	HSAG277437	HSAG277437 Homo sapi	803	202.5	11.2	4340	3	AV118645	AV118645 Drosophi
731	209	11.6	3112	6	AX287608	AX287608 Sequence	804	202.5	11.2	8487	6	CQ717135	Sequence
732	209	11.6	3145	6	CQ870833	CQ870833 Sequence	805	202.5	11.2	9645	6	CQ875263	Sequence
733	209	11.6	3305	9	BC036769	BC036769 Homo sapi	806	202.5	11.2	9645	9	AF245505	AF245505 Homo sapi
734	209	11.6	3402	6	AR252460	AR252460 Sequence	807	202.5	11.2	35347	3	CET09B9	Z47070 Caenorhabdi

808	202	11.2	2472	6	CQ592467	Sequence	CQ592467	881	197	10.9	5292	10	AB0933285	AB0933285 Mus muscu
809	202	11.2	2844	5	AY143173	Gallus ga	AY143173	882	197	10.9	43940	3	AY686597	AY686597 Drosophil
810	202	11.2	2847	10	BC052773	Mus muscu	BC052773	883	196.5	10.9	1559	5	CR354016	CR354016 Gallus ga
811	202	11.2	3822	3	AF041053	Caenorhab	AF041053	884	196.5	10.9	3284	6	AX443486	AX443486 Sequence
812	202	11.2	5604	5	AF394058	Danio rer	AF394058	885	196.5	10.9	3651	10	RNU81036	U81036 Rattus norv
813	202	11.2	5680	5	AY082380	Danio rer	AY082380	886	196.5	10.9	4041	5	CGNEUFASC	X65224 G.gallus mr
814	202	11.2	6300	5	AY029280	Danio rer	AY029280	887	196.5	10.9	5822	10	RATANKBEIND	L11002 Rat ankyrin
815	201.5	11.2	1161	6	AX645013	Sequence	AX645013	888	196.5	10.9	6218	9	AB002341	AB002341 Homo sapi
816	201.5	11.2	1307	6	AX512897	Sequence	AX512897	889	196.5	10.9	6219	6	CQ716062	CQ716062 Sequence
817	201.5	11.2	1514	6	AX645011	Sequence	AX645011	890	196.5	10.9	6254	6	BD190781	BD190781 Secreted
818	201.5	11.2	2176	9	AF363368	Homo sapi	AF363368	891	196.5	10.9	6254	6	AX099489	AX099489 Sequence
819	201.5	11.2	2859	6	CQ576375	Sequence	CQ576375	892	196.5	10.9	6384	6	AR448063	AR448063 Sequence
820	201.5	11.2	10242	6	CQ600663	Sequence	CQ600663	c 893	196.5	10.9	6384	6	AR531706	AR531706 Sequence
821	201.5	11.2	10801	10	AF215896	Mus muscu	AF215896	c 894	196.5	10.9	168144	2	CR792456	CR792456 Danio rer
822	201.5	11.2	12603	6	CQ589875	Sequence	CQ589875	895	196	10.9	1064	6	CQ870296	CQ870296 Sequence
823	201.5	11.2	13041	3	DME487018	Sequence	DME487018	896	196	10.9	2351	10	RN0536020	AX536020 Rattus no
824	201	11.1	3400	5	FSCT8KA	L11311 Torpedo cal	L11311 Torpedo cal	897	196	10.9	7631	5	GGFWYLCK	X52876 G.gallus mr
825	201	11.1	3405	5	GA535114	Gallus ga	GA535114	898	196	10.9	96468	2	AC006902	AC006902 Caenorhab
826	201	11.1	4521	9	AK024462	Homo sapi	AK024462	899	195.5	10.8	479	6	AX665358	AX665358 Sequence
827	201	11.1	5130	9	AF230073	Homo sapi	AF230073	900	195.5	10.8	2898	6	CQ587259	CQ587259 Sequence
828	201	11.1	252070	2	AC098426	Sequence	AC098426	901	195	10.8	2313	9	AK097802	AK097802 Homo sapi
829	200.5	11.1	1103	6	CQ728252	Sequence	CQ728252	902	195	10.8	3384	6	AX714308	AX714308 Sequence
830	200.5	11.1	4119	5	AY376856	Danio rer	AY376856	903	195	10.8	3384	6	AK056544	AK056544 Homo sapi
831	200.5	11.1	5414	10	MNMOGEN	Y09535 M.musculus	Y09535 M.musculus	904	195	10.8	4381	6	CQ869962	CQ869962 Sequence
832	200.5	11.1	177476	9	AC010680	Homo sapi	AC010680	905	195	10.8	4569	9	AY509035	AY509035 Homo sapi
833	200.5	11.1	294540	9	HSAT277892	Sequence	HSAT277892	906	195	10.8	5865	3	DMU71001	DMU71001 Drosophila
834	200	11.1	1967	6	AR156834	Sequence	AR156834	907	195	10.8	6279	6	CQ590850	CQ590850 Sequence
835	200	11.1	1967	6	BD269852	The poly	BD269852	908	195	10.8	6318	3	DMU71002	DMU71002 Drosophila
836	200	11.1	2193	10	MUSPGCBMA	J04055 Mouse basem	J04055 Mouse basem	909	195	10.8	37091	6	CQ590849	CQ590849 Sequence
837	200	11.1	2274	10	MMU293947	Mus muscu	MMU293947	c 910	195	10.8	52726	2	AC017352	AC017352 Drosophil
838	200	11.1	2277	6	AX287593	Sequence	AX287593	911	195	10.8	189557	3	AC007356	AC007356 Drosophil
839	200	11.1	2339	10	BC058745	Mus muscu	BC058745	912	195	10.8	221235	3	AC009695	AC009695 Rattus no
840	200	11.1	2359	10	AF321300	Mus muscu	AF321300	c 913	195	10.8	251435	2	AC128510	AC128510 Rattus no
841	199.5	11.0	2173	9	CQ6068457	Homo sapi	CQ6068457	c 914	195	10.8	264547	2	AC094432	AC094432 Rattus no
842	199.5	11.0	3727	6	CQ726408	Sequence	CQ726408	915	195	10.8	294169	3	AE003821	AE003821 Drosophil
843	199.5	11.0	4924	10	RN0588725	U68725 Rattus norv	U68725 Rattus norv	916	194.5	10.8	3211	3	BT001692	BT001692 Drosophil
844	199.5	11.0	5443	10	BC054540	Mus muscu	BC054540	917	194.5	10.8	173690	2	AC011307	AC011307 Homo sapi
845	199.5	11.0	7855	9	AK122586	Homo sapi	AK122586	918	194.5	10.8	178137	9	AC011302	AC011302 Homo sapi
846	199	11.0	2943	10	AY167411	Sequence	AY167411	919	194	10.7	3783	6	AR177819	AR177819 Sequence
847	199	11.0	3726	9	AF190637	Homo sapi	AF190637	920	194	10.7	3783	10	MMNCAM1	X12875 Mouse mRNA
848	199	11.0	4285	6	AR140634	Sequence	AR140634	921	194	10.7	5038	10	BC056988	BC056988 Mus muscu
849	199	11.0	4285	9	AF035835	Homo sapi	AF035835	922	194	10.7	216540	5	BX322647	BX322647 Zebrafish
850	199	11.0	4287	6	CQ721176	Sequence	CQ721176	923	193.5	10.7	826	6	CQ780202	CQ780202 Sequence
851	199	11.0	4871	5	AF337035	Danio rer	AF337035	924	193.5	10.7	826	6	CQ781611	CQ781611 Sequence
852	198.5	11.0	4285	6	CQ607487	Sequence	CQ607487	925	193.5	10.7	826	6	BD124911	BD124911 Primer fo
853	198.5	11.0	6645	10	AK131182	Mus muscu	AK131182	926	193.5	10.7	826	6	BD126320	BD126320 Primer fo
854	198.5	11.0	6729	9	AF304304	Homo sapi	AF304304	927	193.5	10.7	2499	6	CQ583689	CQ583689 Sequence
855	198.5	11.0	48870	2	AC017807	Drosophil	AC017807	928	193.5	10.7	4486	10	MMU543321	MMU543321 Mus muscu
856	198.5	11.0	155666	3	AC007854	Drosophil	AC007854	929	193.5	10.7	4944	10	BC055053	BC055053 Mus muscu
857	198.5	11.0	168471	3	AC006170	Sequence	AC006170	930	193.5	10.7	5608	10	AK122252	AK122252 Mus muscu
858	198.5	11.0	231562	3	AE003767	Drosophil	AE003767	931	193.5	10.7	5925	6	AX921879	AX921879 Sequence
859	198	11.0	3233	6	CQ721186	Sequence	CQ721186	932	193	10.7	2687	3	DME312133	DME312133 Drosophil
860	198	11.0	3260	9	HSRNCAD22	X59350 H.sapiens m	X59350 H.sapiens m	933	193	10.7	3858	5	BC057728	BC057728 Xenopus l
861	198	11.0	4844	6	CQ728171	Sequence	CQ728171	934	193	10.7	4579	3	DME312134	DME312134 Drosophil
862	198	11.0	199446	10	AC125069	Mus muscu	AC125069	935	193	10.7	4846	5	XLU10986	XLU10986 Xenopus lae
863	198	11.0	202887	10	AL928789	Mouse DNA	AL928789	936	193	10.7	4901	9	HSM803665	HSM803665 Homo sapi
864	198	11.0	255090	2	AC033798	Mus muscu	AC033798	937	193	10.7	5099	3	DME312135	DME312135 Drosophil
865	197.5	10.9	1416	5	BX932504	Gallus ga	BX932504	938	193	10.7	5194	3	BT010247	BT010247 Drosophil
866	197.5	10.9	1861	10	AF061260	Mus muscu	AF061260	939	193	10.7	7606	3	DROLARM	DROLARM D.melanogas
867	197.5	10.9	2526	9	HUMDDC	M32292 Human color	M32292 Human color	940	193	10.7	7928	6	AK039412	AK039412 Sequence
868	197.5	10.9	3255	6	CQ715490	Sequence	CQ715490	941	192.5	10.7	2481	6	AR237560	AR237560 Sequence
869	197.5	10.9	4305	6	CQ613728	Sequence	CQ613728	942	192.5	10.7	2715	6	AR237555	AR237555 Sequence
870	197.5	10.9	4344	6	AX054981	Sequence	AX054981	943	192.5	10.7	2724	6	AR237562	AR237562 Sequence
871	197.5	10.9	4608	6	AR153583	Sequence	AR153583	944	192.5	10.7	2958	6	AR237557	AR237557 Sequence
872	197.5	10.9	4608	9	HSDDCG	X76132 H.sapiens D	X76132 H.sapiens D	945	192.5	10.7	2976	6	AR237558	AR237558 Sequence
873	197.5	10.9	4715	3	AY121698	Drosophil	AY121698	946	192.5	10.7	3192	6	BD270852	BD270852 Pollistat
874	197.5	10.9	4726	3	AF210316	Drosophil	AF210316	947	192.5	10.7	3192	6	AR200355	AR200355 Sequence
875	197.5	10.9	4955	9	AB018239	Homo sapi	AB018239	948	192.5	10.7	3210	6	AR237553	AR237553 Sequence
876	197.5	10.9	5013	6	CQ870298	Sequence	CQ870298	949	192.5	10.7	3219	6	AR237561	AR237561 Sequence
877	197.5	10.9	5019	6	CQ870300	Sequence	CQ870300	950	192.5	10.7	3453	6	AR237556	AR237556 Sequence
878	197	10.9	2462	6	AX746553	Sequence	AX746553	951	192.5	10.7	3874	6	AR237568	AR237568 Sequence
879	197	10.9	2462	9	AK090639	Homo sapi	AK090639	952	192.5	10.7	3942	5	CHKBRVO	L08960 Chicken cel
880	197	10.9	3894	6	BD085988	Method of	BD085988	953	192.5	10.7	3943	5	GGNRACAM	X58482 Chicken mRN

954	192.5	10.7	3943	6	AR177825	AR177825 Sequence	c1027	188	10.4	143593	5	BX248311	BX248311 Zebrafish
955	192.5	10.7	4437	6	CQ777490	CQ777490 Sequence	1028	188	10.4	181728	3	AC008003	AC008003 Drosophila
956	192.5	10.7	4437	10	MWLL1L	X943110 M.musculus	c1029	188	10.4	185967	2	BX640499	BX640499 Danio rerio
957	192	10.6	1463	9	AX098838	AX098838 Homo sapi	1030	188	10.4	290034	3	AE003577	AE003577 Drosophila
958	192	10.6	2094	6	AR508344	AR508344 Sequence	1031	187.5	10.4	770	3	CR386810	CR386810 Gallus ga
959	192	10.6	2143	9	BC031063	BC031063 Homo sapi	1032	187.5	10.4	3311	9	AY302131	AY302131 Homo sapi
960	192	10.6	2256	6	AX747900	AX747900 Sequence	1033	187.5	10.4	3914	10	AF090866	AF090866 Mus muscu
961	192	10.6	2256	9	AX093069	AX093069 Homo sapi	1034	187.5	10.4	3991	5	GGNGCAM	GGNGCAM Chicken mRN
962	192	10.6	3450	3	AY095040	AY095040 Drosophila	1035	187.5	10.4	3991	6	AR177805	AR177805 Sequence
963	192	10.6	3531	6	CQ735712	CQ735712 Sequence	1036	187	10.4	1627	6	AX805542	AX805542 Sequence
964	192	10.6	3738	6	CQ715811	CQ715811 Sequence	1037	187	10.4	1746	6	CQ728058	CQ728058 Sequence
965	192	10.6	3864	6	CQ715175	CQ715175 Sequence	1038	187	10.4	1825	10	AF487345	AF487345 Mus muscu
966	192	10.6	3900	9	HSC7NRCAM	AY001057 Homo sapi	1039	187	10.4	2155	6	AX805540	AX805540 Sequence
967	192	10.6	3997	6	AR7637	AR7637 Sequence 1	1040	187	10.4	2337	9	AF480410	AF480410 Homo sapi
968	192	10.6	4134	9	H8U55258	U52528 Human hBRV	1041	187	10.4	2476	6	AX376518	AX376518 Sequence
969	192	10.6	4239	6	CQ572460	CQ572460 Sequence	1042	187	10.4	2476	9	AY358743	AY358743 Homo sapi
970	192	10.6	4300	3	AY229991	AY229991 Drosophila	1043	187	10.4	3354	5	BC044264	BC044264 Xenopus 1
971	192	10.6	4573	10	AF004840	AF004840 Rattus no	1044	187	10.4	3562	6	AX179302	AX179302 Sequence
972	192	10.6	5103	6	AX399250	AX399250 Sequence	1045	187	10.4	3808	9	BD185197	BD185197 Novel gen
973	192	10.6	5598	9	AB046788	AB046788 Homo sapi	1046	187	10.4	3808	9	AB058770	AB058770 Homo sapi
974	192	10.6	6240	9	HSM806153	BX538010 Homo sapi	1047	187	10.4	4346	10	BC055333	BC055333 Mus muscu
975	191.5	10.6	3650	10	AF182037	AF182037 Rattus no	1048	187	10.4	5037	5	AF180354	AF180354 Danio rerio
976	191.5	10.6	4171	10	BC060226	BC060226 Mus muscu	1049	187	10.4	5789	6	AX923367	AX923367 Sequence
977	191.5	10.6	61468	2	AC149898	AC149898 Xenopus t	1050	187	10.4	7100	3	AF205357	AF205357 Drosophila
978	191	10.6	1221	9	BC008124	BC008124 Homo sapi	1051	187	10.4	9530	5	AY578914	AY578914 Danio rer
979	191	10.6	1806	6	AX662327	AX662327 Sequence	1052	186.5	10.3	972	6	CQ611625	CQ611625 Sequence
980	190.5	10.5	1788	6	AX287613	AX287613 Sequence	1053	186.5	10.3	4214	9	AF004841	AF004841 Homo sapi
981	190.5	10.5	1972	10	AY059394	AY059394 Mus muscu	1054	186.5	10.3	4705	5	DRU23839	DRU23839
982	190.5	10.5	4044	10	RNU81037	U81037 Rattus norv	1055	186	10.3	1782	6	AX521482	AX521482 Sequence
983	190.5	10.5	7241	10	AY574276	AY574276 Rattus no	1056	186	10.3	2959	6	AX521478	AX521478 Sequence
984	190.5	10.5	7250	10	AY574273	AY574273 Rattus no	1057	186	10.3	2973	6	AX376516	AX376516 Sequence
985	190.5	10.5	7253	10	AY574274	AY574274 Rattus no	1058	186	10.3	2973	9	AY358742	AY358742 Homo sapi
986	190.5	10.5	7277	10	AY574275	AY574275 Rattus no	1059	186	10.3	3551	9	BC039269	BC039269 Sequence
987	190.5	10.5	7286	10	AY574272	AY574272 Rattus no	1060	186	10.3	4398	5	BC073282	BC073282 Xenopus 1
988	190.5	10.5	7556	10	AY574277	AY574277 Rattus no	c1061	186	10.3	4734	6	CQ592466	CQ592466 Sequence
989	190.5	10.5	15244	3	AB026845	AB026845 Drosophila	1062	186	10.3	5749	9	AK090455	AK090455 Homo sapi
990	190.5	10.5	15272	6	CQ575028	CQ575028 Sequence	1063	186	10.3	7792	3	BT003586	BT003586 Drosophila
991	190	10.5	2857	10	BC044882	BC044882 Mus muscu	1064	186	10.3	60978	2	AC017675	AC017675 Drosophila
992	190	10.5	5381	3	AF312579	AF312579 Drosophila	c1065	186	10.3	209071	3	AC005285	AC005285 Drosophila
993	190	10.5	6055	6	AR489887	AR489887 Sequence	1066	186	10.3	214621	3	AC093100	AC093100 Drosophila
994	190	10.5	6055	10	MUSRTKB	L07237 Mus musculu	c1067	186	10.3	280096	3	AE003613	AE003613 Drosophila
995	190	10.5	6275	10	D88689	D88689 Mus musculu	1068	185.5	10.3	1223	3	BD176670	BD176670 Soluble R
996	190	10.5	7630	6	CQ614817	CQ614817 Sequence	1069	185.5	10.3	1223	9	AB061668	AB061668 Homo sapi
997	190	10.5	90803	5	AL732421	AL732421 Zebrafish	1070	185.5	10.3	1268	9	AB036432	AB036432 Homo sapi
998	190	10.5	125293	2	CQ073582	CQ073582 Homo sapi	1071	185.5	10.3	1436	9	BC020669	BC020669 Homo sapi
999	189.5	10.5	1302	6	CQ591387	CQ591387 Sequence	1072	185.5	10.3	1451	9	AB061669	AB061669 Homo sapi
1000	189.5	10.5	1981	3	AY089628	AY089628 Drosophila	1073	185.5	10.3	2019	6	AX505112	AX505112 Sequence
1001	189.5	10.5	2525	3	APLCAMD12	M89648 Aplysia cal	1074	185.5	10.3	2031	6	A39900	A39900 Sequence 2
1002	189.5	10.5	2725	3	APLCAMD15	M89649 Aplysia cal	1075	185.5	10.3	2031	6	167748	167748 Sequence 2
1003	189.5	10.5	3284	3	DMTITIN1	AF045775 Drosophila	1076	185.5	10.3	2059	6	AX805534	AX805534 Sequence 35
1004	189.5	10.5	3284	3	AY102651	AY102651 Drosophila	1077	185.5	10.3	2097	6	AA3169	AA3169 Sequence
1005	189.5	10.5	3493	3	GPLCAMD19	M89650 Aplysia cal	1078	185.5	10.3	2097	6	AR079553	AR079553 Sequence
1006	189.5	10.5	3843	5	GGNGCMVA	Z75013 G.gallus mR	1079	185.5	10.3	2109	6	CQ859390	CQ859390 Sequence
c1007	189.5	10.5	7412	6	CQ572459	CQ572459 Sequence	1080	185.5	10.3	2109	6	AX133977	AX133977 Sequence
1008	189.5	10.5	33855	2	AC014874	AC014874 Drosophila	1081	185.5	10.3	2109	6	AX468838	AX468838 Sequence
1009	189.5	10.5	151500	3	AC008355	AC008355 Drosophila	1082	185.5	10.3	2140	6	AX805538	AX805538 Sequence
1010	189.5	10.5	169511	3	AC007531	AC007531 Drosophila	1083	185.5	10.3	2160	6	AX805536	AX805536 Sequence
1011	189.5	10.5	29749	3	AE003606	AE003606 Drosophila	1084	185.5	10.3	2220	6	AR044683	AR044683 Sequence
1012	189	10.5	2250	3	AY724774	AY724774 Caenorhab	1085	185.5	10.3	2349	6	AR052808	AR052808 Sequence
1013	189	10.5	3801	5	CAU55211	U52211 Carassius a	1086	185.5	10.3	2349	6	AR288121	AR288121 Sequence
1014	188.5	10.4	3305	6	CQ608559	CQ608559 Sequence	1087	185.5	10.3	2349	6	AR567108	AR567108 Sequence
1015	188.5	10.4	3099	5	AY138255	AY138255 Danio rer	1088	185.5	10.3	2434	6	AR052807	AR052807 Sequence
1016	188.5	10.4	6096	9	AF304305	AF304305 Homo sapi	1089	185.5	10.3	2434	6	AR288120	AR288120 Sequence
1017	188.5	10.4	98613	2	AC139630	AC139630 Takifugu	1090	185.5	10.3	2434	6	AR567107	AR567107 Sequence
1018	188	10.4	1218	6	CQ730900	CQ730900 Sequence	1091	185.5	10.3	2839	6	I08156	I08156 Sequence 2
1019	188	10.4	1263	10	AY017368	AY017368 Mus muscu	1092	185.5	10.3	2839	6	I08166	I08166 Sequence 8
1020	188	10.4	2228	10	BC023765	BC023765 Mus muscu	1093	185.5	10.3	2888	9	BC034671	BC034671 Homo sapi
1021	188	10.4	2384	10	AY243095	AY243095 Mus muscu	1094	185.5	10.3	2928	6	E01630	E01630 cDNA encodi
1022	188	10.4	3369	6	CQ598917	CQ598917 Sequence	1095	185.5	10.3	2928	6	E13123	E13123 Human gen
1023	188	10.4	4494	5	BC072835	BC072835 Xenopus 1	1096	185.5	10.3	2929	9	HUMCEA	HUMCEA Human carci
1024	188	10.4	5028	2	AC014370	AC014370 Drosophila	1097	185.5	10.3	2974	6	CQ833969	CQ833969 Sequence
1025	188	10.4	5093	10	RNNCAMLI	X59149 Rat mRNA fo	1098	185.5	10.3	2974	6	AX332574	AX332574 Sequence
c1026	188	10.4	5589	6	CQ580169	CQ580169 Sequence	1099	185.5	10.3	2974	6	AX409670	AX409670 Sequence

1100	185.5	10.3	2974	6	AX658324	Sequence	1173	182	10.1	3475	3	AF303661	AF303661
1101	185.5	10.3	2974	6	AX677147	Sequence	1174	182	10.1	3906	5	AY056466	AY056466
1102	185.5	10.3	2974	6	AX805532	Sequence	1175	182	10.1	63209	2	CQ598304	CQ598304
1103	185.5	10.3	2974	9	HUMCRAP	M29540 Human carci	1176	182	10.1	65758	2	AC019956	AC019956
1104	185.5	10.3	3036	6	CQ800159	Sequence	1177	182	10.1	172641	3	AC009739	AC009739
1105	185.5	10.3	3036	9	HUMANTCE	M17303 Human carci	1178	182	10.1	286426	3	AE003841	AE003841
1106	185.5	10.3	6215	6	AX556709	Sequence	1179	181.5	10.0	1364	3	MOTP4A	M64346 Manduca sex
1107	185.5	10.3	105000	6	BS000599	Pan trogl	1180	181.5	10.0	3009	6	AX060540	AX060540
1108	185.5	10.3	173078	9	AC146249	Pan trogl	1181	181.5	10.0	3146	10	AF026465	AF026465
1109	185.5	10.3	171719	5	AX950396	Gallus ga	1182	181.5	10.0	3198	10	BC053057	BC053057
1110	185.5	10.2	2092	9	HSCEAASP	X16455 Human mRNA	1183	181.5	10.0	3379	6	AX359721	AX359721
1111	185.5	10.2	2106	6	AX133657	Sequence	1184	181.5	10.0	3430	6	AX359719	AX359719
1112	185.5	10.2	2106	6	AX192349	Sequence	1185	181.5	10.0	4122	5	DRNADML1	DRNADML1
1113	185.5	10.2	2370	10	AY249056	Rattus norv	1186	181	10.0	4260	6	AX665356	AX665356
1114	185.5	10.2	2370	10	AF480411	Mus muscu	1187	181	10.0	1764	6	CQ728797	CQ728797
1115	185.5	10.2	3585	10	BC063072	Sequence	1188	181	10.0	1859	6	AX179640	AX179640
1116	185.5	10.2	4146	6	BD085987	Sequence	1189	181	10.0	1952	6	CQ095169	CQ095169
1117	185.5	10.2	4992	6	CQ869959	Sequence	1190	181	10.0	1952	6	CQ133915	CQ133915
1118	185.5	10.2	5259	10	AF060570	Mus muscu	1191	181	10.0	1952	6	CQ172446	CQ172446
1119	185.5	10.2	135055	2	AC010056	Drosophil	1192	181	10.0	1952	6	CQ201614	CQ201614
1120	185.5	10.2	135055	2	AC011909	Drosophil	1193	181	10.0	1952	6	CQ217152	CQ217152
1121	185.5	10.2	184266	2	AX571737	Drosophil	1194	181	10.0	1952	6	CQ255729	CQ255729
1122	184.5	10.2	198	6	AR030587	Sequence	1195	181	10.0	1952	6	CQ292826	CQ292826
1123	184.5	10.2	198	6	AR030588	Sequence	1196	181	10.0	1952	6	CQ329804	CQ329804
1124	184.5	10.2	1391	6	AX321600	Sequence	1197	181	10.0	2944	6	AX747451	AX747451
1125	184.5	10.2	1391	6	HUMRAGE	Sequence	1198	181	10.0	2944	6	AK092284	AK092284
1126	184.5	10.2	2139	5	CQ073724	Xenopus l	1199	181	10.0	3153	9	HSM804421	HSM804421
1127	184.5	10.2	3015	9	CQ842363	Sequence	1200	181	10.0	3261	3	AF456360	AF456360
1128	184.5	10.2	3015	9	AX123850	Homo sapi	1201	181	10.0	3570	9	HSM803401	HSM803401
1129	184.5	10.2	9282	9	AX603755	Homo sapi	1202	181	10.0	4591	9	HSM803659	HSM803659
1130	184	10.2	1524	6	CQ827992	Sequence	1203	181	10.0	4988	9	HSM806135	HSM806135
1131	184	10.2	1818	9	AY017369	Homo sapi	1204	181	10.0	5929	9	HSM804605	HSM804605
1132	184	10.2	2013	10	RATWAG	M14871 Rat myelin-	1205	181	10.0	11008	3	AF078161	AF078161
1133	184	10.2	2348	10	RATWAGB	X05301 Rat mRNA fo	1206	181	10.0	113063	2	AC010946	AC010946
1134	184	10.2	2468	10	RATWAGB	M22357 Rat LB236/m	1207	181	10.0	122493	2	AP000912	AP000912
1135	184	10.2	2475	6	AX700174	Sequence	1208	181	10.0	202505	2	AF000912	AF000912
1136	184	10.2	2475	10	RATWAGA	M16800 Rat LB236/m	1209	180.5	10.0	2547	3	HVU59448	HVU59448
1137	184	10.2	2934	6	CQ828004	Sequence	1210	180.5	10.0	3729	10	AF168466	AF168466
1138	184	10.2	4640	3	DNDRTRK	X63453 D.melanogas	1211	180.5	10.0	3943	10	AF172256	AF172256
1139	184	10.2	4645	6	CQ591393	Sequence	1212	180.5	10.0	4052	5	AY376855	AY376855
1140	184	10.2	4645	6	CQ847776	Sequence	1213	180.5	10.0	4239	6	E40577	E40577
1141	184	10.2	4775	3	EF015249	Drosophil	1214	180.5	10.0	4239	6	E40577	E40577
1142	184	10.2	5505	5	AF487829	Sequence	1215	180.5	10.0	4603	10	AF191090	AF191090
1143	184	10.2	7789	6	AX746187	Sequence	1216	180	10.0	1776	6	AX521472	AX521472
1144	183.5	10.2	1357	3	MSU11879	U11879 Manduca sex	1217	180	10.0	2106	11	BV177759	BV177759
1145	183.5	10.2	2728	6	CQ413817	Sequence	1218	180	10.0	2350	11	BV177759	BV177759
1146	183.5	10.2	3631	6	BD170702	Sequence	1219	180	10.0	2656	6	BD157949	BD157949
1147	183.5	10.2	5303	9	AC017561	Sequence	1220	180	10.0	2656	6	AX277406	AX277406
1148	183.5	10.2	6999	6	CQ874027	Sequence	1221	180	10.0	2656	6	AX879647	AX879647
1149	183.5	10.2	6999	9	AY310398	Sequence	1222	180	10.0	2656	9	AK022708	AK022708
1150	183	10.1	822	5	AX931320	Gallus ga	1223	180	10.0	6445	6	AX556703	AX556703
1151	183	10.1	2748	6	CQ869976	Sequence	1224	179.5	9.9	921	5	CR352648	CR352648
1152	183	10.1	69145	3	AF260530	Drosophil	1225	179.5	9.9	1086	10	RNO401157	RNO401157
1153	183	10.1	79405	10	AL928721	Sequence	1226	179.5	9.9	1515	6	CQ603762	CQ603762
1154	182.5	10.1	1565	5	AX364048	Gallus ga	1227	179.5	9.9	2118	6	CQ859389	CQ859389
1155	182.5	10.1	2118	6	CQ859385	Sequence	1228	179.5	9.9	2526	5	AY197498	AY197498
1156	182.5	10.1	2783	6	CQ580170	Sequence	1229	179.5	9.9	2532	5	AF389400	AF389400
1157	182.5	10.1	2931	10	MWU06483	U06483 Mus muscu	1230	179.5	9.9	2784	3	AK112938	AK112938
1158	182.5	10.1	3252	3	AF188751	Caenorhab	1231	179.5	9.9	156150	5	BX322540	BX322540
1159	182.5	10.1	4188	3	AY051656	Drosophil	1232	179.5	9.9	174574	2	BX927363	BX927363
1160	182.5	10.1	4734	10	RATFLT1	D28498 Rattus norv	1233	179	9.9	900	6	AY1702	AY1702
1161	182.5	10.1	4901	9	HSM807328	Sequence	1234	179	9.9	900	6	BD023445	BD023445
1162	182.5	10.1	5201	3	AF275903	Drosophil	1235	179	9.9	1374	6	AY1700	AY1700
1163	182.5	10.1	5923	5	AY603753	Drosophil	1236	179	9.9	1374	6	BD023443	BD023443
1164	182.5	10.1	6374	6	AX497861	Sequence	1237	179	9.9	1851	10	BC021876	BC021876
1165	182	10.1	1904	6	CQ721212	Sequence	1238	179	9.9	2029	10	MMU89915	MMU89915
1166	182	10.1	1969	9	AX05301	Homo sapi	1239	179	9.9	2429	10	MUSNAGX	MUSNAGX
1167	182	10.1	2275	9	AX094545	Homo sapi	1240	179	9.9	2700	6	AX497857	AX497857
1168	182	10.1	2350	6	AX335887	Sequence	1241	179	9.9	2967	9	BC042054	BC042054
1169	182	10.1	2350	6	AX658213	Sequence	1242	179	9.9	3022	9	BC067107	BC067107
1170	182	10.1	2350	9	HUMWAG	M29273 Human myeli	1243	179	9.9	3887	9	BC070119	BC070119
1171	182	10.1	2400	9	BC053347	Homo sapi	1244	179	9.9	5494	6	CQ721268	CQ721268
1172	182	10.1	3464	6	AX359697	Sequence	1245	178.5	9.9	1401	9	AK000845	AK000845

1246	178.5	9.9	2958	9	HSM801204	AL117666 Homo sapi	1319	175	9.7	2224	5	CR848573
1247	178.5	9.9	3236	9	AK095256	AK095256 Homo sapi	1320	175	9.7	5754	9	HSM805275
1248	178.5	9.9	3705	10	AF125521	AF125521 Rattus no	1321	175	9.7	117951	9	AL359821
1249	178.5	9.9	3970	10	AF122255	AF122255 Rattus no	1322	174.5	9.7	4094	6	CQ714181
1250	178.5	9.9	5820	10	AF161715	AF161715 Rattus no	1323	174	9.6	785	6	AR496309
1251	178.5	9.9	6847	6	CQ714785	CQ714785 Sequence	1324	174	9.6	785	6	AR511591
1252	178.5	9.9	140127	2	AC141742	AC141742 Apis mell	1325	174	9.6	868	5	BX933478
1253	178	9.9	1580	10	AF205078	AF205078 Mus muscu	1326	174	9.6	1034	5	CR387777
1254	178	9.9	2107	10	AV271309	AV271309 Rattus no	1327	174	9.6	1744	5	BX935017
1255	178	9.9	2684	10	BC076588	BC076588 Mus muscu	1328	174	9.6	2716	5	BC056023
1256	178	9.9	3581	10	AK173081	AK173081 Mus muscu	1329	174	9.6	3128	3	AF113638
1257	177.5	9.8	1752	4	AB039957	AB039957 Bos tauru	1330	174	9.6	3550	6	AX133825
1258	177.5	9.8	2525	3	AY052120	AY052120 Drosophil	1331	174	9.6	3562	6	AX179300
1259	177.5	9.8	2763	5	PF06FR3	X75603 P.waltlii m	1332	174	9.6	3698	10	AY169782
1260	177.5	9.8	3749	10	AF525412	AF525412 Rattus no	1333	174	9.6	4023	9	AF129167
1261	177.5	9.8	4980	3	AY060637	AY060637 Drosophil	1334	174	9.6	5831	3	AY047563
1262	177.5	9.8	5164	6	CQ572346	CQ572346 Sequence	1335	174	9.6	14985	2	HSTITIN
1263	177.5	9.8	7080	10	AY353236	AY353236 Mus muscu	1336	174	9.6	16799	2	AC020355
1264	177.5	9.8	7158	6	CQ714120	CQ714120 Sequence	1337	174	9.6	23546	6	CQ573465
1265	177.5	9.8	20448	6	CQ599466	CQ599466 Sequence	1338	174	9.6	23546	6	CQ847884
1266	177.5	9.8	24971	6	CQ599465	CQ599465 Sequence	1339	174	9.6	68727	3	AC004516
1267	177.5	9.8	27060	3	AB055927	AB055927 Procamb	1340	174	9.6	71023	2	AC004426
1268	177.5	9.8	53757	2	AC017325	AC017325 Drosophil	1341	174	9.6	97698	2	AC019670
1269	177.5	9.8	70398	3	DME271740	AY271740 Drosophil	1342	174	9.6	113320	2	AC010662
1270	177.5	9.8	121584	2	AC008232	AC008232 Drosophil	1343	174	9.6	166417	10	AC127685
1271	177.5	9.8	144056	3	AC091222	AC091222 Drosophil	1344	174	9.6	193262	3	AC007579
1272	177.5	9.8	194006	3	AC010063	AC010063 Drosophil	1345	174	9.6	260367	3	AE003808
1273	177.5	9.8	315108	3	AE003473	AE003473 Drosophil	1346	173.5	9.6	1962	10	AK311121
1274	177	9.8	1129	5	AF337034	AF337034 Danio rer	1347	173.5	9.6	2550	6	AR008527
1275	177	9.8	2899	10	BC049361	BC049361 Mus muscu	1348	173.5	9.6	2550	6	AR014315
1276	177	9.8	2959	9	BC064925	BC064925 Homo sapi	1349	173.5	9.6	2550	6	AR068074
1277	177	9.8	3757	9	AF151909	AF151909 Homo sapi	1350	173.5	9.6	2550	6	186161
1278	177	9.8	3768	9	AB103655	AB102655 Pongo pyg	1351	173.5	9.6	2550	6	186871
1279	177	9.8	6726	9	AB037718	AB037718 Homo sapi	1352	173.5	9.6	2550	6	AX746327
1280	177	9.8	7710	6	AX056397	AX056397 Sequence	1353	173.5	9.6	2550	6	AX816907
1281	177	9.8	153114	2	BX927068	BX927068 Danio rer	1354	173.5	9.6	2550	6	BD064497
1282	177	9.8	158241	3	AC115483	AC115483 Drosophil	1355	173.5	9.6	2565	6	BD064497
1283	177	9.8	161682	3	AC092326	AC092326 Drosophil	1356	173.5	9.6	2598	9	AK365516
1284	177	9.8	180190	2	CB626902	CB626902 Danio rer	1357	173.5	9.6	2764	6	AK000681
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1291	176.5	9.8	1409	9	AK025843	AK025843 Homo sapi	1364	173.5	9.6	2988	6	186863
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## ALIGNMENTS

RESULT 1  
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LOCUS Sequence 1 from patent US 6664383.  
DEFINITION AR439648  
ACCESSION AR439648  
VERSION AR439648.1 GI:42665572  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1032)  
AUTHORS Fukushima,D., Shibayama,S. and Tada,H.  
TITLE Polypeptides, cDNA encoding the same and utilization thereof  
JOURNAL Patent: US 6664383-A 1 16-DEC-2003;  
FEATURES Location/Qualifiers  
source 1..1032  
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Pred. No.: 1806.00 Matches: 344  
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Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6  
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Db 1 ATGAAACCATCCAGCCAAAATGCACAAATCTATCTCTTTGGGCAATCTTCACGGGGCTG 60

Qy 21 AlaAlaLeuCyLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40  
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Qy 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
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Qy 61 AenArgValThrArgValAlaAlaThrLeuAenArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
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Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrGlnTyrSerIle 100  
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Qy 101 GluIleGlnAenValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
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Qy 121 AenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
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Db 421 ATTCTTCAGATATCTCCATTAATGAGGAGAACATATTAGCTTCACTGATAGCAACT 480  
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Qy 201 CysSerAlaSerAenAspValAlaAlaProValValArgValLysValThrValAen 220  
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RESULT 2

CQ768055

LOCUS

DEFINITION

Sequence 522 from Patent EP1386931.

ACCESSION CQ768055  
VERSION CQ768055.1 GI:45108887

KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Wood, W. I., Goddard, A., Gurney, A., Yuan, J., Baker, K. P. and Chen, J.

TITLE Human neurotrophin homologue

JOURNAL Patent: EP 1386931-A 522 04-FEB-2004;

Genentech, Inc. (US)

FEATURES

Location/Qualifiers

source 1..1679

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 1.19e-157 Length: 1679

Score: 1806.00 Matches: 344

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x CQ768055 (1-1679)

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Db 134 ATGAAACCATCCAGCCAAATAATGCAATCTATCTCTTGGGCAATCTTCCAGGGGCTG 193

Qy 21 AlaAlaLeuCyLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40

Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCCAAA 253

Qy 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

Db 254 GCTATGGACAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTTCAAGTGCACCTATTGAC 313

Qy 61 AenArgValThrArgValAlaAlaTrpLeuAenArgSerThrIleLeuTyrAlaGlyAsnAsp 80

Db 314 AACCGGTCCACCGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373

Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrGlnTyrSerIle 100

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Qy 101 GluIleGlnAenValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120

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Qy 121 AenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140

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Qy 141 IleSerSerAspIleSerIleAenGluGlyAenAenIleSerLeuThrCysIleAlaThr 160

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Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180

Db 614 GGTAGACACAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673

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Qy 341 LeuLeuLysPhe 344
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RESULT 3
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LOCUS Sequence 375 from patent US 6725730.
DEFINITION AR528639
ACCESSION AR528639
VERSION AR528639.1 GI:53916717
FEATURES
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x AR528639 (1-1679)

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Db 194 GCTGCTCTGTCTCTTCCAGGAGTGGCCGTGCGCAGGGAGATGCCACCTTCCCCAAA 253
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Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAAACGTGGATGTGTATGACGAGGGGCCCTTACACCTCTCGTGGTGCACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db 1154 CTTCTCAAAATTT 1165
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RESULT 4
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LOCUS Sequence 125 from Patent WO0193983.
DEFINITION AX358872
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS
Baker, K.P., Desnovers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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Genentech Inc. (US)  
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VERSION AX362365.1 GI:18694640  
KEYWORDS Homo sapiens (human)  
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1 Baker, K. P., Desnoyers, L., Gerritsen, M. E., Goddard, A.,  
Godowski, P. J., Grimaldi, J. C., Gurney, A. L., Smith, V., Stephan, J. P.,  
Watanabe, C. K. and Wood, W. I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
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Patent: WO 0208288-A 125 31-JAN-2002;  
Genentech, Inc. (US)

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REFERENCE  
AUTHORS Ashkenazi, A., Baker, K., Botstein, D., Desnovers, L., Eaton, D.L.,  
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,  
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TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
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Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL PUBMED 12975309
REFERENCE 2 (bases 1 to 1679)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
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AUTHORS Fukushima,D., Shibayama,S. and Tada,H.
TITLE Polypeptides, cDNA encoding the same and utilization thereof
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Db 250 GCTATGACCAACGTGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 309
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db 370 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTTGAGCAACCCCAACCGCAGTACGACATC 429
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 490 AACCAACCAAGACCTCTAGGGTCCACTCATTTGCAAGTATCTCCCAAAATTTGTAGAG 549
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 550 ATTTCTTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCAGCTGATGCAACT 609
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Db 670 AGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 729
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Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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RESULT 12  
AX665342  
LOCUS AX665342 1839 bp DNA linear PAT 26-MAR-2003  
DEFINITION Sequence 100 from Patent WO03002765.  
ACCESSION AX665342  
VERSION AX665342.1 GI:292290464  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Sellar,G.C. and Gabra,H.  
TITLE Cancer  
JOURNAL Cancer Research Technology Limited (GB)  
FEATURES  
source  
Location/Qualifiers  
1. .1839  
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ORIGIN

Alignment Scores:  
Pred. No.: 1,446-144 Length: 1839  
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Query Match: 92.22% Indels: 2  
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US-10-017-084A-523 (1-344) x AX665342 (1-1839)

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Qy 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50  
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Db 355 GTGCGCAGCGGAGATGCCACCTTCCCGAAGATATGGACACGTGACGTCGGCAGGGG 414  
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Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70  
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Qy 71 ArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90  
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Qy 311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgAlaGlyCysVal 330  
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RESULT 13  
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DEFINITION Homo sapiens neurotrophin (HNT) mRNA, complete cds.  
ACCESSION AF126426  
VERSION AF126426.1 GI:7158997  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1839)  
TITLE Cloning and identification of human neurotrophin full length cDNA  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1839)  
AUTHORS Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.  
TITLE Direct Submission  
JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical  
Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China  
FEATURES  
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Qy	171	HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly	190	
Db	511	CACATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGATATCTTGGAAATTCAGGCG	570	
Qy	191	IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro	210	
Db	571	ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCCAATGACGTGGCCGCGCC	630	
Qy	211	ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly	230	
Db	631	GTGGTACGGAGAGTAAAGGTACCGTGAACACTATCCACCATACATTTCCAGAACCCAAAGGT	690	
Qy	231	ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer	250	
Db	691	ACAGGTGTCCTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCA	750	
Qy	251	AlaGluPheGlnTrpTyrLysAspLysArgLeuIleGluGlyLysGlyValLys	270	
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Qy	271	ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr	290	
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Qy	291	GlyAsnTyrThrCysValAlaSerAsnLysValGlyHisThrAsnAlaSerIleMetLeu	310	
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Qy	311	Phe-----GlyProGlyAlaValSerGluVal	319	
Db	931	TTTGAAGTGAAAACTACAGCCCTGACCCCTTGGAAAGGTCCAGGCGCGTCCAGCGAGGTG	990	
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LOCUS	BC023307			
DEFINITION	Mus musculus neurotrophin, mRNA (cdna clone MGC:30504 linear ROD 06-OCT-2003 IMAGE:4480983), complete cds.			
ACCESSION	BC023307			
VERSION	BC023307.1			
KEYWORDS	GI:23958300			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 1615)			
	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.J., Schuler, G.D., Altachul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, I., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ussdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S.G., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalley, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length			

JOURNAL	human and mouse cdna sequences
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	22388257
REFERENCE	12477932
AUTHORS	2 (bases 1 to 1615)
TITLE	Straussberg, R.
JOURNAL	Direct Submission
	Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: The Cepko Laboratory cdna Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 41 Row: n Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26986610. Location/Qualifiers 1..1615 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="MGC:30504 IMAGE:4480983" /tissue_type="Eye, retina, mouse strain C57Bl/6" /clone_lib="NIH MGC_94" /lab_host="DH10B" /note="vector: PCMV-SPORT6" 1..1615 /gene="Hnt-pending" /db_xref="LocusID:235106" /db_xref="MGI:2446259" 44..1078 /gene="Hnt-pending" /codon_start=1 /product="Hnt-pending protein" /protein_id="AAH23307.1" /db_xref="GI:23958301" /db_xref="LocusID:235106" /db_xref="MGI:2446259" /translation="MGVCGYILFLPWKLVVSLRLFLVPTGVFVRSGDATPPKAMDNVTVQGESATLRCTIDNRVTKRSLVAMLRSTILYAGNDKCLDPVRLVLLNGTQYSLIEI QNVYDGGPTCSQTDNHPKTSRVHLIVQSPKIVISDISINEGNNISLTCTAT GRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGEYECSSANDVAAPVVRVKVTVNYPISEAKGTGVPCKQKTLQCEASAVPSAEQWFQKDKRLVEGKKGVKVENRPF LSKPTFFNVSEHDYGNITYCVASANKLGHNTNASIMLFGPNAVSEVNGTSRRAGCIIWLLP LLVHLHLIKF" 173..442 /gene="Hnt-pending" /note="IG; Region: Immunoglobulin" /db_xref="CDD:smart00409" 485..664 /gene="Hnt-pending" /note="IGC2; Region: Immunoglobulin C-2 Type" /db_xref="CDD:smart00408" 740..973 /gene="Hnt-pending" /note="IG; Region: Immunoglobulin" /db_xref="CDD:smart00409"
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CDS	
misc_feature	
misc_feature	
misc_feature	
ORIGIN	

Alignment Scores:

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Percent Similarity: 95.83% Conservative: 8  
Best Local Similarity: 93.45% Mismatches: 11  
Query Match: 91.22% Indels: 3  
DB: 10 Gaps: 1

US-10-017-084A-523 (1-344) x BC023307 (1-1615)

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QY 29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
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   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Db 968 ATGCTATTGGTCCCGGTGCTGCTCAGTGAGGTCAACAATGGGACATCAAGGAGGGCAGGC 1027

QY - 329 CysValTrrLeuLeuProLeuLeuValLeuHisLeuLeuLysPhe 344

Db 1028 TGCATTGGCTCCTCCCTCTTCTGGTCTTACACCTGCTCCTCAAAATTT 1075

Search completed: October 30, 2005, 14:01:02  
Job time : 5317 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
OM protein - nucleic search, using frame plus.p2n model  
Run on: October 30, 2005, 11:25:06 ; Search time 641 Seconds  
(without alignments)  
3176.897 Million cell updates/sec

Title: US-10-017-084A-523  
Perfect score: 1806  
Sequence: 1 MKTIQPKMNSISWIFTGL.....RRAGCVMLPLVLHLLKLF 344  
Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0  
Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:  
-MODEL=frame+ p2n model -DRV=xlh  
-Q/cgn2\_1/USPTO spool/US10017084/runat\_28102005\_112650\_9393/app\_query.fasta\_1.519  
-DB=N\_Geneseq\_16Dec04 -Qfmt=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi  
-LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1500  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10017084 @CGN 1.1 644 @runat\_28102005\_112650\_9393 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7  
Database : N\_Geneseq\_16Dec04 :  
1: Geneseqn1980s :  
2: Geneseqn1990s :  
3: Geneseqn2000s :  
4: Geneseqn2001as :  
5: Geneseqn2001bs :  
6: Geneseqn2002as :  
7: Geneseqn2002bs :  
8: Geneseqn2003as :  
9: Geneseqn2003bs :  
10: Geneseqn2003cs :  
11: Geneseqn2003ds :  
12: Geneseqn2004as :  
13: Geneseqn2004bs :  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAZ47892	standard;	cDNA;	1032	BP.	
DE	Human	protein	encoding	cDNA	SEQ ID NO:2.	
PN	WO9958668	-A2.				
PD	18-NOV-1999.					
PA	(ONCY ) ONO PHARM CO LTD.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 2						
ID	AAZ34324	standard;	cDNA;	1679	BP.	
DE	Human	PRO337	nucleotide	sequence.		
PN	WO9946281	-A2.				
PD	16-SEP-1999.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 3						
ID	AAC78590	standard;	cDNA;	1679	BP.	
DE	Human	PRO337	nucleotide	sequence	SEQ ID NO:522.	
PN	WO200053756	-A2.				

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PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 4						
ID	AAC87037	standard;	cDNA;	1679	BP.	
DE	Nucleotide	sequence	of	human	polypeptide	PRO337.
PN	WO200077037	-A2.				
PD	21-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 5						
ID	AAS21431	standard;	cDNA;	1679	BP.	
DE	Human	cDNA	sequence	encoding	for	PRO337 polypeptide.
PN	WO200140466	-A2.				
PD	07-JUN-2001.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 6						
ID	ABK33598	standard;	cDNA;	1679	BP.	
DE	cDNA	encoding	human	PRO	protein,	Seq ID No 125.
PN	WO200208288	-A2.				
PD	31-JAN-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 7						
ID	ABL88099	standard;	cDNA;	1679	BP.	
DE	Human	PRO337	cDNA	sequence	SEQ ID NO:55.	
PN	WO200206930	-A2.				
PD	03-JAN-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 8						
ID	ABL95588	standard;	cDNA;	1679	BP.	
DE	Human	angiogenesis	related	cDNA	PRO337	SEQ ID NO: 55.
PN	WO200208284	-A2.				
PD	31-JAN-2002.					
PA	(GETH ) GENENTECH INC.					
PA	(BAKE ) BAKER K P.					
PA	(FERR ) FERRARA N.					
PA	(GERB ) GERBER H.					
PA	(GERR ) GERRITSEN M E.					
PA	(GODD ) GODDARD A.					
PA	(GODO ) GODOWSKI P J.					
PA	(GURN ) GURNEY A L.					
PA	(HILL ) HILLAN K J.					
PA	(MARS ) MARSTERS S A.					
PA	(PANJ ) PAN J.					
PA	(PAON ) PAONI N F.					
PA	(STEP ) STEPHAN J F.					
PA	(WATA ) WATANABE C K.					
PA	(WILL ) WILLIAMS P M.					
PA	(WOOD ) WOOD W I.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0
RESULT 9						
ID	ACA63892	standard;	cDNA;	1679	BP.	
DE	Novel	human	secreted	and	transmembrane	protein
PN	US2002192706	-A1.				
PD	19-DEC-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.00%					Conservative: 0
Best Local Similarity:	100.00%					Mismatches: 0
Query Match:	100.00%					Indels: 0

```
Query Match: 100.00% Indels: 0
RESULT 10
ID ACA03790 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 11
ID ACA04996 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 12
ID ACA72056 standard; cDNA; 1679 BP.
DE Human secreted and transmembrane PRO polypeptide #37 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 13
ID ABX89328 standard; cDNA; 1679 BP.
DE DNA encoding novel secreted and transmembrane protein PRO337.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 14
ID ABX92696 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO337 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACD41982 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #188.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACA60526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ACA04516 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ACA66437 standard; cDNA; 1679 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO337.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACA68559 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ACA04211 standard; cDNA; 1679 BP.
DE Human CDNA encoding a secreted/transmembrane protein, SEQ ID 375.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACA65657 standard; cDNA; 1679 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO337.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ADA45894 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ADA76325 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ABT44288 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ADA18975 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
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ID	ADA61598 standard; cDNA; 1679 BP.		
DE	Homo sapiens.		
FN	US2003049816-A1.		
PD	13-MAR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 27			
ID	ABD19383 standard; cDNA; 1679 BP.		
DE	Novel human secreted and transmembrane protein PRO337 cDNA.		
FN	US2003068796-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 28			
ID	ABD27924 standard; cDNA; 1679 BP.		
DE	cDNA encoding human PRO polypeptide #188.		
FN	US2003082704-A1.		
PD	01-MAY-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 29			
ID	ADA86403 standard; cDNA; 1679 BP.		
DE	Novel human secreted and transmembrane protein PRO337 cDNA.		
FN	US2003082711-A1.		
PD	01-MAY-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 30			
ID	ABD15967 standard; cDNA; 1679 BP.		
DE	Human PRO polynucleotide #188.		
FN	US2003087350-A1.		
PD	08-MAY-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 31			
ID	ADA47753 standard; cDNA; 1679 BP.		
DE	Human PRO polynucleotide #188.		
FN	US2003073215-A1.		
PD	17-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 32			
ID	ADA67548 standard; cDNA; 1679 BP.		
DE	Human PRO polynucleotide #188.		
FN	US2003068795-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 33			
ID	ADB30555 standard; cDNA; 1679 BP.		
DE	cDNA encoding human PRO polypeptide #188.		
FN	US2003068794-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 34			
ID	ADA85851 standard; cDNA; 1679 BP.		
DE	Novel human secreted and transmembrane protein PRO337 cDNA.		
FN	US2003082704-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

DE	Novel human secreted and transmembrane protein PRO337 cDNA.
FN	US2003082693-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 35	
ID	ADA97063 standard; cDNA; 1679 BP.
DE	Human PRO polynucleotide #188.
FN	US2003082705-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 36	
ID	ADA79367 standard; cDNA; 1679 BP.
DE	Human PRO polynucleotide #188.
FN	US2003082763-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 37	
ID	ADA87506 standard; cDNA; 1679 BP.
DE	Novel human secreted and transmembrane protein PRO337 cDNA.
FN	US2003087345-A1.
PD	08-MAY-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 38	
ID	ADBI6708 standard; cDNA; 1679 BP.
DE	Human PRO polynucleotide #188.
FN	US2003087349-A1.
PD	08-MAY-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 39	
ID	ADA91800 standard; cDNA; 1679 BP.
DE	Novel human secreted and transmembrane protein PRO337 cDNA.
FN	US2003082694-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 40	
ID	ADBI4863 standard; cDNA; 1679 BP.
DE	Human PRO polynucleotide #188.
FN	US2003087351-A1.
PD	08-MAY-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 41	
ID	ADA25061 standard; cDNA; 1679 BP.
DE	Novel human secreted and transmembrane protein PRO337 cDNA.
FN	US2003050241-A1.
PD	13-MAR-2003.
PA	(GETH ) GENENTECH INC.
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
RESULT 42	
ID	ADA47275 standard; cDNA; 1679 BP.
DE	Human secreted/transmembrane polypeptide PRO337 cDNA.

PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 43  
ID ADB18824 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 44  
ID ADA94039 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 45  
ID ADB19935 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 46  
ID ADB13247 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 47  
ID ACD98611 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 48  
ID ACD30038 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 49  
ID ADA12722 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO337.  
PN US200305216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 50  
ID ADA74501 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003068798-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 51  
ID ADB24734 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 52  
ID ADA82258 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 53  
ID ADA75221 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 54  
ID ADA85299 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 55  
ID ADA84747 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 56  
ID ADB30003 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 57  
ID ADA80531 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 58  
ID ADA75773 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003082703-A1.  
PD 01-MAY-2003.





```
Query Match: 100.00% Indels: 0
RESULT 75
ID ADB18272 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US200307710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADA86955 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 77
ID ADA88058 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADB28476 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ADB29028 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADA88610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADB27372 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003022339-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADB22305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 86
ID ACD30273 standard; cDNA; 1679 BP.
DE Human CDNA encoding Pro337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ABT43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ADA66996 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ADB22857 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ADB23630 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADA92352 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
```



PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 108  
ID ADB47123 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 109  
ID ADB83861 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 110  
ID ADB86730 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 111  
ID ADB73016 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 112  
ID ADB76744 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide sequence #133.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 113  
ID ADB77335 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 114  
ID ADB34492 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 115  
ID ADB35596 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 116  
ID ADB33940 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 117  
ID ADB35044 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 118  
ID ADB36148 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide SEQ ID NO 375.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 119  
ID ADB46543 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 120  
ID ADC44170 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 121  
ID ADC61930 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 122  
ID ADC63894 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 123  
ID ADC66994 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

Best Local Similarity: 100.00%	Mismatches: 0	Query Match: 100.00%	Indels: 0
Query Match: 100.00%	Indels: 0	RESULT 132	
ID ADC69118 standard; cDNA; 1679 BP.		ID ADC21844 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.		DE Human PRO polynucleotide #63.	
PN US2003064407-A1.		PN US2003096969-A1.	
PD 03-APR-2003.		PD 22-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
RESULT 125		RESULT 133	
ID ADC63178 standard; cDNA; 1679 BP.		ID ADC50416 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.		DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003068648-A1.		PN US2003092106-A1.	
PD 10-APR-2003.		PD 15-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
RESULT 126		RESULT 134	
ID ADC68243 standard; cDNA; 1679 BP.		ID ADC71963 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.		DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003069178-A1.		PN US2003092107-A1.	
PD 10-APR-2003.		PD 15-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
RESULT 127		RESULT 135	
ID ADC41563 standard; cDNA; 1679 BP.		ID ADC59942 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.		DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003072745-A1.		PN US2003092105-A1.	
PD 17-APR-2003.		PD 15-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
RESULT 128		RESULT 136	
ID ADC67618 standard; cDNA; 1679 BP.		ID ADC49875 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.		DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003073131-A1.		PN US2003088064-A1.	
PD 17-APR-2003.		PD 08-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
RESULT 129		RESULT 137	
ID ADC62554 standard; cDNA; 1679 BP.		ID ADC49074 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.		DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003073624-A1.		PN US2003088070-A1.	
PD 17-APR-2003.		PD 08-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
RESULT 130		RESULT 138	
ID ADC36854 standard; cDNA; 1679 BP.		ID ADC49591 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #63.		DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003088065-A1.		PN US2003088071-A1.	
PD 08-MAY-2003.		PD 08-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
RESULT 131		RESULT 139	
ID ADC42187 standard; cDNA; 1679 BP.		ID ADC47452 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.		DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003104998-A1.		PN US2003088072-A1.	
PD 05-JUN-2003.		PD 08-MAY-2003.	
PA (GETH ) GENENTECH INC.		PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
Best Local Similarity: 100.00%	Conservative: 0	Query Match: 100.00%	Indels: 0
Indels: 0			

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RESULT 140
ID ADC52949 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 141
ID ADC57303 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 142
ID ADC60494 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 143
ID ADC50969 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 144
ID ADC65496 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 145
ID ADC54594 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 146
ID ADC53555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 147
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 148
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 149
ID ADC58526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 150
ID ADC47197 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 151
ID ADD03200 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 152
ID ADC90192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 153
ID ADC69611 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 154
ID ADC48500 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 155
ID ADD10029 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 156
ID ADC78072 standard; cDNA; 1679 BP.
```

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DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 157
ID ADD04604 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 158
ID ADD06307 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 159
ID ADC80560 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 160
ID ADD11067 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 161
ID ADD10344 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 162
ID ADC47948 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 163
ID ADC77826 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 164
ID ADC80008 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 165
ID ADD11304 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 166
ID ADD09477 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 167
ID ADD50789 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 168
ID ADD41190 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 169
ID ADD52329 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 170
ID ADD51035 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 171
ID ADD53069 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 172
ID ADD53621 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203437-A1.
```

PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 173  
ID ADD37097 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #28.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 174  
ID ADD51777 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 175  
ID ADD02576 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 176  
ID ADD50516 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 177  
ID ADD02010 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 178  
ID ADD54192 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 179  
ID ADD50270 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 180  
ID ADD51281 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003105289-A1.  
PD 05-JUN-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 181  
ID ADE49556 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 182  
ID ADD92509 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 183  
ID ADD91405 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 184  
ID ADE04019 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 185  
ID ADE32316 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 186  
ID ADE22248 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 187  
ID ADD79472 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 188  
ID ADE35610 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.



Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 189	
ID ADE16724 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003203435-A1.	
PD 30-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 190	
ID ADD73339 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003203436-A1.	
PD 30-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 191	
ID ADE42008 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003194772-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 192	
ID ADE17825 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199023-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 193	
ID ADD91957 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199053-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 194	
ID ADE33420 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003194767-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 195	
ID ADE33972 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003194791-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 196	
ID ADD80024 standard; cDNA; 1679 BP.	
DE cDNA encoding human PRO polypeptide #188.	
PN US2003207417-A1.	
PD 06-NOV-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 197	
ID ADD93061 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003194768-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 198	
ID ADD72697 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003194781-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 199	
ID ADE19481 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199025-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 200	
ID ADE18929 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199026-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 201	
ID ADE43125 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199033-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 202	
ID ADD95914 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199059-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 203	
ID ADE22800 standard; cDNA; 1679 BP.	
DE cDNA encoding human PRO polypeptide #188.	
PN US2003199064-A1.	
PD 23-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 204	
ID ADD78918 standard; cDNA; 1679 BP.	
DE cDNA encoding human PRO polypeptide #188.	
PN US2003203429-A1.	
PD 30-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 205	
ID ADE33972 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003194791-A1.	
PD 16-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 206	
ID ADD80024 standard; cDNA; 1679 BP.	
DE cDNA encoding human PRO polypeptide #188.	
PN US2003207417-A1.	
PD 06-NOV-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0

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Query Match: 100.00% Indels: 0
RESULT 205
ID ADE32868 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ADE42560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 207
ID ADE17348 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 208
ID ADD80576 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 209
ID ADD89604 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 210
ID ADE40888 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 211
ID ADE04687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 212
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 213
ID ADF47362 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADG21525 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADG23166 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADF97501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADG80565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADG53119 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADG60439 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADG80013 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
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ID ADG63784 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADH55305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADH55857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADI61199 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADI64076 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADI65025 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ADI63524 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADH81938 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 229
ID ADH81386 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 230
ID ACD24040 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 231
ID ACA66903 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #63.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 232
ID ACD42387 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 233
ID ACD42857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 234
ID ACD68655 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 235
ID ACA67181 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 236
ID ADM82555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 237
ID ADNI5954 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
```

PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 238  
ID ADN16583 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 239  
ID ADN15402 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 240  
ID ADN14850 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 241  
ID ADC48828 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 242  
ID ADC81112 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 243  
ID ADE20999 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 244  
ID ADE05843 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 245  
ID ADD76560 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003100087-A1.

PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 246  
ID ADD75072 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 247  
ID ADD75818 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 248  
ID ADD85050 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 249  
ID ADD86876 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 250  
ID ADE20753 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 251  
ID ADE39050 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 252  
ID ADD87924 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 253  
ID ADD86328 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003203440-A1.  
PD 30-OCT-2003.



```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 270
ID ADE24547 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 271
ID ADD87372 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 272
ID ADE05105 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 273
ID ADD75318 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 274
ID ADD76862 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 275
ID ADD86630 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 276
ID ADE89238 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 277
ID ADE41198 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 278
ID ADD78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 279
ID ADE18377 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 280
ID ADE88686 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 281
ID ADE89957 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOM/) GAO W.
PA (GERR/) GERRITSEN H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 282
ID ADD77606 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 283
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ID ADD77852 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 284  
ID ADD85310 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 285  
ID ADD73842 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 286  
ID ADD74580 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 287  
ID ADD77108 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 288  
ID ADD85802 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 289  
ID ADE05351 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 290  
ID ADD74826 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #63.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 291  
ID ADF61597 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 292  
ID ADF40289 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 293  
ID ADF46095 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 294  
ID ADE94706 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 295  
ID ADE91117 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 296  
ID ADE95258 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 297  
ID ADE93368 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 298  
ID ADF24481 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 299  
ID ADF40913 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.

```
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 300
ID ADF23857 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 301
ID ADF33840 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 302
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 303
ID ADF27307 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 304
ID ADF27943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 305
ID ADE92264 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 306
ID ADE90565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 307
ID ADF41537 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199435-A1.
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 308
ID ADF33216 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 309
ID ADF25582 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 310
ID ADF26683 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 311
ID ADF34472 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 312
ID ADF46709 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 313
ID ADE91712 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 314
ID ADG05638 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 315
ID ADG27192 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
```



PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 316  
ID ADG02291 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207352-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 317  
ID ADG22077 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 318  
ID ADG20147 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207376-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 319  
ID ADF98053 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207422-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 320  
ID ADG24270 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 321  
ID ADF98624 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003208055-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 322  
ID ADG03455 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207351-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 323  
ID ADF99176 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207353-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 324  
ID ADG16761 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207359-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 325  
ID ADG05220 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207375-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 326  
ID ADG19487 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207425-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 327  
ID ADG11255 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096967-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 328  
ID ADG13324 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003207357-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 329  
ID ADG08381 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 330  
ID ADG15551 standard; cDNA; 1679 BP.  
DE cDNA encoding human PRO polypeptide #188.  
PN US2003219885-A1.  
PD 27-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 331  
ID ADG12034 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096963-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0



RESULT 348  
ID ADG58564 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 349  
ID ADG70930 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 350  
ID ADH39031 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 351  
ID ADG58012 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 352  
ID ADG53596 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 353  
ID ADG71482 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 354  
ID ADG50695 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 355  
ID ADG81669 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 356  
ID ADH30631 standard; cDNA; 1679 BP.

DE Human PRO polynucleotide #188.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 357  
ID ADG63633 standard; cDNA; 1679 BP.  
DE Human secreted/transmembrane polypeptide PRO337 cDNA.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 358  
ID ADH11998 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 359  
ID ADG50071 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 360  
ID ADG51943 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 361  
ID ADG52420 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 362  
ID ADG54148 standard; cDNA; 1679 BP.  
DE Novel human secreted and transmembrane protein PRO337 cDNA.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 363  
ID ADG49447 standard; cDNA; 1679 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO337.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 364  
ID ADG81117 standard; cDNA; 1679 BP.  
DE Human PRO polynucleotide #188.

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PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 365
ID ADG56356 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 366
ID ADH12622 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 367
ID ADG48823 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 368
ID ADG61468 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 369
ID ADH28555 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 370
ID ADG54700 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 371
ID ADG59740 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 372
ID ADG51319 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
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PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 373
ID ADH43488 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 374
ID ADG59263 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 375
ID ADG34121 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 376
ID ADG62719 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 377
ID ADI81164 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 378
ID ADI33591 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 379
ID ADH69685 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 380
ID ADH25744 standard; cDNA; 1679 BP.
DE Human PRO337 encoding cDNA SEQ ID NO:522.
PN EP1386931-A1.
PD 04-FEB-2004.
```





RESULT 413  
ID ADN39137 standard; cDNA; 1839 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 97.31%  
Best Local Similarity: 96.41%  
Query Match: 92.22%  
Conservative: 3  
Mismatches: 8  
Indels: 2  
RESULT 414  
ID ADI21817 standard; cDNA; 2884 BP.  
DE Novel human protein cDNA #76.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 97.31%  
Best Local Similarity: 96.41%  
Query Match: 92.22%  
Conservative: 3  
Mismatches: 8  
Indels: 2  
RESULT 415  
ID ADQ22984 standard; DNA; 3987 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 97.31%  
Best Local Similarity: 96.41%  
Query Match: 92.22%  
Conservative: 3  
Mismatches: 8  
Indels: 2  
RESULT 416  
ID ADQ24601 standard; DNA; 3987 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 97.31%  
Best Local Similarity: 96.41%  
Query Match: 92.22%  
Conservative: 3  
Mismatches: 8  
Indels: 2  
RESULT 417  
ID ADG63210 standard; DNA; 1068 BP.  
DE Human neurotrophin DNA +33bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Percent Similarity: 94.20%  
Best Local Similarity: 93.33%  
Query Match: 91.36%  
Conservative: 3  
Mismatches: 8  
Indels: 13  
RESULT 418  
ID ABT17391 standard; DNA; 1094 BP.  
DE Human IG gene related nucleic acid SEQ ID No 17.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 94.20%  
Best Local Similarity: 93.33%  
Query Match: 91.36%  
Conservative: 3  
Mismatches: 8  
Indels: 13  
RESULT 419  
ID ADI35771 standard; DNA; 2129 BP.  
DE Human neurotrophin DNA.  
PN US2003100485-A1.  
PD 29-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 94.20%  
Best Local Similarity: 93.33%  
Query Match: 91.36%  
Conservative: 3  
Mismatches: 8  
Indels: 13  
RESULT 420  
ID ADG63212 standard; DNA; 1104 BP.  
DE Human neurotrophin DNA +69bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Percent Similarity: 91.04%  
Best Local Similarity: 90.20%  
Query Match: 91.03%  
Conservative: 3  
Mismatches: 8  
Indels: 25  
RESULT 421

ID ABT17392 standard; DNA; 1130 BP.  
DE Human IG gene related nucleic acid SEQ ID No 18.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 91.04%  
Best Local Similarity: 90.20%  
Query Match: 91.03%  
Conservative: 3  
Mismatches: 8  
Indels: 25  
RESULT 422  
ID AAZ47894 standard; cDNA; 939 BP.  
DE Human protein encoding cDNA SEQ ID NO:5.  
PN WO9558668-A1.  
PD 18-NOV-1999.  
PA (ONCY) ONO PHARM CO LTD.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 90.92%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 423  
ID ADG63214 standard; DNA; 1140 BP.  
DE Human neurotrophin DNA +108bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Percent Similarity: 88.08%  
Best Local Similarity: 87.26%  
Query Match: 90.70%  
Conservative: 3  
Mismatches: 8  
Indels: 37  
RESULT 424  
ID ADE07017 standard; DNA; 3298 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #83.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 82.89%  
Best Local Similarity: 71.39%  
Query Match: 71.73%  
Conservative: 39  
Mismatches: 57  
Indels: 1  
RESULT 425  
ID AAQ51015 standard; cDNA; 3069 BP.  
DE Rat opioid receptor gene.  
PN WO9321309-A1.  
PD 28-OCT-1993.  
PA (LEEN/) LEE N M.  
PA (LOHH/) LOH H H.  
PA (LIPP/) LIPPMAN D.  
Percent Similarity: 82.01%  
Best Local Similarity: 71.39%  
Query Match: 71.23%  
Conservative: 36  
Mismatches: 60  
Indels: 1  
RESULT 426  
ID ABT17408 standard; DNA; 1071 BP.  
DE Human IG gene related nucleic acid SEQ ID No 34.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 83.28%  
Best Local Similarity: 72.24%  
Query Match: 70.21%  
Conservative: 37  
Mismatches: 54  
Indels: 3  
RESULT 427  
ID ABT17407 standard; DNA; 1080 BP.  
DE Human IG gene related nucleic acid SEQ ID No 33.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 83.28%  
Best Local Similarity: 72.24%  
Query Match: 70.21%  
Conservative: 37  
Mismatches: 54  
Indels: 3  
RESULT 428  
ID ABT17409 standard; DNA; 1478 BP.  
DE Human IG gene related nucleic acid SEQ ID No 35.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 83.28%  
Best Local Similarity: 72.24%  
Query Match: 70.21%  
Conservative: 37  
Mismatches: 54  
Indels: 3

RESULT 429  
ID ABT17406 standard; DNA; 3110 BP.  
DE Human IG gene related nucleic acid SEQ ID No 32.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 83.28%  
Best Local Similarity: 72.24%  
Query Match: 70.21%  
Indels: 3  
RESULT 430  
ID ADG63206 standard; DNA; 3110 BP.  
DE Opioid-binding protein/cell adhesion molecule-like DNA.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Percent Similarity: 83.28%  
Best Local Similarity: 72.24%  
Query Match: 70.21%  
Indels: 3  
RESULT 431  
ID AAO51017 standard; cDNA; 2179 BP.  
DE Rat opioid receptor gene.  
PN WO9321309-A1.  
PD 28-OCT-1993.  
PA (LEEN/) LEE N M.  
PA (LOHH/) LOH H H.  
PA (LIPP/) LIPPMAN D.  
Percent Similarity: 81.31%  
Best Local Similarity: 71.22%  
Query Match: 69.77%  
Indels: 4  
RESULT 432  
ID AAO51016 standard; cDNA; 2337 BP.  
DE Rat opioid receptor gene.  
PN WO9321309-A1.  
PD 28-OCT-1993.  
PA (LEEN/) LEE N M.  
PA (LOHH/) LOH H H.  
PA (LIPP/) LIPPMAN D.  
Percent Similarity: 81.31%  
Best Local Similarity: 71.22%  
Query Match: 69.77%  
Indels: 4  
RESULT 433  
ID AAA44536 standard; cDNA; 832 BP.  
DE Human secreted expressed sequence tag SEQ ID NO:1111.  
PN WO200021991-A1.  
PD 20-APR-2000.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 99.56%  
Best Local Similarity: 99.11%  
Query Match: 64.95%  
Indels: 0  
RESULT 434  
ID ABT17404 standard; DNA; 1017 BP.  
DE Human IG gene related nucleic acid SEQ ID No 30.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 73.85%  
Best Local Similarity: 55.38%  
Query Match: 51.63%  
Indels: 5  
RESULT 435  
ID AAL50356 standard; cDNA; 1411 BP.  
DE Human limbic system associated membrane protein 36-85 coding sequence.  
PN CN1345756-A.  
PD 24-APR-2002.  
PA (SHAN-) SHANGHAI BLOWNDOW GENE DEV INC.  
Percent Similarity: 72.62%  
Best Local Similarity: 53.87%  
Query Match: 51.63%  
Indels: 7  
RESULT 436  
ID ABT17402 standard; DNA; 1017 BP.  
DE Human IG gene related nucleic acid SEQ ID No 28.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.

Percent Similarity: 73.85%  
Best Local Similarity: 55.38%  
Query Match: 51.58%  
Indels: 5  
RESULT 437  
ID ABX63560 standard; cDNA; 1195 BP.  
DE Human cDNA #560 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Percent Similarity: 73.85%  
Best Local Similarity: 55.38%  
Query Match: 51.58%  
Indels: 5  
RESULT 438  
ID ADL12674 standard; cDNA; 1195 BP.  
DE Human steroid-induced C3A liver cell cDNA #403.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 73.85%  
Best Local Similarity: 55.38%  
Query Match: 51.58%  
Indels: 5  
RESULT 439  
ID AAT42081 standard; cDNA to mRNA; 1014 BP.  
DE Rat LAMP coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 73.54%  
Best Local Similarity: 55.08%  
Query Match: 51.30%  
Indels: 5  
RESULT 440  
ID AAT42080 standard; cDNA to mRNA; 1238 BP.  
DE Rat LAMP coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 73.54%  
Best Local Similarity: 55.08%  
Query Match: 51.30%  
Indels: 5  
RESULT 441  
ID ABT17403 standard; DNA; 1075 BP.  
DE Human IG gene related nucleic acid SEQ ID No 29.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 71.51%  
Best Local Similarity: 53.71%  
Query Match: 51.19%  
Indels: 17  
RESULT 442  
ID AAT42079 standard; cDNA to mRNA; 977 BP.  
DE Human LAMP residues 8-332 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 74.06%  
Best Local Similarity: 55.31%  
Query Match: 51.14%  
Indels: 5  
RESULT 443  
ID AAT42116 standard; cDNA to mRNA; 1307 BP.  
DE Rat LAMP clone 6c coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 68.97%  
Best Local Similarity: 53.72%  
Query Match: 50.55%  
Indels: 28  
RESULT 444  
ID AAT42084 standard; cDNA to mRNA; 924 BP.  
DE Human LAMP residues 8-315 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 68.97%  
Best Local Similarity: 53.72%  
Query Match: 50.55%  
Indels: 28  
RESULT 445  
ID AAT42084 standard; cDNA to mRNA; 924 BP.  
DE Human LAMP residues 8-315 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 75.50%  
Conservative: 58



Best Local Similarity: 56.29% Mismatches: 70  
 Query Match: 50.28% Indels: 4  
 RESULT 445  
 ID AAT42085 standard; cDNA to mRNA; 945 BP.  
 DE Rat LAMP residues 1-315 coding sequence.  
 PN WO9630052-A1.  
 PD 03-OCT-1996.  
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
 Percent Similarity: 75.50% Conservative: 58  
 Best Local Similarity: 56.29% Mismatches: 70  
 Query Match: 50.22% Indels: 4  
 RESULT 446  
 ID AAT42083 standard; cDNA to mRNA; 930 BP.  
 DE Rat mature LAMP coding sequence.  
 PN WO9630052-A1.  
 PD 03-OCT-1996.  
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
 Percent Similarity: 74.12% Conservative: 59  
 Best Local Similarity: 55.27% Mismatches: 77  
 Query Match: 50.11% Indels: 4  
 RESULT 447  
 ID AAT42082 standard; cDNA to mRNA; 912 BP.  
 DE Human mature LAMP coding sequence.  
 PN WO9630052-A1.  
 PD 03-OCT-1996.  
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
 Percent Similarity: 74.68% Conservative: 59  
 Best Local Similarity: 55.52% Mismatches: 74  
 Query Match: 49.94% Indels: 4  
 RESULT 448  
 ID ABZ76264 standard; cDNA; 1757 BP.  
 DE Human GENSET cDNA clone name SLAMP.  
 PN WO2003014151-A2.  
 PD 20-FEB-2003.  
 PA (GEST ) GENSET SA.  
 Percent Similarity: 72.14% Conservative: 61  
 Best Local Similarity: 53.25% Mismatches: 76  
 Query Match: 49.45% Indels: 14  
 RESULT 449  
 ID AAT42086 standard; cDNA to mRNA; 861 BP.  
 DE Human LAMP residues 29-315 coding sequence.  
 PN WO9630052-A1.  
 PD 03-OCT-1996.  
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
 Percent Similarity: 76.21% Conservative: 57  
 Best Local Similarity: 56.55% Mismatches: 66  
 Query Match: 49.09% Indels: 3  
 RESULT 450  
 ID AAT42087 standard; cDNA to mRNA; 861 BP.  
 DE Rat LAMP residues 29-315 coding sequence.  
 PN WO9630052-A1.  
 PD 03-OCT-1996.  
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
 Percent Similarity: 76.21% Conservative: 57  
 Best Local Similarity: 56.55% Mismatches: 66  
 Query Match: 49.03% Indels: 3  
 RESULT 451  
 ID AAH34425 standard; cDNA; 1153 BP.  
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1507.  
 PN WO200122920-A2.  
 PD 05-APR-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 68.68% Conservative: 60  
 Best Local Similarity: 51.44% Mismatches: 81  
 Query Match: 49.00% Indels: 29  
 RESULT 452  
 ID ADM47274 standard; DNA; 617 BP.  
 DE Oestrogen regulated protein like NOVX 25b gene.  
 PN WO2003083039-A2.  
 PD 09-OCT-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 56.59% Conservative: 4  
 Best Local Similarity: 55.39% Mismatches: 8

Query Match: 48.37% Indels: 138  
 RESULT 453  
 ID AAZ34325 standard; DNA; 503 BP.  
 DE Human EST DNA42301.  
 PN WO9946281-A2.  
 PD 16-SEP-1999.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0  
 RESULT 454  
 ID AAC78591 standard; cDNA; 503 BP.  
 DE Human EST DNA42301 nucleotide sequence SEQ ID NO:524.  
 PN WO200053756-A2.  
 PD 14-SEP-2000.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0  
 RESULT 455  
 ID ACA63893 standard; cDNA; 503 BP.  
 DE Novel human secreted and transmembrane protein DNA42301.  
 PN US2002192706-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0  
 RESULT 456  
 ID ACA72057 standard; DNA; 503 BP.  
 DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.  
 PN US2002177553-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0  
 RESULT 457  
 ID ABX92697 standard; cDNA; 503 BP.  
 DE Human PRO337 EST polynucleotide sequence.  
 PN US2002169284-A1.  
 PD 14-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0  
 RESULT 458  
 ID ACA66438 standard; cDNA; 503 BP.  
 DE Human secreted/transmembrane protein EST DNA42301.  
 PN US2003004102-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0  
 RESULT 459  
 ID ADA25063 standard; cDNA; 503 BP.  
 DE Novel human secreted and transmembrane protein EST DNA42301.  
 PN US2003050241-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0  
 RESULT 460  
 ID ACD30039 standard; cDNA; 503 BP.  
 DE Novel human secreted and transmembrane protein EST DNA42301.  
 PN US2003050240-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.56% Indels: 0

RESULT 461  
ID ADA12724 standard; cDNA; 503 BP.  
DE Human secreted/transmembrane polypeptide PRO337 EST.  
PN US200305216-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 462  
ID ACD29454 standard; cDNA; 503 BP.  
DE Novel human secreted and transmembrane polypeptide cDNA #134.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 463  
ID ADB74030 standard; cDNA; 503 BP.  
DE Human PRO polynucleotide sequence #134.  
PN US200304542-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 464  
ID ADB76746 standard; cDNA; 503 BP.  
DE Human PRO polynucleotide sequence #134.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 465  
ID ADC44172 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 466  
ID ADC61932 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 467  
ID ADC63896 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 468  
ID ADC66996 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 469  
ID ADC69120 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 470  
ID ADC63180 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 471  
ID ADC68245 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 472  
ID ADC41565 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 473  
ID ADC67620 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 474  
ID ADC62556 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 475  
ID ADC42189 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 476  
ID ADE49558 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 477  
ID ADE35612 standard; cDNA; 503 BP.  
DE Human EST from secreted/transmembrane protein, PRO337.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 47.56%  
Conservative: 0  
Mismatch: 0  
Indels: 0

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PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 478
ID ADE16726 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 479
ID ADD73341 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 480
ID ADD72699 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 481
ID ADE17350 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 482
ID ADF47364 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 483
ID ADG53121 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 484
ID ADG60441 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 485
ID ADI61201 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 486
ID ACD42858 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 487
ID ADE48858 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 488
ID ADE89959 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 489
ID ADF61599 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 490
ID ADF40291 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
```

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 491
ID ADF46087 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 492
ID ADF24483 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 493
ID ADF40915 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 494
ID ADF23859 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 495
ID ADF3842 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 496
ID ADF27309 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 497
ID ADF27945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 498
ID ADF41539 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 499
ID ADF33218 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 500
ID ADF25584 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 501
ID ADF26685 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 502
ID ADF34474 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 503
ID ADF46711 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 504
ID ADG50697 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 505
ID ADG50073 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
RESULT 506
ID ADG51945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
```

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Query Match: 47.56% Indels: 0
RESULT 507
ID ADG49449 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 508
ID ADG48825 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 509
ID ADG51321 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 510
ID ADG59265 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 511
ID ADG62721 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 512
ID ADH25746 standard; cDNA; 503 BP.
DE Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 513
ID ADH17523 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 514
ID ADL07357 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 515
ID ABT17405 standard; DNA; 898 BP.
DE Human IG gene related nucleic acid SEQ ID NO 31.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 74.65%
Best Local Similarity: 55.56%
Query Match: 47.12%
Conservative: 55
Mismatch: 71
Indels: 2
RESULT 516
ID ABQ82337 standard; cDNA; 1196 BP.
DE Human NOV12a encoding cDNA SEQ ID NO:23.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 517
ID ADI28059 standard; cDNA; 1327 BP.
DE ECMAD gene clone 7087904CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCI-) INCIYTE GENOMICS INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 518
ID AAC87055 standard; cDNA; 4834 BP.
DE Nucleotide sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 519
ID ABK33536 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO protein, Seq ID No 1.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 520
ID ACA05014 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 521
ID ACA60544 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 522
ID ACA04534 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatch: 105
Indels: 2
RESULT 523
```

ID ACA68497 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 524  
ID ACA65675 standard; cDNA; 4834 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO6004.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 525  
ID ABT44226 standard; cDNA; 4834 BP.  
DE Human PRO6004 cDNA.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 526  
ID ADA47301 standard; cDNA; 4834 BP.  
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 527  
ID ABT44509 standard; cDNA; 4834 BP.  
DE Human PRO6004 cDNA.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 528  
ID ACD82176 standard; cDNA; 4834 BP.  
DE Human secreted/transmembrane polypeptide PRO 6004 cDNA.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 529  
ID ACD30291 standard; cDNA; 4834 BP.  
DE Human cDNA encoding Pro6004.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 530  
ID ABT43982 standard; cDNA; 4834 BP.  
DE Human membrane bound receptor/protein PRO6004 cDNA sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 531  
ID ADB83491 standard; cDNA; 4834 BP.

DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 532  
ID ADB80597 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 533  
ID ADB73138 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 534  
ID ADB78220 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 535  
ID ADB84868 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 536  
ID ADB7974 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 537  
ID ADB87040 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 538  
ID ADB84622 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Indels: 2  
RESULT 539  
ID ADB83737 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.

[illegible]

PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 556  
ID ADG63810 standard; cDNA; 4834 BP.  
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 557  
ID ACA66841 standard; cDNA; 4834 BP.  
DE cDNA encoding human PRO polypeptide #1.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 558  
ID ACD42405 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 559  
ID ACD68593 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 560  
ID ADC48704 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 561  
ID ADE20875 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 562  
ID ADE05719 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 563  
ID ADD74948 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 564  
ID ADD75694 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 565  
ID ADD84926 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 566  
ID ADD86752 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 567  
ID ADE20629 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 568  
ID ADE38926 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 569  
ID ADE05473 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 570  
ID ADD73458 standard; cDNA; 4834 BP.  
DE Human PRO polynucleotide #1.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2  
RESULT 571  
ID ADD78298 standard; cDNA; 4834 BP.  
DE Novel human secreted and transmembrane protein PRO6004 cDNA.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 67.18%  
Best Local Similarity: 47.85%  
Query Match: 45.57%  
Conservative: 63  
Mismatches: 105  
Indels: 2



Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 572	
ID ADE21121 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100736-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 573	
ID ADD77236 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100732-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 574	
ID ADE20383 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100733-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 575	
ID ADD75448 standard; cDNA; 4834 BP.	
DE Human PRO polynucleotide #1.	
PN US2003100064-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 576	
ID ADD73964 standard; cDNA; 4834 BP.	
DE Human PRO polynucleotide #1.	
PN US2003100708-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 577	
ID ADD74210 standard; cDNA; 4834 BP.	
DE Human PRO polynucleotide #1.	
PN US2003100709-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 578	
ID ADD75940 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100718-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 579	
ID ADD85432 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100721-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 580	
ID ADE04981 standard; cDNA; 4834 BP.	
DE Human PRO polynucleotide #1.	
PN US2003100726-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 581	
ID ADD75194 standard; cDNA; 4834 BP.	
DE Human PRO polynucleotide #1.	
PN US2003100714-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 582	
ID ADD76738 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100715-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 583	
ID ADD86506 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100719-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 584	
ID ADE41224 standard; cDNA; 4834 BP.	
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.	
PN US2003104558-A1.	
PD 05-JUN-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 585	
ID ADD77974 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100731-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 586	
ID ADD77482 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100729-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 587	
ID ADD77728 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100730-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2
RESULT 588	
ID ADD77728 standard; cDNA; 4834 BP.	
DE Novel human secreted and transmembrane protein PRO6004 cDNA.	
PN US2003100730-A1.	
PD 29-MAY-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 67.18%	Conservative: 63
Best Local Similarity: 47.85%	Mismatches: 105
Query Match: 45.57%	Indels: 2

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RESULT 588
ID ADD85186 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 589
ID ADD73718 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 590
ID ADD74456 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 591
ID ADD76984 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 592
ID ADD85678 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 593
ID ADE05227 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 594
ID ADD74702 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 595
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 596
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 597
ID ADG11131 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 598
ID ADG11910 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 599
ID ADP94467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 600
ID ADG06563 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 601
ID ADH38907 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 602
ID ADG63658 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 603
ID ADG33997 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Conservative: 63
Mismatches: 105
Indels: 2
Query Match: 45.57%
RESULT 604
ID ADI33467 standard; cDNA; 4834 BP.
```

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DE Human PRO polynucleotide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 605
ID ADH69561 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 606
ID ADI29722 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 607
ID ADM27119 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 608
ID ADK66477 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 609
ID ADS82049 standard; DNA; 4891 BP.
DE Human cancer-associated protein coding sequence #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS ) LG LIFE SCI LTD.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 610
ID ABN85384 standard; DNA; 1119 BP.
DE Human NOV6, KILON-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.51%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 611
ID ADB62841 standard; cDNA; 2383 BP.
DE Human cDNA encoding clone OCBPF20110210.
PN EPL308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 66.87%
Best Local Similarity: 47.85%
Query Match: 45.40%
Indels: 2
Conservative: 62
Mismatches: 106
Indels: 2
RESULT 612
ID ABQ82338 standard; cDNA; 1165 BP.
DE Human NOV6, KILON-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 613
ID ABT17401 standard; DNA; 1809 BP.
DE Human IG gene related nucleic acid SEQ ID NO 27.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 67.06%
Best Local Similarity: 47.48%
Query Match: 45.13%
Indels: 10
Conservative: 66
Mismatches: 101
Indels: 10
RESULT 614
ID AAC78596 standard; cDNA; 2840 BP.
DE Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN WO200003756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 615
ID ACA63979 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 616
ID ACA72143 standard; cDNA; 2840 BP.
DE Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 617
ID ABX92783 standard; cDNA; 2840 BP.
DE cDNA encoding human PRO4993 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 618
ID ACA66524 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 619
ID ADA25149 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 620
ID ACD30125 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
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PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 621  
ID ADA12811 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO4993.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 622  
ID ADC29540 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide cDNA #139.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 623  
ID ADB74117 standard; cDNA; 2840 BP.  
DE Human PRO polynucleotide sequence #139.  
PN US2003045482-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 624  
ID ADB76833 standard; cDNA; 2840 BP.  
DE Human PRO polynucleotide sequence #139.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 625  
ID ADC44259 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 626  
ID ADC62019 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 627  
ID ADC63983 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003054408-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 628  
ID ADC67083 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003060406-A1.  
PD 27-MAR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 629  
ID ADC69207 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 630  
ID ADC63267 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 631  
ID ADC68332 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 632  
ID ADC41652 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 633  
ID ADC67707 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 634  
ID ADC62643 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 635  
ID ADC42276 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 636  
ID ADE49645 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 637  
 ID ADE35699 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003203434-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 638  
 ID ADE16813 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003203435-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 639  
 ID ADD73428 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003203436-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 640  
 ID ADD72786 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003194781-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 641  
 ID ADE17437 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003203433-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 642  
 ID ADF47451 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003195333-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 643  
 ID ADG53208 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003216561-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 644  
 ID ADG60528 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003206915-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63

Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 645  
 ID ADI61288 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003077700-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 646  
 ID ACD42944 standard; cDNA; 2840 BP.  
 DE Novel human secreted and transmembrane protein PRO4993 cDNA.  
 PN US2003050239-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 647  
 ID ADE48945 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003104536-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 648  
 ID ADE90046 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003130181-A1.  
 PD 10-JUL-2003.  
 PA (ASHK/) ASHENAZI A J.  
 PA (BAKE/) BAKER K P.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GIRM/) GIRMALDI J C.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (KUOS/) KUO S S.  
 PA (NAPI/) NAPIER M A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (SHEL/) SHELTON D L.  
 PA (STEW/) STEWART T A.  
 PA (TUNA/) TUNAS D.  
 PA (WOOD/) WILLIAMS P M.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2  
 RESULT 649  
 ID ADF61686 standard; cDNA; 2840 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
 PN US2003195345-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 66.87% Conservative: 63  
 Best Local Similarity: 47.55% Mismatches: 106  
 Query Match: 45.13% Indels: 2

RESULT 650  
ID ADF40378 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003198934-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 651  
ID ADF46174 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 652  
ID ADF24570 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 653  
ID ADF41002 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 654  
ID ADF23946 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 655  
ID ADF33929 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 656  
ID ADF27396 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 657  
ID ADF28032 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 658  
ID ADF41626 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 659  
ID ADF33305 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 660  
ID ADF25671 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 661  
ID ADF26772 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 662  
ID ADF34561 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 663  
ID ADF46798 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 664  
ID ADG50784 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 665  
ID ADG50160 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87%  
Best Local Similarity: 47.55%  
Query Match: 45.13%  
Conservative: 63  
Mismatches: 106  
Indels: 2  
RESULT 666  
ID ADG52032 standard; cDNA; 2840 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 667  
ID ADG49536 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 668  
ID ADG48912 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 669  
ID ADG51408 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 670  
ID ADG59352 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 671  
ID ADG62808 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 672  
ID ADM17610 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 673  
ID ADL07444 standard; cDNA; 2840 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 674  
ID AAT42094 standard; cDNA to mRNA; 756 BP.  
DE Human LAMP residues 46-294 coding sequence.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 66.87% Conservative: 63  
Best Local Similarity: 47.55% Mismatches: 106  
Query Match: 45.13% Indels: 2  
RESULT 675  
ID AAT42095 standard; cDNA to mRNA; 756 BP.  
DE Rat LAMP residues 46-294 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDNJ ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 76.68% Conservative: 50  
Best Local Similarity: 56.92% Mismatches: 58  
Query Match: 44.05% Indels: 1  
RESULT 676  
ID ADH71417 standard; DNA; 1030 BP.  
DE Human gene of the invention NOV1lg SEQ ID NO:313.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 64.20% Conservative: 44  
Best Local Similarity: 50.62% Mismatches: 104  
Query Match: 42.25% Indels: 12  
RESULT 677  
ID ADH71411 standard; DNA; 1033 BP.  
DE Human gene of the invention NOV1ln SEQ ID NO:307.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 64.20% Conservative: 44  
Best Local Similarity: 50.62% Mismatches: 104  
Query Match: 42.25% Indels: 12  
RESULT 678  
ID ADH71413 standard; DNA; 1035 BP.  
DE Human gene of the invention NOV1lo SEQ ID NO:309.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 64.20% Conservative: 44  
Best Local Similarity: 50.62% Mismatches: 104  
Query Match: 42.25% Indels: 12  
RESULT 679  
ID ABS76364 standard; DNA; 1427 BP.  
DE DNA encoding human immunoglobulin superfamily protein IGSPF-9.  
PN WO200272794-A2.  
PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 64.20% Conservative: 44  
Best Local Similarity: 50.62% Mismatches: 104  
Query Match: 42.25% Indels: 12  
RESULT 680  
ID AAD47371 standard; DNA; 2653 BP.  
DE Human LP289 DNA.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 64.20% Conservative: 44  
Best Local Similarity: 50.62% Mismatches: 104  
Query Match: 42.25% Indels: 12  
RESULT 681  
ID ADH71395 standard; DNA; 976 BP.  
DE Human gene of the invention NOV1lf SEQ ID NO:291.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 64.40% Conservative: 45  
Best Local Similarity: 50.46% Mismatches: 103  
Query Match: 42.19% Indels: 12  
RESULT 682  
ID ADH71389 standard; DNA; 976 BP.  
DE Human gene of the invention NOV1lc SEQ ID NO:285.  
PN WO2003102155-A2.

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PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.40% Conservative: 45
Best Local Similarity: 50.46% Mismatches: 103
Query Match: 42.19% Indels: 12
RESULT 683
ID ADH71401 standard; DNA; 926 BP.
DE Human gene of the invention NOV111 SEQ ID NO:297.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 684
ID ADH71405 standard; DNA; 927 BP.
DE Human gene of the invention NOV11k SEQ ID NO:301.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 685
ID ADH71409 standard; DNA; 946 BP.
DE Human gene of the invention NOV1lm SEQ ID NO:305.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 686
ID ADH71393 standard; DNA; 946 BP.
DE Human gene of the invention NOV1le SEQ ID NO:289.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 687
ID ADH71415 standard; DNA; 976 BP.
DE Human gene of the invention NOV1lp SEQ ID NO:311.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 688
ID ADH71397 standard; DNA; 976 BP.
DE Human gene of the invention NOV1lg SEQ ID NO:293.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 689
ID ABS71699 standard; DNA; 1017 BP.
DE DNA encoding human NOV5b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 690
ID ADL35978 standard; cDNA; 1017 BP.
DE Human NOVX cDNA #12.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
(PA (SHEN/) SHENOV S G.
(PA (SPVT/) SPYTEK K A.
(PA (ZERH/) ZERHUSEN B D.
(PA (PATI/) PATTURAJAN M.
(PA (GUOX/) GUO X.
(PA (KEKU/) KEKUDA R.
(PA (GANG/) GANGOLLI E A.
(PA (SHIM/) SHIMKETS R A.
(PA (TAUP/) TAUPIER R J.
(PA (LILL/) LI L.
(PA (PADI/) PADIGARU M.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 691
ID ABS71698 standard; DNA; 1018 BP.
DE DNA encoding human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 692
ID ADL35976 standard; cDNA; 1018 BP.
DE Human NOVX cDNA #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
(PA (SHEN/) SHENOV S G.
(PA (SPVT/) SPYTEK K A.
(PA (ZERH/) ZERHUSEN B D.
(PA (PATI/) PATTURAJAN M.
(PA (GUOX/) GUO X.
(PA (KEKU/) KEKUDA R.
(PA (GANG/) GANGOLLI E A.
(PA (SHIM/) SHIMKETS R A.
(PA (TAUP/) TAUPIER R J.
(PA (LILL/) LI L.
(PA (PADI/) PADIGARU M.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 693
ID ADH71399 standard; DNA; 1018 BP.
DE Human gene of the invention NOV1lh SEQ ID NO:295.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 694
ID ADH71387 standard; DNA; 1033 BP.
DE Human gene of the invention NOV1lb SEQ ID NO:283.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 695
ID ADH71385 standard; DNA; 1271 BP.
DE Human gene of the invention NOV1la SEQ ID NO:281.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11% Conservative: 41
Best Local Similarity: 52.49% Mismatches: 94
Query Match: 42.14% Indels: 8
RESULT 696
ID ADH71421 standard; DNA; 1271 BP.
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DE Human gene of the invention NOV11s SEQ ID NO:317.  
PN WO2003102155-A2.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 63.89% Conservative: 43  
Best Local Similarity: 50.62% Mismatches: 105  
Query Match: 42.08% Indels: 12  
RESULT 697  
ID ABS71700 standard; DNA; 1136 BP.  
DE DNA encoding human NOV5c protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 65.78% Conservative: 40  
Best Local Similarity: 52.49% Mismatches: 95  
Query Match: 41.92% Indels: 8  
RESULT 698  
ID ADH71403 standard; DNA; 1171 BP.  
DE Human gene of the invention NOV11j SEQ ID NO:299.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 65.78% Conservative: 40  
Best Local Similarity: 52.49% Mismatches: 95  
Query Match: 41.92% Indels: 8  
RESULT 699  
ID ADH71419 standard; DNA; 1271 BP.  
DE Human gene of the invention NOV11r SEQ ID NO:315.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 63.89% Conservative: 44  
Best Local Similarity: 50.31% Mismatches: 105  
Query Match: 41.92% Indels: 12  
RESULT 700  
ID ADP28685 standard; DNA; 834 BP.  
DE Human secreted protein encoding sequence SEQ ID #683.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 68.33% Conservative: 40  
Best Local Similarity: 54.09% Mismatches: 84  
Query Match: 41.67% Indels: 5  
RESULT 701  
ID ABK35606 standard; DNA; 1011 BP.  
DE Gene encoding novel human secreted or membrane-associated protein #25.  
PN WO200204600-A2.  
PD 17-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Percent Similarity: 65.12% Conservative: 44  
Best Local Similarity: 50.50% Mismatches: 97  
Query Match: 40.20% Indels: 8  
RESULT 702  
ID ABS71701 standard; DNA; 1169 BP.  
DE DNA encoding human NOV5d protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 64.78% Conservative: 43  
Best Local Similarity: 50.50% Mismatches: 98  
Query Match: 39.92% Indels: 8  
RESULT 703  
ID ADH71407 standard; DNA; 1169 BP.  
DE Human gene of the invention NOV11l SEQ ID NO:303.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 64.78% Conservative: 43  
Best Local Similarity: 50.50% Mismatches: 98  
Query Match: 39.92% Indels: 8  
RESULT 704  
ID ABK35605 standard; DNA; 1056 BP.  
DE Gene encoding novel human secreted or membrane-associated protein #24.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 64.78% Conservative: 43  
Best Local Similarity: 50.50% Mismatches: 99  
Query Match: 37.76% Indels: 10  
RESULT 705  
ID ABV83812 standard; cDNA; 2813 BP.  
DE Human polynucleotide SEQ ID NO 141.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Percent Similarity: 70.45% Conservative: 53  
Best Local Similarity: 50.38% Mismatches: 77  
Query Match: 39.89% Indels: 1  
RESULT 706  
ID AAD47374 standard; DNA; 2601 BP.  
DE Human LP319b DNA.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 65.12% Conservative: 44  
Best Local Similarity: 50.50% Mismatches: 97  
Query Match: 39.04% Indels: 9  
RESULT 707  
ID ACH15238 standard; cDNA; 437 BP.  
DE Human adult brain cDNA #2450.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Percent Similarity: 99.25% Conservative: 0  
Best Local Similarity: 99.25% Mismatches: 1  
Query Match: 38.21% Indels: 0  
RESULT 708  
ID ADH71391 standard; DNA; 760 BP.  
DE Human gene of the invention NOV11d SEQ ID NO:287.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 68.40% Conservative: 32  
Best Local Similarity: 55.60% Mismatches: 74  
Query Match: 38.07% Indels: 5  
RESULT 709  
ID ADL35982 standard; cDNA; 1168 BP.  
DE Human NOVX cDNA #14.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOV S G.  
PA (SPVT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PAITURAJAN M.  
PA (GUOX/) GUO X.  
PA (KEKU/) KEGUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (LILL/) LI L.  
PA (PADI/) PADIGARU M.  
Percent Similarity: 64.24% Conservative: 43  
Best Local Similarity: 50.00% Mismatches: 99  
Query Match: 37.76% Indels: 10  
RESULT 710  
ID ABK35605 standard; DNA; 1056 BP.  
DE Gene encoding novel human secreted or membrane-associated protein #24.

PN WO200204600-A2.  
PD 17-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (GLAX ) GLAXO GROUP LTD.  
Percent Similarity: 64.26%  
Best Local Similarity: 51.89%  
Query Match: 37.74%  
Indels: 19  
Conservative: 36  
Mismatches: 86  
Indels: 19

RESULT 711  
ID ADL35980 standard; cDNA; 1133 BP.  
DE Human NOVX cDNA #13.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (GUOX/) GUO X.  
PA (KEKU/) KEXUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (LILL/) LI L.  
PA (PADI/) PADIGARU M.  
Percent Similarity: 64.78%  
Best Local Similarity: 51.16%  
Query Match: 37.71%  
Indels: 11  
Conservative: 41  
Mismatches: 98  
Indels: 11

RESULT 712  
ID AAS28811 standard; cDNA; 4656 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID NO 57.  
PN WO20015315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 69.81%  
Best Local Similarity: 49.43%  
Query Match: 37.35%  
Indels: 3  
Conservative: 54  
Mismatches: 78  
Indels: 3

RESULT 713  
ID ADB31536 standard; cDNA; 4656 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 57.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 69.81%  
Best Local Similarity: 49.43%  
Query Match: 37.35%  
Indels: 3  
Conservative: 54  
Mismatches: 78  
Indels: 3

RESULT 714  
ID AAD47373 standard; DNA; 2597 BP.  
DE Human LP319a DNA.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 59.57%  
Best Local Similarity: 45.90%  
Query Match: 36.68%  
Indels: 28  
Conservative: 45  
Mismatches: 106  
Indels: 28

RESULT 715  
ID ABL99899 standard; cDNA; 5666 BP.  
DE Human secretory polynucleotide (sptm) 154.  
PN WO20020756-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 63.61%  
Best Local Similarity: 44.08%  
Query Match: 36.10%  
Indels: 14  
Conservative: 66  
Mismatches: 109  
Indels: 14

RESULT 716  
ID AAC91321 standard; cDNA; 537 BP.  
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.  
PN WO200073509-A2.  
PD 07-DEC-2000.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 97.54%  
Best Local Similarity: 97.54%  
Query Match: 34.99%  
Indels: 0  
Conservative: 0  
Mismatches: 3  
Indels: 0

RESULT 717  
ID AAD47372 standard; DNA; 754 BP.  
DE Human LP289 splice variant (LP343) DNA.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 69.27%  
Best Local Similarity: 55.96%  
Query Match: 33.58%  
Indels: 5  
Conservative: 29  
Mismatches: 62  
Indels: 5

RESULT 718  
ID AAS78035 standard; cDNA; 484 BP.  
DE DNA encoding novel human diagnostic protein #13839.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 90.30%  
Best Local Similarity: 86.57%  
Query Match: 33.22%  
Indels: 0  
Conservative: 5  
Mismatches: 13  
Indels: 0

RESULT 719  
ID ADP28686 standard; DNA; 666 BP.  
DE Human secreted protein encoding sequence SEQ ID #684.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 67.70%  
Best Local Similarity: 53.98%  
Query Match: 33.19%  
Indels: 5  
Conservative: 31  
Mismatches: 68  
Indels: 5

RESULT 720  
ID ACH46276 standard; cDNA; 409 BP.  
DE Human infant brain cDNA #339.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Percent Similarity: 95.87%  
Best Local Similarity: 94.21%  
Query Match: 32.06%  
Indels: 0  
Conservative: 2  
Mismatches: 5  
Indels: 0

RESULT 721  
ID AAF93346 standard; cDNA; 452 BP.  
DE Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.  
PN WO200107611-A2.  
PD 01-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 32.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0

RESULT 722  
ID AAS78034 standard; cDNA; 443 BP.  
DE DNA encoding novel human diagnostic protein #13838.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 88.89%  
Best Local Similarity: 88.89%  
Query Match: 31.53%  
Indels: 11  
Conservative: 0  
Mismatches: 3  
Indels: 11

RESULT 723  
ID ADQ83739 standard; cDNA; 919 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #553.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 64.96%  
Best Local Similarity: 50.00%  
Query Match: 30.79%  
Indels: 8  
Conservative: 35  
Mismatches: 74  
Indels: 8

RESULT 724  
ID AAC19214 standard; cDNA; 333 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 23289.  
PN EP1033401-A2.

PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Percent Similarity: 95.50%  
Best Local Similarity: 94.59%  
Query Match: 30.18%  
Indels: 1  
Conservative: 1  
Mismatches: 4  
Indels: 1  
RESULT 725  
ID AAS78003 standard; cDNA; 2883 BP.  
DE DNA encoding novel human diagenetic protein #13807.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 56.58%  
Best Local Similarity: 45.58%  
Query Match: 29.10%  
Indels: 50  
Conservative: 31  
Mismatches: 74  
Indels: 50  
RESULT 726  
ID ADE08816 standard; DNA; 2883 BP.  
DE Novel DNA-related contig nucleotide sequence #60.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 56.58%  
Best Local Similarity: 45.58%  
Query Match: 29.10%  
Indels: 50  
Conservative: 31  
Mismatches: 74  
Indels: 50  
RESULT 727  
ID AAF93597 standard; cDNA; 585 BP.  
DE Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.  
PN WO200107611-A2.  
PD 01-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 71.58%  
Best Local Similarity: 50.58%  
Query Match: 27.16%  
Indels: 4  
Conservative: 40  
Mismatches: 50  
Indels: 4  
RESULT 728  
ID ABS2769 standard; cDNA; 408 BP.  
DE Murine tuberosus sclerosis complex 8 (TSC8) DNA.  
PN WO200246475-A2.  
PD 13-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 75.00%  
Best Local Similarity: 55.88%  
Query Match: 22.18%  
Indels: 1  
Conservative: 26  
Mismatches: 33  
Indels: 1  
RESULT 729  
ID ADG63283 standard; DNA; 540 BP.  
DE Human OBCAM gene exon 2.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Percent Similarity: 78.38%  
Best Local Similarity: 69.37%  
Query Match: 21.68%  
Indels: 13  
Conservative: 10  
Mismatches: 11  
Indels: 13  
RESULT 730  
ID AAC02777 standard; cDNA; 352 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 2775.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Percent Similarity: 82.80%  
Best Local Similarity: 73.12%  
Query Match: 19.05%  
Indels: 1  
Conservative: 9  
Mismatches: 16  
Indels: 1  
RESULT 731  
ID ABL25337 standard; DNA; 1242 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27484.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 42.93%  
Best Local Similarity: 27.99%  
Query Match: 18.74%  
Indels: 63  
Conservative: 55  
Mismatches: 147  
Indels: 63  
RESULT 732  
ID ABL17651 standard; DNA; 948 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4426.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 50.17%  
Best Local Similarity: 31.86%  
Query Match: 18.44%  
Indels: 22  
Conservative: 54  
Mismatches: 125  
Indels: 22  
RESULT 733  
ID ABL11515 standard; cDNA; 2010 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 47.64%  
Best Local Similarity: 28.72%  
Query Match: 16.97%  
Indels: 30  
Conservative: 56  
Mismatches: 125  
Indels: 30  
RESULT 734  
ID ABX71182 standard; cDNA; 913 BP.  
DE Novel human cDNA sequence #407.  
PN WO200281731-A2.  
PD 17-OCT-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 66.13%  
Best Local Similarity: 46.77%  
Query Match: 16.75%  
Indels: 1  
Conservative: 24  
Mismatches: 41  
Indels: 1  
RESULT 735  
ID ABL04261 standard; cDNA; 1110 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7265.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 44.37%  
Best Local Similarity: 29.69%  
Query Match: 16.47%  
Indels: 27  
Conservative: 43  
Mismatches: 136  
Indels: 27  
RESULT 736  
ID ABL04260 standard; cDNA; 3426 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7262.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 44.37%  
Best Local Similarity: 29.69%  
Query Match: 16.47%  
Indels: 27  
Conservative: 43  
Mismatches: 136  
Indels: 27  
RESULT 737  
ID ABX56303 standard; DNA; 8243 BP.  
DE Human NOV25b CG93858-02 DNA SEQ ID 85.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 42.47%  
Best Local Similarity: 30.14%  
Query Match: 16.47%  
Indels: 63  
Conservative: 36  
Mismatches: 105  
Indels: 63  
RESULT 738  
ID ADK60477 standard; DNA; 8546 BP.  
DE Angiogenesis differentially expressed gene GS-N52.  
PN FR2836687-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
Percent Similarity: 42.12%  
Best Local Similarity: 29.79%  
Query Match: 16.09%  
Indels: 63  
Conservative: 36  
Mismatches: 106  
Indels: 63  
RESULT 739  
ID ADK60778 standard; DNA; 8546 BP.  
DE Angiogenesis differentially expressed gene GS-N52.  
PN FR2836686-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
Percent Similarity: 42.12%  
Best Local Similarity: 29.79%  
Query Match: 16.09%  
Indels: 63  
Conservative: 36  
Mismatches: 106  
Indels: 63  
RESULT 740  
ID ADP73100 standard; DNA; 8546 BP.  
DE Angiogenesis inhibitor human DNA sequence, GS-N52.

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PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 741
ID ADS09799 standard; DNA; 8546 BP.
DE Human therapeutic DNA - SEQ ID 36.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 742
ID ADO08272 standard; cDNA; 15659 BP.
DE Human NOVX polynucleotide #10.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOV S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERHUSEN B D.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 743
ID ACA10120 standard; cDNA; 15660 BP.
DE Human NOVX polynucleotide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 744
ID ADH72105 standard; DNA; 15660 BP.
DE Human gene of the invention NOV43c SEQ ID NO:1001.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 745
ID ADK60455 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 746
ID ADK60756 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 747
ID ADP73078 standard; DNA; 18207 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 748
ID ADH72103 standard; DNA; 2136 BP.
DE Human gene of the invention NOV43b SEQ ID NO:999.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 749
ID ACA10119 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 750
ID ADH72101 standard; DNA; 2153 BP.
DE Human gene of the invention NOV43a SEQ ID NO:997.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 751
ID ADO08270 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.

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PA (LILL/) LI L.  
PA (LIUX/) LIU X.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLER C E.  
PA (MILL/) MILLER I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (RIEG/) RIEGER D K.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (SPYT/) SPYTEK K A.  
PA (TAUP/) TAUPIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 752  
ID ACD03633 standard; cDNA; 2916 BP.  
DE Human GPCR related protein NOV9b cDNA.  
PN WO200299116-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.97%  
Best Local Similarity: 30.50%  
Query Match: 15.97%  
Conservative: 38  
Mismatches: 117  
Indels: 41  
RESULT 753  
ID AAS68120 standard; cDNA; 3910 BP.  
DE DNA encoding novel human diagnostic protein #3924.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 754  
ID AA172024 standard; cDNA; 4073 BP.  
DE Human thrombospondin protein, BTL012, coding sequence.  
PN WO200174852-A2.  
PD 11-OCT-2001.  
PA (FARB) BAYER CORP.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 755  
ID ADL93996 standard; cDNA; 5877 BP.  
DE Human g-coupled protein receptor-related gene #44.  
PN US2004006205-A1.  
PD 08-JAN-2004.  
PA (LILL/) LI L.  
PA (GERL/) GERLACH V.  
PA (LIUX/) LIU X.  
PA (MILL/) MILLER C E.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (ZHON/) ZHONG H.  
PA (SMIT/) SMITHSON G.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (VOSS/) VOSS E Z.  
PA (VERN/) VERNET C A.  
PA (MACD/) MACDOUGALL J R.  
PA (RAST/) RASTELLI L.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (MEZE/) MEZES P S.  
PA (FURT/) FURTAK K.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.

PA (MALY/) MALYANKAR U M.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (EDIN/) EDINGER S.  
PA (MAZU/) MAZUR A.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 756  
ID ADB16057 standard; DNA; 5935 BP.  
DE G-coupled protein receptor related polypeptide DNA, SEQ ID No 87.  
PN WO200283841-A2.  
PD 24-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 757  
ID ABX56304 standard; DNA; 6343 BP.  
DE Human NOV25c CG56914-03 DNA SEQ ID 87.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 758  
ID ADH72107 standard; DNA; 6343 BP.  
DE Human gene of the invention NOV43d SEQ ID NO:1003.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 759  
ID ABO86156 standard; DNA; 16908 BP.  
DE Novel human gene. SEQ ID 27.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (GLAX) GLAXO GROUP LTD.  
Percent Similarity: 43.36%  
Best Local Similarity: 31.12%  
Query Match: 15.97%  
Conservative: 35  
Mismatches: 111  
Indels: 51  
RESULT 760  
ID ADQ22570 standard; DNA; 18248 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 43.77%  
Best Local Similarity: 30.25%  
Query Match: 15.92%  
Conservative: 38  
Mismatches: 117  
Indels: 41  
RESULT 761  
ID ADM93822 standard; DNA; 2916 BP.  
DE DNA encoding human NOV protein #21.  
PN US2004009480-A1.  
PD 15-JAN-2004.  
PA (ANDE/) ANDERSON D W.  
PA (BAUM/) BAUMGARTNER J C.  
PA (BOLD/) BOLDOG F L.  
PA (CASM/) CASMAN S J.  
PA (EDIN/) EDINGER S R.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUOX/) GUO X S.  
PA (HJAL/) HJALT T.  
PA (KEKU/) KEKUDA R.  
PA (LILL/) LI L.  
PA (MACD/) MACDOUGALL J R.

PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATI/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
PA (STON/) STONE D J.  
PA (SPYT/) SPYTEK K A.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
Percent Similarity: 43.01%  
Best Local Similarity: 30.07%  
Query Match: 15.86%  
RESULT 762  
ID ABL12455 standard; cDNA; 1710 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31847.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE/) PE CORP NY.  
Percent Similarity: 43.10%  
Best Local Similarity: 26.15%  
Query Match: 15.75%  
RESULT 763  
ID ADB53259 standard; DNA; 3170 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3801.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 42.52%  
Best Local Similarity: 25.51%  
Query Match: 15.37%  
RESULT 764  
ID ADI24496 standard; cDNA; 2960 BP.  
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:46.  
PN WO2004004785-A1.  
PD 15-JAN-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.28%  
RESULT 765  
ID ADA53985 standard; cDNA; 3309 BP.  
DE Human coding sequence, SEQ ID 1553.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.28%  
RESULT 766  
ID AAH98595 standard; cDNA; 4710 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 452.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.28%  
RESULT 767  
ID AAH98610 standard; cDNA; 4710 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 467.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.28%  
RESULT 768  
ID AAD14203 standard; DNA; 8513 BP.  
DE MESVR/EGFP/IRESNCAPro(ori) vector.

PN WO200155371-A1.  
PD 02-AUG-2001.  
PA (SCRI-) SCRIPPS RES INST.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.28%  
RESULT 769  
ID ADD25618 standard; DNA; 2633 BP.  
DE Binding domain-immunoglobulin fusion protein-associated DNA #93.  
PN US2003118592-A1.  
PD 26-JUN-2003.  
PA (GENE-) GENE CRAFT INC.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.23%  
RESULT 770  
ID ADI31624 standard; cDNA; 2633 BP.  
DE Human cDNA #950.  
PN US6607879-B1.  
PD 19-AUG-2003.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.23%  
RESULT 771  
ID ADL12516 standard; cDNA; 5807 BP.  
DE Human steroid-induced C3A liver cell cDNA #245.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 43.31%  
Best Local Similarity: 25.70%  
Query Match: 15.17%  
RESULT 772  
ID AAD56185 standard; DNA; 6801 BP.  
DE Human LRRCAPS DNA #2.  
PN WO2003035831-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 39.58%  
Best Local Similarity: 29.17%  
Query Match: 15.17%  
RESULT 773  
ID ADH48823 standard; DNA; 7097 BP.  
DE NOV45B coding sequence, SEQ ID 107.  
PN WO200268652-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 41.99%  
Best Local Similarity: 29.00%  
Query Match: 15.14%  
RESULT 774  
ID ADH48921 standard; DNA; 4321 BP.  
DE NOV45A coding sequence, SEQ ID 105.  
PN WO200268652-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 41.74%  
Best Local Similarity: 28.97%  
Query Match: 15.03%  
RESULT 775  
ID AAL62047 standard; cDNA; 3360 BP.  
DE Human cell adhesion and extracellular matrix protein (CADECM)-35 cDNA.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 41.84%  
Best Local Similarity: 24.83%  
Query Match: 15.01%  
RESULT 776  
ID ABL23499 standard; DNA; 2190 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21970.  
PN WO200171042-A2.

PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 41.18% Conservative: 49  
Best Local Similarity: 26.01% Mismatches: 131  
Query Match: 14.95% Indels: 60  
RESULT 777  
ID ADQ89919 standard; DNA; 4491 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #175.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 778  
ID ADQ89913 standard; DNA; 4491 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #172.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 779  
ID AA251671 standard; cDNA; 5510 BP.  
DE Human p53 target molecule, PRG2 cDNA.  
PN WO200012526-A1.  
PD 09-MAR-2000.  
PA (UYPR-) UNIV PRINCETON.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 780  
ID ABK83723 standard; cDNA; 5510 BP.  
DE Human cDNA differentially expressed in granulocytic cells #294.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 781  
ID ABN95260 standard; DNA; 5510 BP.  
DE Gene #1758 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 782  
ID ADD89099 standard; cDNA; 5510 BP.  
DE Encoding sequence TAT264.  
PN WO2003057160-A2.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 783  
ID ABX08782 standard; cDNA; 5510 BP.  
DE Angiogenesis-associated human polynucleotide sequence #44.  
PN WO200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 784  
ID ADQ18901 standard; DNA; 5510 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1720.  
PN WO2004048938-A2.  
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 785  
ID ABA08831 standard; cDNA; 5530 BP.  
DE Human peroxidase homologous-encoding cDNA, SEQ ID NO:607.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 786  
ID ACD05839 standard; cDNA; 5530 BP.  
DE Novel human contig #13.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 787  
ID ADL35716 standard; DNA; 6807 BP.  
DE Human peroxidase-melanoma antigen-related DNA.  
PN WO2004019893-A2.  
PD 11-MAR-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 788  
ID AAV99922 standard; cDNA; 6847 BP.  
DE Melanoma associated antigen MG50 gene.  
PN WO9855133-A1.  
PD 10-DEC-1998.  
PA (REGC ) UNIV CALIFORNIA.  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 789  
ID ABQ88160 standard; cDNA; 6847 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 67.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC ) PROCTER & GAMBLE CO.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 790  
ID ADR66609 standard; DNA; 6847 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 121 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 791  
ID ADR65865 standard; DNA; 6847 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 61 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51

PA (PILA/) PILARSKY C. 38.70% Conservative: 32  
Percent Similarity: 28.79% Mismatches: 147  
Best Local Similarity: 14.87% Indels: 51  
Query Match: 14.87%  
RESULT 792  
ID ADR666267 standard; DNA; 6847 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 121 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 793  
ID ADR66768 standard; DNA; 6847 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 61 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 794  
ID ADF81722 standard; DNA; 6939 BP.  
DE Leukaemia-related DNA sequence #2278.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 795  
ID ADF81721 standard; DNA; 6939 BP.  
DE Leukaemia-related DNA sequence #2277.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Percent Similarity: 38.70% Conservative: 32  
Best Local Similarity: 28.79% Mismatches: 147  
Query Match: 14.87% Indels: 51  
RESULT 796  
ID ABL17650 standard; DNA; 3060 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4423.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 44.74% Conservative: 54  
Best Local Similarity: 28.53% Mismatches: 124  
Query Match: 14.78% Indels: 62  
RESULT 797  
ID ABS70409 standard; cDNA; 6814 BP.  
DE Human bone remodelling gene #66.  
PN US6426186-B1.  
PD 30-JUL-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 38.39% Conservative: 32  
Best Local Similarity: 28.48% Mismatches: 148

Query Match: 14.59% Indels: 51  
RESULT 798  
ID ABX63089 standard; cDNA; 4978 BP.  
DE Human CDNA #89 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Percent Similarity: 43.15% Conservative: 50  
Best Local Similarity: 26.03% Mismatches: 133  
Query Match: 14.56% Indels: 33  
RESULT 799  
ID AAX55767 standard; cDNA; 4188 BP.  
DE Drosophila Robo 1 polypeptide encoding CDNA.  
PN WO9925833-A1.  
PD 27-MAY-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 42.16% Conservative: 49  
Best Local Similarity: 26.14% Mismatches: 127  
Query Match: 14.45% Indels: 50  
RESULT 800  
ID AAX57350 standard; cDNA; 4188 BP.  
DE Drosophila sp. ROBO1 CDNA.  
PN WO9920764-A1.  
PD 29-APR-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 42.16% Conservative: 49  
Best Local Similarity: 26.14% Mismatches: 127  
Query Match: 14.45% Indels: 50  
RESULT 801  
ID ABL10471 standard; cDNA; 2113 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25895.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 42.34% Conservative: 58  
Best Local Similarity: 26.18% Mismatches: 134  
Query Match: 14.42% Indels: 73  
RESULT 802  
ID ABL22881 standard; DNA; 4355 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20116.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 42.16% Conservative: 49  
Best Local Similarity: 26.14% Mismatches: 127  
Query Match: 14.40% Indels: 50  
RESULT 803  
ID ABX13540 standard; DNA; 93801 BP.  
DE Human RGS11 DNA.  
PN WO2002103355-A1.  
PD 27-DEC-2002.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Percent Similarity: 42.96% Conservative: 37  
Best Local Similarity: 29.60% Mismatches: 132  
Query Match: 14.34% Indels: 26  
RESULT 804  
ID ADQ89963 standard; DNA; 103052 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #197.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Percent Similarity: 42.96% Conservative: 37  
Best Local Similarity: 29.60% Mismatches: 132  
Query Match: 14.34% Indels: 26  
RESULT 805  
ID ADM74170 standard; DNA; 1140 BP.  
DE Human NOV3A gene sequence SegID9.  
PN WO2004015079-A2.  
PD 19-FEB-2004.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.38% Conservative: 52  
Best Local Similarity: 27.38% Mismatches: 123  
Query Match: 14.31% Indels: 61



RESULT 806  
ID AAZ06640 standard; cDNA; 1335 BP.  
DE Beta-secretase polynucleotide.  
PN US5942400-A.  
PD 24-AUG-1999.  
PA (ELAN-) ELAN PHARM INC.  
Percent Similarity: 42.39%  
Best Local Similarity: 26.63%  
Query Match: 14.17%  
Conservative: 58  
Mismatches: 137  
Indels: 76  
RESULT 807  
ID AAC65809 standard; cDNA; 1335 BP.  
DE Beta-secretase cDNA.  
PN US6221645-B1.  
PD 24-APR-2001.  
PA (ELAN-) ELAN PHARM INC.  
Percent Similarity: 42.39%  
Best Local Similarity: 26.63%  
Query Match: 14.17%  
Conservative: 58  
Mismatches: 137  
Indels: 76  
RESULT 808  
ID ABL14207 standard; cDNA; 2131 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37103.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.78%  
Best Local Similarity: 24.93%  
Query Match: 14.17%  
Conservative: 53  
Mismatches: 131  
Indels: 84  
RESULT 809  
ID ADM74176 standard; DNA; 918 BP.  
DE Human NOV3D gene sequence SeqID15.  
PN WO2004015079-A2.  
PD 19-FEB-2004.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.38%  
Best Local Similarity: 27.08%  
Query Match: 14.04%  
Conservative: 53  
Mismatches: 123  
Indels: 61  
RESULT 810  
ID ABT17377 standard; DNA; 1216 BP.  
DE Human IG gene related nucleic acid SEQ ID No 3.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 43.60%  
Best Local Similarity: 26.83%  
Query Match: 14.04%  
Conservative: 55  
Mismatches: 124  
Indels: 61  
RESULT 811  
ID ABT17376 standard; DNA; 1242 BP.  
DE Human IG gene related nucleic acid SEQ ID No 2.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 812  
ID ADI19787 standard; DNA; 2113 BP.  
DE Human NOV12 DNA.  
PN US2004002134-A1.  
PD 01-JAN-2004.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 813  
ID AAF27862 standard; cDNA; 2116 BP.  
DE Human NOV12 cDNA.  
PN WO200075321-A2.  
PD 14-DEC-2000.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 814  
ID ABL54191 standard; cDNA; 2196 BP.

ID ABT17375 standard; DNA; 2116 BP.  
DE Human IG gene related nucleic acid SEQ ID No 1.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 815  
ID ACD40265 standard; DNA; 2116 BP.  
DE Human breast tumour associated protein 47-like polypeptide NOV12 DNA.  
PN US2003027158-A1.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 816  
ID ADM56388 standard; cDNA; 2116 BP.  
DE Human CDNA encoding cell adhesion molecule NOV12.  
PN US2003082554-A1.  
PD 01-MAY-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 817  
ID ADF66750 standard; cDNA; 2116 BP.  
DE CDNA encoding novel human protein NOV12.  
PN US2003199103-A1.  
PD 23-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 818  
ID ADO60260 standard; DNA; 2116 BP.  
DE Human NOV12 DNA.  
PN US2003134430-A1.  
PD 17-JUL-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 819  
ID ABK94901 standard; cDNA; 2422 BP.  
DE Human novel polynucleotide #12.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 43.06%  
Best Local Similarity: 26.91%  
Query Match: 14.04%  
Conservative: 57  
Mismatches: 137  
Indels: 65  
RESULT 820  
ID AAS86623 standard; cDNA; 16421 BP.  
DE DNA encoding novel human diagnostic protein #22427.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 42.86%  
Best Local Similarity: 26.19%  
Query Match: 14.04%  
Conservative: 42  
Mismatches: 115  
Indels: 29  
RESULT 821  
ID ADO47373 standard; DNA; 1761 BP.  
DE Human neurotrophin-like protein-related DNA SeqID8.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Percent Similarity: 43.97%  
Best Local Similarity: 27.36%  
Query Match: 14.01%  
Conservative: 51  
Mismatches: 132  
Indels: 40  
RESULT 822  
ID ABL54191 standard; cDNA; 2196 BP.

DE Neurotrophin-like protein splice variant coding sequence.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC. Conservative: 51  
Best Local Similarity: 43.97% Mismatches: 132  
Query Match: 27.36% Indels: 40  
RESULT 823  
ID ADO47371 standard; DNA; 2196 BP.  
DE Human neurotrophin-like protein-related gene SeqID6.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO. Conservative: 51  
Best Local Similarity: 43.97% Mismatches: 132  
Query Match: 27.36% Indels: 40  
RESULT 824  
ID ABL09371 standard; cDNA; 2658 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22595.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PERE-) PE CORP NY. Conservative: 54  
Best Local Similarity: 42.56% Mismatches: 122  
Query Match: 26.49% Indels: 71  
RESULT 825  
ID ABL54189 standard; cDNA; 1124 BP.  
DE Neurotrophin-like protein partial coding sequence.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 826  
ID ADO47367 standard; DNA; 1124 BP.  
DE Human neurotrophin-like protein-related gene SeqID2.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 827  
ID ADO47370 standard; cDNA; 1377 BP.  
DE Human neurotrophin-like protein-related cDNA SeqID5.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 828  
ID ABL54190 standard; cDNA; 1699 BP.  
DE Neurotrophin-like protein coding sequence.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 829  
ID ADO47368 standard; cDNA; 1699 BP.  
DE Human neurotrophin-like protein-related cDNA SeqID3.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 830  
ID ADS09923 standard; DNA; 1699 BP.  
DE Human therapeutic DNA - SEQ ID 160.

PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 831  
ID ADO47384 standard; DNA; 2868 BP.  
DE Human neurotrophin-like protein-related DNA SeqID12.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 832  
ID AAL62046 standard; cDNA; 3257 BP.  
DE Human cell adhesion and extracellular matrix protein (CADECM)-34 cDNA.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 833  
ID ADO47382 standard; DNA; 3312 BP.  
DE Human neurotrophin-like protein-related gene SeqID17.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 834  
ID ADS09924 standard; DNA; 3312 BP.  
DE Human therapeutic DNA - SEQ ID 161.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 835  
ID ADS10423 standard; DNA; 3386 BP.  
DE Human therapeutic DNA - SEQ ID 660.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 836  
ID AAS76287 standard; cDNA; 3868 BP.  
DE DNA encoding novel human diagnostic protein #12091.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 837  
ID ADH72133 standard; DNA; 4141 BP.  
DE Human gene of the invention NOV46f SEQ ID NO:1029.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. Conservative: 47  
Best Local Similarity: 44.89% Mismatches: 123  
Query Match: 27.74% Indels: 28  
RESULT 838  
ID ABX70427 standard; DNA; 4169 BP.  
DE DNA encoding human GPCR related protein NOV13a.  
PN WO200279398-A2.

PD 10-OCT-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 44.89%  
 Best Local Similarity: 27.74%  
 Query Match: 13.84%  
 Indels: 28  
 RESULT 839  
 ID ADH72137 standard; DNA; 4169 BP.  
 DE Human gene of the invention NOV46h SEQ ID NO:1033.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 44.89%  
 Best Local Similarity: 27.74%  
 Query Match: 13.84%  
 Indels: 28  
 RESULT 840  
 ID ADL24006 standard; cDNA; 4169 BP.  
 DE Human NOVX cDNA #26.  
 PN US2004002120-A1.  
 PD 01-JAN-2004.  
 PA (KEKU/) KEKUDA R.  
 PA (TCHE/) TCHERNEV V T.  
 PA (LIUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.  
 PA (PATT/) PATTURAJAN M.  
 PA (BURG/) BURGESS C E.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (MALLY/) MALYANKAR U M.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (PADI/) PADIGARU M.  
 PA (MILL/) MILLER C E.  
 PA (CASM/) CASMAN S J.  
 PA (PENNA/) PENNA C E A.  
 PA (GANG/) GANGOLLI E A.  
 PA (GUSE/) GUSEV V V.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERRH/) ZERHUSEN B D.  
 PA (GERL/) GERLACH V.  
 PA (POCH/) POCHART P F.  
 PA (FERN/) FERNANDES E R.  
 PA (SHIM/) SHIMKETS R A.  
 PA (RAST/) RASTELLI L.  
 PA (SPAD/) SPADERNA S K.  
 PA (LARO/) LAROCHHELLE W J.  
 PA (ZHON/) ZHONG M.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (VOSS/) VOSS E Z.  
 PA (HERR/) HERRMANN J L.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (PADI/) PADIGARU M.  
 PA (TAUP/) TAUPIER R J.  
 PA (MILL/) MILLER C E.  
 PA (CASM/) CASMAN S J.  
 PA (PENNA/) PENNA C E A.  
 PA (GANG/) GANGOLLI E A.  
 PA (GUSE/) GUSEV V V.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERRH/) ZERHUSEN B D.  
 PA (GERL/) GERLACH V.  
 PA (POCH/) POCHART P F.  
 PA (FERN/) FERNANDES E R.  
 PA (SHIM/) SHIMKETS R A.  
 PA (RAST/) RASTELLI L.  
 PA (SPAD/) SPADERNA S K.  
 PA (LARO/) LAROCHHELLE W J.  
 PA (ZHON/) ZHONG M.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (VOSS/) VOSS E Z.  
 PA (HERR/) HERRMANN J L.  
 Percent Similarity: 44.89%  
 Best Local Similarity: 27.74%  
 Query Match: 13.84%  
 Indels: 28  
 RESULT 841  
 ID ABX70420 standard; DNA; 4295 BP.  
 DE DNA encoding human GPCR related protein NOV12a.  
 PN WO200279398-A2.  
 PD 10-OCT-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 44.89%  
 Best Local Similarity: 27.74%  
 Query Match: 13.84%  
 Indels: 28  
 RESULT 842  
 ID ADL23992 standard; cDNA; 4295 BP.  
 DE Human NOVX cDNA #19.  
 PN US2004002120-A1.  
 PD 01-JAN-2004.  
 PA (KEKU/) KEKUDA R.  
 PA (TCHE/) TCHERNEV V T.  
 PA (LIUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.

PA (PATT/) PATTURAJAN M.  
 PA (BURG/) BURGESS C E.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (MALLY/) MALYANKAR U M.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (PADI/) PADIGARU M.  
 PA (MILL/) MILLER C E.  
 PA (CASM/) CASMAN S J.  
 PA (PENNA/) PENNA C E A.  
 PA (GANG/) GANGOLLI E A.  
 PA (GUSE/) GUSEV V V.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERRH/) ZERHUSEN B D.  
 PA (GERL/) GERLACH V.  
 PA (POCH/) POCHART P F.  
 PA (FERN/) FERNANDES E R.  
 PA (SHIM/) SHIMKETS R A.  
 PA (RAST/) RASTELLI L.  
 PA (SPAD/) SPADERNA S K.  
 PA (LARO/) LAROCHHELLE W J.  
 PA (ZHON/) ZHONG M.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (VOSS/) VOSS E Z.  
 PA (HERR/) HERRMANN J L.  
 Percent Similarity: 44.89%  
 Best Local Similarity: 27.74%  
 Query Match: 13.84%  
 Indels: 28  
 RESULT 843  
 ID ABD33040 standard; cDNA; 3588 BP.  
 DE Human cancer-associated cDNA HR22-025.1.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 40.70%  
 Best Local Similarity: 26.67%  
 Query Match: 13.82%  
 Indels: 59  
 RESULT 844  
 ID AAI64283 standard; DNA; 4548 BP.  
 DE Human transient axonal glycoprotein (tag-1) DNA.  
 PN WO200188546-A2.  
 PD 22-NOV-2001.  
 PA (UNMI) UNIV MICHIGAN.  
 Percent Similarity: 40.70%  
 Best Local Similarity: 26.67%  
 Query Match: 13.82%  
 Indels: 59  
 RESULT 845  
 ID ABD33041 standard; cDNA; 6137 BP.  
 DE Human cancer-associated cDNA HR22-025.2.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 40.70%  
 Best Local Similarity: 26.67%  
 Query Match: 13.82%  
 Indels: 59  
 RESULT 846  
 ID ADQ23368 standard; DNA; 7625 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6188.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 40.70%  
 Best Local Similarity: 26.67%  
 Query Match: 13.82%  
 Indels: 59  
 RESULT 847  
 ID ADQ24513 standard; DNA; 7625 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 40.70% Conservative: 40  
Best Local Similarity: 26.67% Mismatches: 110  
Query Match: 13.82% Indels: 59  
RESULT 848  
ID ADO28580 standard; cDNA; 7650 BP.  
DE Human axonin-1 precursor (AXO1) encoding cDNA SEQ ID NO:9.  
PN WO200404178-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 40.70% Conservative: 40  
Best Local Similarity: 26.67% Mismatches: 110  
Query Match: 13.82% Indels: 59  
RESULT 849  
ID ADA53286 standard; cDNA; 1880 BP.  
DE Human coding sequence, SEQ ID 854.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 44.31% Conservative: 58  
Best Local Similarity: 26.46% Mismatches: 126  
Query Match: 13.78% Indels: 55  
RESULT 850  
ID ABL24131 standard; DNA; 1404 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 23866.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE ) PE CORP NY.  
Percent Similarity: 42.08% Conservative: 38  
Best Local Similarity: 27.41% Mismatches: 72  
Query Match: 13.73% Indels: 78  
RESULT 851  
ID ABK94709 standard; DNA; 3314 BP.  
DE Neurodegenerative disease associated polynucleotide #18.  
PN WO200240996-A2.  
PD 23-MAY-2002.  
PA (MITO-) MITOKOR.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 852  
ID ABK94710 standard; DNA; 3335 BP.  
DE Neurodegenerative disease associated polynucleotide #19.  
PN WO200240996-A2.  
PD 23-MAY-2002.  
PA (MITO-) MITOKOR.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 853  
ID AAQ74440 standard; cDNA; 3360 BP.  
DE Human contactin cDNA (EMBL Accession #Z21488).  
PN EP618293-A1.  
PD 05-OCT-1994.  
PA (BECT ) BECTON DICKINSON CO.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 854  
ID ABL64109 standard; DNA; 3360 BP.  
DE Breast cancer related gene sequence SEQ ID NO:2446.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 855  
ID ABL63715 standard; DNA; 3360 BP.  
DE Breast cancer related gene sequence SEQ ID NO:2052.  
PN WO200194629-A2.  
PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 856  
ID ABK94708 standard; DNA; 3360 BP.  
DE Neurodegenerative disease associated polynucleotide #17.  
PN WO200240996-A2.  
PD 23-MAY-2002.  
PA (MITO-) MITOKOR.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 857  
ID ADE71112 standard; DNA; 3360 BP.  
DE Contactin gene, SEQ ID 66.  
PN WO2003070889-A2.  
PD 28-AUG-2003.  
PA (IDEC-) IDEC PHARM CORP.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 858  
ID ADJ75287 standard; DNA; 3360 BP.  
DE Marker gene SEQ ID NO:539.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 859  
ID AAT07313 standard; cDNA; 3395 BP.  
DE Human contactin coding sequence.  
PN WO9535373-A2.  
PD 28-DEC-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 860  
ID ADO28658 standard; cDNA; 3427 BP.  
DE Human CONT encoding cDNA SEQ ID NO:87.  
PN WO200404178-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 41.85% Conservative: 54  
Best Local Similarity: 24.60% Mismatches: 133  
Query Match: 13.65% Indels: 49  
RESULT 861  
ID ADR66243 standard; DNA; 4015 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 97 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Percent Similarity: 39.04% Conservative: 40  
Best Local Similarity: 27.03% Mismatches: 146  
Query Match: 13.62% Indels: 57  
RESULT 862  
ID ADR66585 standard; DNA; 4015 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 97 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Percent Similarity: 39.04% Conservative: 40

Best Local Similarity: 27.03% Mismatches: 146  
Query Match: 13.62% Indels: 57  
RESULT 863  
ID AAG67246 standard; cDNA; 2678 BP.  
DE DNA encoding novel human diagnostic protein #3050.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 45.21% Conservative: 60  
Best Local Similarity: 27.25% Mismatches: 99  
Query Match: 13.43% Indels: 87  
RESULT 864  
ID AAS71723 standard; cDNA; 2678 BP.  
DE DNA encoding novel human diagnostic protein #7527.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 45.21% Conservative: 60  
Best Local Similarity: 27.25% Mismatches: 99  
Query Match: 13.43% Indels: 87  
RESULT 865  
ID AAG64445 standard; cDNA; 3131 BP.  
DE DNA encoding novel human diagnostic protein #249.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 45.21% Conservative: 60  
Best Local Similarity: 27.25% Mismatches: 99  
Query Match: 13.43% Indels: 87  
RESULT 866  
ID AAS64798 standard; cDNA; 3131 BP.  
DE DNA encoding novel human diagnostic protein #602.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 45.21% Conservative: 60  
Best Local Similarity: 27.25% Mismatches: 99  
Query Match: 13.43% Indels: 87  
RESULT 867  
ID ABK90037 standard; cDNA; 7764 BP.  
DE Human OCP cDNA.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Percent Similarity: 40.47% Conservative: 46  
Best Local Similarity: 26.98% Mismatches: 129  
Query Match: 13.40% Indels: 74  
RESULT 868  
ID ABK90051 standard; cDNA; 7770 BP.  
DE Coding sequence of human OCP protein.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Percent Similarity: 40.47% Conservative: 46  
Best Local Similarity: 26.98% Mismatches: 129  
Query Match: 13.40% Indels: 74  
RESULT 869  
ID ADL02243 standard; cDNA; 7770 BP.  
DE Human OCP cDNA #5.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Percent Similarity: 40.47% Conservative: 46  
Best Local Similarity: 26.98% Mismatches: 129  
Query Match: 13.40% Indels: 74  
RESULT 870  
ID AAT15929 standard; cDNA; 2178 BP.  
DE Neural cell adhesion molecule splice variant cDNA.  
PN WO9604396-A1.  
PD 15-FEB-1996.  
PA (SYST-) SYSTEMIX INC.  
Percent Similarity: 41.98% Conservative: 57  
Best Local Similarity: 24.38% Mismatches: 157  
Query Match: 13.37% Indels: 31

Query Match: 13.37% Indels: 31  
RESULT 871  
ID AAT15928 standard; cDNA; 2450 BP.  
DE Neural cell adhesion molecule full-length DNA.  
PN WO9604396-A1.  
PD 15-FEB-1996.  
PA (SYST-) SYSTEMIX INC.  
Percent Similarity: 41.98% Conservative: 57  
Best Local Similarity: 24.38% Mismatches: 157  
Query Match: 13.37% Indels: 31  
RESULT 872  
ID ADJ76119 standard; DNA; 3843 BP.  
DE Marker gene SEQ ID NO:1371.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Percent Similarity: 41.85% Conservative: 55  
Best Local Similarity: 24.28% Mismatches: 133  
Query Match: 13.37% Indels: 49  
RESULT 873  
ID ADA53434 standard; cDNA; 3870 BP.  
DE Human coding sequence, SEQ ID 1002.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 44.33% Conservative: 48  
Best Local Similarity: 27.84% Mismatches: 109  
Query Match: 13.37% Indels: 53  
RESULT 874  
ID ADI24497 standard; cDNA; 4723 BP.  
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:47.  
PN WO2004004785-A1.  
PD 15-JAN-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 41.67% Conservative: 55  
Best Local Similarity: 24.69% Mismatches: 158  
Query Match: 13.37% Indels: 31  
RESULT 875  
ID AB211468 standard; cDNA; 6599 BP.  
DE Human polynucleotide SEQ ID NO 350.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 42.60% Conservative: 44  
Best Local Similarity: 26.71% Mismatches: 131  
Query Match: 13.34% Indels: 28  
RESULT 876  
ID ADM43986 standard; cDNA; 6599 BP.  
DE Novel human arginine-rich protein cDNA #350.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Percent Similarity: 42.60% Conservative: 44  
Best Local Similarity: 26.71% Mismatches: 131  
Query Match: 13.34% Indels: 28  
RESULT 877  
ID AAD04326 standard; DNA; 2766 BP.  
DE Human nuclear cell adhesion molecule homologue, NCAM\_c\_2 DNA.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Percent Similarity: 41.28% Conservative: 52  
Best Local Similarity: 25.38% Mismatches: 109  
Query Match: 13.21% Indels: 83  
RESULT 878  
ID AAD04325 standard; DNA; 2771 BP.  
DE Human cell adhesion molecule homologue (CAM-H) DNA #2.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.

Percent Similarity: 41.28% Conservative: 52  
Best Local Similarity: 25.38% Mismatches: 109  
Query Match: 13.21% Indels: 83  
RESULT 879  
ID AAD04327 standard; DNA; 2771 BP.  
DE Human nuclear cell adhesion molecule homologue, NCAM\_c\_1 DNA.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Percent Similarity: 41.28% Conservative: 52  
Best Local Similarity: 25.38% Mismatches: 109  
Query Match: 13.21% Indels: 83  
RESULT 880  
ID AAD04328 standard; DNA; 3060 BP.  
DE Human nuclear cell adhesion molecule homologue, NCAM\_d\_2 DNA.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Percent Similarity: 41.28% Conservative: 52  
Best Local Similarity: 25.38% Mismatches: 109  
Query Match: 13.21% Indels: 83  
RESULT 881  
ID AAD04324 standard; DNA; 3065 BP.  
DE Human cell adhesion molecule homologue (CAM-H) DNA #1.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Percent Similarity: 41.28% Conservative: 52  
Best Local Similarity: 25.38% Mismatches: 109  
Query Match: 13.21% Indels: 83  
RESULT 882  
ID ADJ56383 standard; cDNA; 6829 BP.  
DE C elegans cDNA differentially expressed in MYCN activated cells SeqID189.  
PN US2003119009-A1.  
PD 26-JUN-2003.  
PA (STUA/) STUART S G.  
PA (NUCH/) NUCHTERN J G.  
PA (PLON/) PLON S E.  
PA (SHOH/) SHOHET J M.  
Percent Similarity: 38.39% Conservative: 32  
Best Local Similarity: 28.48% Mismatches: 148  
Query Match: 13.18% Indels: 52  
RESULT 883  
ID ABS54189 standard; cDNA; 8180 BP.  
DE Human osteoclast protein (OCP) cDNA 5+3 corrected.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Percent Similarity: 40.64% Conservative: 47  
Best Local Similarity: 26.90% Mismatches: 128  
Query Match: 13.15% Indels: 75  
RESULT 884  
ID ADL02228 standard; cDNA; 8180 BP.  
DE Human OCP cDNA #3.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Percent Similarity: 40.64% Conservative: 47  
Best Local Similarity: 26.90% Mismatches: 128  
Query Match: 13.15% Indels: 75  
RESULT 885  
ID ABK90038 standard; cDNA; 8262 BP.  
DE Human 5+3 corrected OCP cDNA.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Percent Similarity: 40.64% Conservative: 47  
Best Local Similarity: 26.90% Mismatches: 128  
Query Match: 13.15% Indels: 75

RESULT 886  
ID AAI72586 standard; cDNA; 8262 BP.  
DE Human OCP cDNA.  
PN US200202026-A1.  
PD 21-FEB-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Percent Similarity: 40.64% Conservative: 47  
Best Local Similarity: 26.90% Mismatches: 128  
Query Match: 13.15% Indels: 75  
RESULT 887  
ID ABS54187 standard; cDNA; 8262 BP.  
DE Human osteoclast protein (OCP) cDNA.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Percent Similarity: 40.64% Conservative: 47  
Best Local Similarity: 26.90% Mismatches: 128  
Query Match: 13.15% Indels: 75  
RESULT 888  
ID ADJ02226 standard; cDNA; 8262 BP.  
DE Human OCP cDNA #2.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Percent Similarity: 40.64% Conservative: 47  
Best Local Similarity: 26.90% Mismatches: 128  
Query Match: 13.15% Indels: 75  
RESULT 889  
ID AAT42088 standard; cDNA to mRNA; 219 BP.  
DE Human LAMP residues 46-118 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 77.78% Conservative: 14  
Best Local Similarity: 58.33% Mismatches: 16  
Query Match: 13.12% Indels: 0  
RESULT 890  
ID AAT42089 standard; cDNA to mRNA; 219 BP.  
DE Rat LAMP residues 46-118 coding sequence.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Percent Similarity: 77.78% Conservative: 14  
Best Local Similarity: 58.33% Mismatches: 16  
Query Match: 13.12% Indels: 0  
RESULT 891  
ID ADR07797 standard; cDNA; 2451 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1303.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 40.83% Conservative: 34  
Best Local Similarity: 29.07% Mismatches: 133  
Query Match: 13.07% Indels: 39  
RESULT 892  
ID ADH71831 standard; DNA; 2902 BP.  
DE Human gene of the invention NOV29af SEQ ID NO:727.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.59% Conservative: 46  
Best Local Similarity: 27.06% Mismatches: 127  
Query Match: 13.04% Indels: 75  
RESULT 893  
ID ADH71817 standard; DNA; 2902 BP.

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DE Human gene of the invention NOV29y SEQ ID NO:713.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.59%
Best Local Similarity: 27.06%
Query Match: 13.04%
Conservative: 46
Mismatch: 127
Indels: 75
RESULT 894
ID ABK90046 standard; DNA; 3518 BP.
DE Middle fragment (B) comprising central region of human OCP DNA.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatch: 128
Indels: 75
RESULT 895
ID ADL02247 standard; cDNA; 3518 BP.
DE Human OCP cDNA #7.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatch: 128
Indels: 75
RESULT 896
ID ADR07921 standard; cDNA; 4086 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1427.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatch: 128
Indels: 75
RESULT 897
ID ADL02251 standard; cDNA; 7872 BP.
DE Human OCP cDNA #10.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatch: 128
Indels: 75
RESULT 898
ID ADS09892 standard; DNA; 7996 BP.
DE Human therapeutic DNA - SEQ ID 129.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatch: 128
Indels: 75
RESULT 899
ID ADS09893 standard; DNA; 8782 BP.
DE Human therapeutic DNA - SEQ ID 130.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatch: 128
Indels: 75
RESULT 900
ID ADB62179 standard; cDNA; 2420 BP.
DE Human cDNA encoding clone CTONG20036990.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 43.35%
Best Local Similarity: 26.62%
Query Match: 12.98%
Conservative: 44
Mismatch: 103
Indels: 46
RESULT 901
ID ABL98109 standard; cDNA; 1427 BP.
DE Human PRO7261 cDNA sequence SEQ ID NO:75.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatch: 132
Indels: 43
RESULT 902
ID ABL95598 standard; cDNA; 1427 BP.
DE Human anglogenesis related cDNA PRO7261 SEQ ID NO: 75.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatch: 132
Indels: 43
RESULT 903
ID ADD10364 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatch: 132
Indels: 43
RESULT 904
ID ADD11324 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatch: 132
Indels: 43
RESULT 905
ID ADD37117 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatch: 132
Indels: 43
RESULT 906
ID ADE41325 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatch: 132
Indels: 43
RESULT 907
ID ADH43508 standard; cDNA; 1427 BP.
DE Human PRO polynucleotide #38.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
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Percent Similarity: 39.45% Conservative: 42  
Best Local Similarity: 24.91% Mismatches: 132  
Query Match: 12.93% Indels: 43  
RESULT 908  
ID ADK82853 standard; cDNA; 1427 BP.  
DE Human PRO polynucleotide #38.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 39.45% Conservative: 42  
Best Local Similarity: 24.91% Mismatches: 132  
Query Match: 12.93% Indels: 43  
RESULT 909  
ID ADK67151 standard; DNA; 3904 BP.  
DE Human bladder cancer associated nucleotide sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAU B.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Percent Similarity: 39.45% Conservative: 42  
Best Local Similarity: 24.91% Mismatches: 132  
Query Match: 12.93% Indels: 43  
RESULT 910  
ID ABL22880 standard; DNA; 8410 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20113.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NV.  
Percent Similarity: 38.84% Conservative: 49  
Best Local Similarity: 23.85% Mismatches: 121  
Query Match: 12.93% Indels: 79  
RESULT 911  
ID ADH71829 standard; DNA; 2902 BP.  
DE Human gene of the invention NOV29ae SEQ ID NO:725.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.71% Conservative: 47  
Best Local Similarity: 26.84% Mismatches: 126  
Query Match: 12.87% Indels: 75  
RESULT 912  
ID ADH71815 standard; DNA; 2902 BP.  
DE Human gene of the invention NOV29x SEQ ID NO:711.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.71% Conservative: 47  
Best Local Similarity: 26.84% Mismatches: 126  
Query Match: 12.87% Indels: 75  
RESULT 913  
ID ADH71819 standard; DNA; 7831 BP.  
DE Human gene of the invention NOV29z SEQ ID NO:715.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35% Conservative: 46  
Best Local Similarity: 26.90% Mismatches: 132  
Query Match: 12.85% Indels: 72  
RESULT 914  
ID ABS51089 standard; cDNA; 7876 BP.  
DE cDNA encoding human NOV12a protein.  
PN WO200250277-A2.  
PD 27-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35% Conservative: 46  
Best Local Similarity: 26.90% Mismatches: 132  
Query Match: 12.85% Indels: 72  
RESULT 915  
ID ADJ83054 standard; DNA; 7876 BP.

Human NOVX NOV12a DNA.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLEY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Percent Similarity: 40.35% Conservative: 46  
Best Local Similarity: 26.90% Mismatches: 132  
Query Match: 12.85% Indels: 72  
RESULT 916  
ID ADH71843 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29al SEQ ID NO:739.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35% Conservative: 46  
Best Local Similarity: 26.90% Mismatches: 132  
Query Match: 12.85% Indels: 72  
RESULT 917  
ID ADH71769 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29a SEQ ID NO:665.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35% Conservative: 46  
Best Local Similarity: 26.90% Mismatches: 132  
Query Match: 12.85% Indels: 72  
RESULT 918  
ID ADH71839 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29aj SEQ ID NO:735.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35% Conservative: 46  
Best Local Similarity: 26.90% Mismatches: 132  
Query Match: 12.85% Indels: 72  
RESULT 919  
ID ADH71847 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29an SEQ ID NO:743.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35% Conservative: 46  
Best Local Similarity: 26.90% Mismatches: 132  
Query Match: 12.85% Indels: 72  
RESULT 920  
ID ADH71853 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29aq SEQ ID NO:749.  
PN WO2003102155-A2.  
PD 11-DEC-2003.



PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 921  
ID ADH71841 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29ak SEQ ID NO:737.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 922  
ID ADH71845 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29am SEQ ID NO:741.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 923  
ID ADH71849 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29ao SEQ ID NO:745.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 924  
ID ADH71835 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29ah SEQ ID NO:731.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 925  
ID ADH71851 standard; DNA; 7876 BP.  
DE Human gene of the invention NOV29ap SEQ ID NO:747.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 926  
ID ADH71837 standard; DNA; 7877 BP.  
DE Human gene of the invention NOV29ai SEQ ID NO:733.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 927  
ID ABS51094 standard; cDNA; 8270 BP.  
DE cDNA encoding human NOV12f protein.  
FN WO200250277-A2.  
PD 27-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 928  
ID ADJ383064 standard; DNA; 8270 BP.  
DE Human NOVX NOV12f DNA.  
FN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.

PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLEY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASHMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (PERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 929  
ID ADH71821 standard; DNA; 8270 BP.  
DE Human gene of the invention NOV29aa SEQ ID NO:717.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 40.35%  
Best Local Similarity: 26.90%  
Query Match: 12.85%  
Conservative: 46  
Mismatches: 132  
Indels: 72  
RESULT 930  
ID ABX10231 standard; cDNA; 11796 BP.  
DE Human cDNA encoding protein NOV9.  
FN WO200285922-A2.  
PD 31-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 39.55%  
Best Local Similarity: 28.30%  
Query Match: 12.85%  
Conservative: 35  
Mismatches: 128  
Indels: 60  
RESULT 931  
ID AAV40528 standard; cDNA; 3442 BP.  
DE Homo sapiens DL185\_1 clone secreted protein coding region.  
FN WO9830695-A2.  
PD 16-JUL-1998.  
PA (GEMY-) GENETICS INST INC.  
Percent Similarity: 42.01%  
Best Local Similarity: 26.74%  
Query Match: 12.79%  
Conservative: 44  
Mismatches: 135  
Indels: 32  
RESULT 932  
ID ADO38613 standard; DNA; 13650 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 276.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 38.91%  
Best Local Similarity: 26.05%  
Query Match: 12.79%  
Conservative: 40  
Mismatches: 148  
Indels: 42  
RESULT 933  
ID ADQ38612 standard; DNA; 13711 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 275.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 38.91%  
Best Local Similarity: 26.05%  
Query Match: 12.79%  
Conservative: 40  
Mismatches: 148  
Indels: 42

Query Match: 12.79% Indels: 42  
RESULT 934  
ID AD038614 standard; DNA; 13793 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 277.  
PN WO20004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 38.91% Conservative: 40  
Best Local Similarity: 26.05% Mismatches: 148  
Query Match: 12.79% Indels: 42  
RESULT 935  
ID AD038611 standard; DNA; 14194 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 274.  
PN WO20004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 38.91% Conservative: 40  
Best Local Similarity: 26.05% Mismatches: 148  
Query Match: 12.79% Indels: 42  
RESULT 936  
ID AAT87074 standard; cDNA; 2869 BP.  
DE Rat Dmk receptor cDNA.  
PN US5656473-A.  
PD 12-AUG-1997.  
PA (REGE-) REGENERON PHARM INC.  
Percent Similarity: 39.13% Conservative: 45  
Best Local Similarity: 25.16% Mismatches: 145  
Query Match: 12.76% Indels: 51  
RESULT 937  
ID AAT90472 standard; cDNA; 2869 BP.  
DE Rat muscle-specific kinase (MusK) cDNA.  
PN WO9721811-A2.  
PD 19-JUN-1997.  
PA (REGE-) REGENERON PHARM INC.  
Percent Similarity: 39.13% Conservative: 45  
Best Local Similarity: 25.16% Mismatches: 145  
Query Match: 12.76% Indels: 51  
RESULT 938  
ID AB033038 standard; cDNA; 8455 BP.  
DE Mouse cancer-associated cDNA WR22-025.1.  
PN WO20004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 38.78% Conservative: 39  
Best Local Similarity: 25.51% Mismatches: 103  
Query Match: 12.78% Indels: 77  
RESULT 939  
ID AB032650 standard; cDNA; 10976 BP.  
DE Human cancer-associated cDNA HR13-036.1.  
PN WO20004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 36.96% Conservative: 50  
Best Local Similarity: 24.30% Mismatches: 134  
Query Match: 12.76% Indels: 116  
RESULT 940  
ID AAT87073 standard; DNA; 2610 BP.  
DE Human Dmk receptor gene.  
PN US5656473-A.  
PD 12-AUG-1997.  
PA (REGE-) REGENERON PHARM INC.  
Percent Similarity: 39.88% Conservative: 44  
Best Local Similarity: 26.17% Mismatches: 138  
Query Match: 12.74% Indels: 55  
RESULT 941  
ID AAT90473 standard; cDNA; 2610 BP.  
DE Human muscle-specific kinase (MusK) cDNA.  
PN WO9721811-A2.  
PD 19-JUN-1997.  
PA (REGE-) REGENERON PHARM INC.  
Percent Similarity: 39.88% Conservative: 44  
Best Local Similarity: 26.17% Mismatches: 138  
Query Match: 12.74% Indels: 55

RESULT 942  
ID AD089843 standard; DNA; 2610 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #137.  
PN WO20004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Percent Similarity: 39.88% Conservative: 44  
Best Local Similarity: 26.17% Mismatches: 138  
Query Match: 12.74% Indels: 55  
RESULT 943  
ID ADL13698 standard; DNA; 13182 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #230.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 38.91% Conservative: 40  
Best Local Similarity: 26.05% Mismatches: 148  
Query Match: 12.74% Indels: 42  
RESULT 944  
ID ADL13697 standard; DNA; 13793 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #229.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 38.91% Conservative: 40  
Best Local Similarity: 26.05% Mismatches: 148  
Query Match: 12.74% Indels: 42  
RESULT 945  
ID ADL35757 standard; DNA; 13793 BP.  
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) DNA.  
PN WO2004019893-A2.  
PD 11-MAR-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Percent Similarity: 38.91% Conservative: 40  
Best Local Similarity: 26.05% Mismatches: 148  
Query Match: 12.74% Indels: 42  
RESULT 946  
ID AAS87452 standard; cDNA; 14586 BP.  
DE DNA encoding novel human diagnostic protein #23256.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 38.91% Conservative: 40  
Best Local Similarity: 26.05% Mismatches: 148  
Query Match: 12.74% Indels: 42  
RESULT 947  
ID ADM03329 standard; cDNA; 2004 BP.  
DE Human cDNA of the invention SEQ ID NO:2014.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 37.60% Conservative: 36  
Best Local Similarity: 27.58% Mismatches: 146  
Query Match: 12.71% Indels: 78  
RESULT 948  
ID ACN42337 standard; cDNA; 6144 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1212.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 39.74% Conservative: 44  
Best Local Similarity: 25.64% Mismatches: 139  
Query Match: 12.71% Indels: 49  
RESULT 949  
ID ADL16583 standard; cDNA; 6487 BP.  
DE Human 282P1G3 polynucleotide #16.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Percent Similarity: 39.74% Conservative: 44  
Best Local Similarity: 25.64% Mismatches: 139  
Query Match: 12.71% Indels: 49  
RESULT 950

ID ADL16581 standard; cDNA; 6487 BP. DE Human 282PiG3 polynucleotide #14. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 951 ID ADL16430 standard; cDNA; 6487 BP. DE Human 282PiG3 polynucleotide #4. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 952 ID ADL16587 standard; cDNA; 7329 BP. DE Human 282PiG3 polynucleotide #17. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 953 ID ADL16432 standard; cDNA; 7329 BP. DE Human 282PiG3 polynucleotide #5. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 954 ID ADL16589 standard; cDNA; 7329 BP. DE Human 282PiG3 polynucleotide #19. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 955 ID ADL16601 standard; cDNA; 7527 BP. DE Human 282PiG3 polynucleotide #25. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 956 ID ADL16436 standard; cDNA; 7527 BP. DE Human 282PiG3 polynucleotide #7. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 957 ID ADL16599 standard; cDNA; 7527 BP. DE Human 282PiG3 polynucleotide #23. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 958 ID ADL16442 standard; cDNA; 7570 BP.	Conservative: 44 Mismatch: 139 Indels: 49
DE Human 282PiG3 polynucleotide #10. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 959 ID ADL16617 standard; cDNA; 7570 BP. DE Human 282PiG3 polynucleotide #32. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 960 ID ADL16619 standard; cDNA; 7570 BP. DE Human 282PiG3 polynucleotide #34. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 961 ID ADL16434 standard; cDNA; 7602 BP. DE Human 282PiG3 polynucleotide #6. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 962 ID ADL16593 standard; cDNA; 7602 BP. DE Human 282PiG3 polynucleotide #20. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 963 ID ADL16595 standard; cDNA; 7602 BP. DE Human 282PiG3 polynucleotide #22. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 964 ID ADL16576 standard; cDNA; 7650 BP. DE Human 282PiG3 polynucleotide #12. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 965 ID ADL16582 standard; cDNA; 7650 BP. DE Human 282PiG3 polynucleotide #15. PN WO2004016734-A2. PD 26-FEB-2004. PA (AGEN-) AGENSYS INC. Percent Similarity: 39.74% Best Local Similarity: 25.64% Query Match: 12.71% RESULT 966 ID ADL16612 standard; cDNA; 7650 BP.	Conservative: 44 Mismatch: 139 Indels: 49
Conservative: 44 Mismatch: 139 Indels: 49	

PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 967  
 ID ADL16426 standard; cDNA; 7650 BP.  
 DE Human 282PIG3 polynucleotide #2.  
 PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 968  
 ID ADL16594 standard; cDNA; 7650 BP.  
 DE Human 282PIG3 polynucleotide #21.  
 PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 969  
 ID ADL16588 standard; cDNA; 7650 BP.  
 DE Human 282PIG3 polynucleotide #18.  
 PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 970  
 ID ADL16618 standard; cDNA; 7650 BP.  
 DE Human 282PIG3 polynucleotide #33.  
 PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 971  
 ID ADL16600 standard; cDNA; 7650 BP.  
 DE Human 282PIG3 polynucleotide #24.  
 PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 972  
 ID ADL16606 standard; cDNA; 7650 BP.  
 DE Human 282PIG3 polynucleotide #27.  
 PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 973  
 ID ADL16631 standard; cDNA; 7651 BP.  
 DE Human 282PIG3 polynucleotide #35.  
 PN WO2004016734-A2.  
 PD 26-FEB-2004.  
 PA (AGEN-) AGENSYS INC.  
 Percent Similarity: 39.74%  
 Best Local Similarity: 25.64%  
 Query Match: 12.71%  
 RESULT 974  
 ID ADQ97818 standard; DNA; 109661 BP.  
 DE Human cancer associated sequence HD11-002, SEQ ID 795.  
 PN WO2004060304-A2.

PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 39.94%  
 Best Local Similarity: 26.15%  
 Query Match: 12.71%  
 RESULT 975  
 ID ADG39785 standard; cDNA; 11796 BP.  
 DE Human cDNA encoding NOV9.  
 PN US2003203843-A1.  
 PD 30-OCT-2003.  
 PA (PENA) PENA C E A.  
 PA (GUOX) GUO X.  
 PA (SHIM) SHIMKETS R A.  
 PA (PADI) PADIGARU M.  
 PA (KEKU) KEKUDA R.  
 PA (SEYT) SPYTEK K A.  
 PA (MEHR) MEHRABAN F.  
 PA (TOPP) TOPPER J N.  
 PA (MALY) MALYANKAR U M.  
 PA (WASS) WASSERMAN S M.  
 PA (EDIN) EDINGER S R.  
 PA (SMIT) SMITHSON G.  
 PA (GUNT) GUNTHER E.  
 PA (KOMU) KOMUVES L.  
 Percent Similarity: 39.55%  
 Best Local Similarity: 27.97%  
 Query Match: 12.68%  
 RESULT 976  
 ID AAS92794 standard; cDNA; 4452 BP.  
 DE DNA encoding novel human diagnostic protein #28598.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 33.24%  
 Best Local Similarity: 24.10%  
 Query Match: 12.62%  
 RESULT 977  
 ID AAS80523 standard; cDNA; 4452 BP.  
 DE DNA encoding novel human diagnostic protein #16327.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 33.24%  
 Best Local Similarity: 24.10%  
 Query Match: 12.62%  
 RESULT 978  
 ID ABN59991 standard; cDNA; 4009 BP.  
 DE Novel human coding sequence SEQ ID NO: 402.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 39.43%  
 Best Local Similarity: 25.71%  
 Query Match: 12.57%  
 RESULT 979  
 ID ABT17394 standard; DNA; 4045 BP.  
 DE Human IG gene related nucleic acid SEQ ID No 20.  
 PN WO200299040-A2.  
 PD 12-DEC-2002.  
 PA (EXEL-) EXELIXIS INC.  
 Percent Similarity: 39.43%  
 Best Local Similarity: 25.71%  
 Query Match: 12.57%  
 RESULT 980  
 ID ACN37528 standard; cDNA; 4045 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA323962, SEQ ID NO:476.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 39.43%  
 Best Local Similarity: 25.71%  
 Query Match: 12.57%  
 RESULT 981

Best Local Similarity:	25.32%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 989			
ID ADP28189 standard; DNA; 4752 BP.			
DE Human secreted protein encoding sequence SEQ ID #187.			
PN WO2004035732-A2.			
PD 29-FEB-2004.			
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 990			
ID ADP28123 standard; DNA; 4752 BP.			
DE Human secreted protein encoding sequence SEQ ID #121.			
PN WO2004035732-A2.			
PD 29-APR-2004.			
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 991			
ID AAS84195 standard; cDNA; 5298 BP.			
DE DNA encoding novel human diagnostic protein #19999.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 992			
ID AAS86818 standard; cDNA; 5298 BP.			
DE DNA encoding novel human diagnostic protein #22622.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 993			
ID AAS76204 standard; cDNA; 6040 BP.			
DE DNA encoding novel human diagnostic protein #12008.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 994			
ID ADL16575 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #11.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 995			
ID ADL16577 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #13.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 996			
ID ADL16428 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #3.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 997			
ID ADL16428 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #3.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49

Query Match: 12.43% Indels: 49  
RESULT 997  
ID ADL15033 standard; DNA; 7642 BP.  
DE Human neural cell adhesion molecule DNA for cancer treatment.  
PN WO2003068268-A2.  
PD 21-AUG-2003.  
PA (BIOI-) BIOINVENT INT AB.  
Percent Similarity: 39.42%  
Best Local Similarity: 25.32%  
Conservative: 44  
Mismatch: 140  
Indels: 49  
Query Match: 12.43%  
RESULT 998  
ID ADJ75061 standard; DNA; 7642 BP.  
DE Marker gene SEQ ID NO:313.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Percent Similarity: 39.42%  
Best Local Similarity: 25.32%  
Conservative: 44  
Mismatch: 140  
Indels: 49  
Query Match: 12.43%  
RESULT 999  
ID ADN04061 standard; cDNA; 7642 BP.  
DE Antipsoriatic cDNA sequence #230.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 39.42%  
Best Local Similarity: 25.32%  
Conservative: 44  
Mismatch: 140  
Indels: 49  
Query Match: 12.43%  
RESULT 1000  
ID ADQ19765 standard; DNA; 7642 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2584.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 39.42%  
Best Local Similarity: 25.32%  
Conservative: 44  
Mismatch: 140  
Indels: 49  
Query Match: 12.43%  
RESULT 1001  
ID ADQ23905 standard; DNA; 7642 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6725.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 39.42%  
Best Local Similarity: 25.32%  
Conservative: 44  
Mismatch: 140  
Indels: 49  
Query Match: 12.43%  
RESULT 1002  
ID ADRI4750 standard; DNA; 7642 BP.  
DE Nucleotide sequence of human MAPCAX orthologue #8.  
PN WO2004066948-A2.  
PD 12-AUG-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 39.42%  
Best Local Similarity: 25.32%  
Conservative: 44  
Mismatch: 140  
Indels: 49  
Query Match: 12.43%  
RESULT 1003  
ID ADI61707 standard; cDNA; 7647 BP.  
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 334247.2.  
PN US668288-B1.  
PD 27-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 39.42%  
Best Local Similarity: 25.32%  
Conservative: 44  
Mismatch: 140  
Indels: 49  
Query Match: 12.43%  
RESULT 1004  
ID AAS66304 standard; cDNA; 1464 BP.  
DE DNA encoding novel human diagnostic protein #2108.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.25%  
Best Local Similarity: 25.50%  
Conservative: 41  
Mismatch: 137  
Indels: 82  
Query Match: 12.40%

RESULT 1005  
ID AAS90766 standard; cDNA; 1464 BP.  
DE DNA encoding novel human diagnostic protein #26570.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.25%  
Best Local Similarity: 25.50%  
Conservative: 41  
Mismatch: 137  
Indels: 82  
Query Match: 12.40%  
RESULT 1006  
ID AAS72490 standard; cDNA; 1802 BP.  
DE DNA encoding novel human diagnostic protein #8294.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.25%  
Best Local Similarity: 25.50%  
Conservative: 41  
Mismatch: 137  
Indels: 82  
Query Match: 12.40%  
RESULT 1007  
ID AAS66206 standard; cDNA; 2214 BP.  
DE DNA encoding novel human diagnostic protein #2010.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.25%  
Best Local Similarity: 25.50%  
Conservative: 41  
Mismatch: 137  
Indels: 82  
Query Match: 12.40%  
RESULT 1008  
ID AAK94785 standard; cDNA; 2500 BP.  
DE Human full-length cDNA, SEQ ID NO: 3892.  
PN EPI130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 37.90%  
Best Local Similarity: 23.89%  
Conservative: 44  
Mismatch: 127  
Indels: 68  
Query Match: 12.40%  
RESULT 1009  
ID ADL31859 standard; cDNA; 2500 BP.  
DE Full length human cDNA clone SeqID 3892.  
PN EPI396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 37.90%  
Best Local Similarity: 23.89%  
Conservative: 44  
Mismatch: 127  
Indels: 68  
Query Match: 12.40%  
RESULT 1010  
ID AAX37725 standard; cDNA; 3598 BP.  
DE Human PRO335 DNA fragment #2.  
PN WO9914241-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1011  
ID AAX52264 standard; DNA; 3662 BP.  
DE Protein PRO335 cDNA clone DNA41388-1234.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1012  
ID AAZ52206 standard; cDNA; 3662 BP.  
DE Human PRO335 protein encoding cDNA, UNQ287V.  
PN WO200015797-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1013  
ID AAZ52206 standard; cDNA; 3662 BP.  
DE Human PRO335 protein encoding cDNA, UNQ287V.  
PN WO200015797-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match: 12.40%

ID ADC78601 standard; cDNA; 3662 BP.  
DE Human PRO335 cDNA.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 37.90%      Conservative: 44  
Best Local Similarity: 23.89%      Mismatches: 127  
Query Match: 12.40%      Indels: 68  
RESULT 1014  
ID AAF72422 standard; cDNA; 3662 BP.  
DE Human PRO335 cDNA.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1015  
ID AAS00161 standard; cDNA; 3662 BP.  
DE Human cDNA clone DNA41388-1234 encoding PRO335 (UNQ287).  
PN WO200119991-A1.  
PD 22-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1016  
ID ACA60239 standard; cDNA; 3662 BP.  
DE Human cDNA for secreted/transmembrane protein PRO335.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1017  
ID ADC07639 standard; cDNA; 3662 BP.  
DE Novel human secreted and transmembrane protein PRO335 cDNA.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1018  
ID ABX71687 standard; cDNA; 3662 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO335.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1019  
ID ACH07019 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane polypeptide PRO335 cDNA.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1020  
ID ABX96256 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #52.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1021  
ID ACA05577 standard; cDNA; 3662 BP.

DE cDNA encoding human secreted protein PRO335.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1022  
ID ACD20244 standard; cDNA; 3662 BP.  
DE Human secreted / transmembrane polypeptide PRO335 cDNA.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1023  
ID ACA55047 standard; cDNA; 3662 BP.  
DE Novel human secreted and transmembrane protein PRO335 cDNA.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1024  
ID ACD19882 standard; cDNA; 3662 BP.  
DE Human secreted / transmembrane polypeptide PRO335 cDNA.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1025  
ID ADB29494 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1026  
ID ADA18350 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1027  
ID ACD67029 standard; cDNA; 3662 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO335.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1028  
ID ACD83190 standard; cDNA; 3662 BP.  
DE Human PRO polynucleotide #50.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%      Conservative: 54  
Best Local Similarity: 20.73%      Mismatches: 148  
Query Match: 12.40%      Indels: 146  
RESULT 1029  
ID ADA16325 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.

PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1030  
ID ADA42470 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1031  
ID ACD23368 standard; cDNA; 3662 BP.  
DE Human PRO polynucleotide #50.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1032  
ID ADA16749 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1033  
ID ADA13178 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1034  
ID ADA42046 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1035  
ID ADA17393 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1036  
ID ADA42896 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1037  
ID ACD23730 standard; cDNA; 3662 BP.  
DE Human PRO polynucleotide #50.  
PN US2003064923-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1038  
ID ADB77815 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1039  
ID ADB74951 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1040  
ID ADC28597 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1041  
ID ADC39797 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1042  
ID ADC40311 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1043  
ID ADC19135 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1044  
ID ADC34435 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1045  
ID ADC29490 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003049676-A1.  
PD 13-MAR-2003.





Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1062  
ID ADE79791 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1063  
ID ADE73467 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1064  
ID ADE74002 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1065  
ID ADE99556 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1066  
ID ADE98675 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1067  
ID ADE99102 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1068  
ID ADG40572 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1069  
ID ADE73966 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.

DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1070  
ID ADF73542 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1071  
ID ADG92385 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1072  
ID ADG92812 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1073  
ID ADH20601 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1074  
ID ADH07456 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1075  
ID ADH60001 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1076  
ID ADH07029 standard; cDNA; 3662 BP.  
DE Human secreted/transmembrane protein cDNA, #54.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.

PA (GODD//) GODDARD A.	PD 02-OCT-2003.	PA (GETH ) GENENTECH INC.	
PA (GODO//) GODOWSKI P J.		Percent Similarity: 33.03%	Conservative: 54
PA (GURN//) GURNEY A L.		Best Local Similarity: 20.73%	Mismatches: 148
PA (MATH//) MATHER J P.		Query Match: 12.40%	Indels: 146
PA (WILL//) WILLIAMS P M.		RESULT 1084	
PA (WOOD//) WOOD W I.		ID ADM25252 standard; cDNA; 3662 BP.	
Percent Similarity: 33.03%		DE Human secreted/transmembrane protein cDNA, #54.	
Best Local Similarity: 20.73%		PN US2003096233-A1.	
Query Match: 12.40%		PD 22-MAY-2003.	
RESULT 1077		PA (GETH ) GENENTECH INC.	
ID AD118771 standard; cDNA; 3662 BP.		Percent Similarity: 33.03%	Conservative: 54
DE Human secreted/transmembrane protein cDNA, #54.		Best Local Similarity: 20.73%	Mismatches: 148
PN US2003152999-A1.		Query Match: 12.40%	Indels: 146
PD 14-AUG-2003.		RESULT 1085	
PA (GETH ) GENENTECH INC.		ID ADM30002 standard; cDNA; 3662 BP.	
Percent Similarity: 33.03%		DE Human secreted/transmembrane protein cDNA, #54.	
Best Local Similarity: 20.73%		PN US2003190611-A1.	
Query Match: 12.40%		PD 09-OCT-2003.	
RESULT 1078		PA (GETH ) GENENTECH INC.	
ID AD137750 standard; cDNA; 3662 BP.		Percent Similarity: 33.03%	Conservative: 54
DE Human secreted/transmembrane protein cDNA, #54.		Best Local Similarity: 20.73%	Mismatches: 148
PN US2003096340-A1.		Query Match: 12.40%	Indels: 146
PD 22-MAY-2003.		RESULT 1079	
PA (GETH ) GENENTECH INC.		ID ADH97550 standard; cDNA; 3662 BP.	
Percent Similarity: 33.03%		DE Human secreted/transmembrane protein cDNA, #54.	
Best Local Similarity: 20.73%		PN US2003190610-A1.	
Query Match: 12.40%		PD 09-OCT-2003.	
RESULT 1079		PA (GETH ) GENENTECH INC.	
ID ADI65918 standard; cDNA; 3662 BP.		Percent Similarity: 33.03%	Conservative: 54
DE Human secreted/transmembrane protein cDNA, #54.		Best Local Similarity: 20.73%	Mismatches: 148
PN US2003148371-A1.		Query Match: 12.40%	Indels: 146
PD 07-AUG-2003.		RESULT 1080	
PA (GETH ) GENENTECH INC.		ID ADI65918 standard; cDNA; 3662 BP.	
Percent Similarity: 33.03%		DE Human secreted/transmembrane protein cDNA, #54.	
Best Local Similarity: 20.73%		PN US2003148371-A1.	
Query Match: 12.40%		PD 07-AUG-2003.	
RESULT 1081		PA (GETH ) GENENTECH INC.	
ID ADH60661 standard; cDNA; 3662 BP.		Percent Similarity: 33.03%	Conservative: 54
DE Human secreted/transmembrane protein cDNA, #54.		Best Local Similarity: 20.73%	Mismatches: 148
PN US2004023331-A1.		Query Match: 12.40%	Indels: 146
PD 05-FEB-2004.		RESULT 1081	
PA (DESN//) DESNOYERS L.		ID ADH60661 standard; cDNA; 3662 BP.	
PA (GODD//) GODDARD A.		DE Human secreted/transmembrane protein cDNA, #54.	
PA (GODO//) GODOWSKI P J.		PN US2004023331-A1.	
PA (GURN//) GURNEY A L.		PD 05-FEB-2004.	
PA (MATH//) MATHER J P.		PA (DESN//) DESNOYERS L.	
PA (WILL//) WILLIAMS P M.		PA (GODD//) GODDARD A.	
PA (WOOD//) WOOD W I.		PA (GODO//) GODOWSKI P J.	
Percent Similarity: 33.03%		PA (GURN//) GURNEY A L.	
Best Local Similarity: 20.73%		PA (MATH//) MATHER J P.	
Query Match: 12.40%		PA (WILL//) WILLIAMS P M.	
RESULT 1082		PA (WOOD//) WOOD W I.	
ID ADJ99718 standard; cDNA; 3662 BP.		Percent Similarity: 33.03%	Conservative: 54
DE Human secreted/transmembrane protein cDNA, #54.		Best Local Similarity: 20.73%	Mismatches: 148
PN US2003187238-A1.		Query Match: 12.40%	Indels: 146
PD 02-OCT-2003.		RESULT 1082	
PA (GETH ) GENENTECH INC.		ID ADJ99718 standard; cDNA; 3662 BP.	
Percent Similarity: 33.03%		DE Human secreted/transmembrane protein cDNA, #54.	
Best Local Similarity: 20.73%		PN US2003187238-A1.	
Query Match: 12.40%		PD 02-OCT-2003.	
RESULT 1083		PA (GETH ) GENENTECH INC.	
ID ADL08911 standard; cDNA; 3662 BP.		Percent Similarity: 33.03%	Conservative: 54
DE Human secreted/transmembrane protein cDNA, #54.		Best Local Similarity: 20.73%	Mismatches: 148
PN US2003186358-A1.		Query Match: 12.40%	Indels: 146
		RESULT 1083	
ID ADL08911 standard; cDNA; 3662 BP.		DE Human secreted/transmembrane protein cDNA, #54.	
PN US2003186358-A1.		PN US2003186358-A1.	

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RESULT 1089
ID ADT03761 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003152322-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1090
ID ADS74724 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane cDNA #54.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PRON/) PRONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1091
ID AAX37743 standard; cDNA; 3807 BP.
DE Human PRO326 DNA fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1092
ID AAX52266 standard; DNA; 4053 BP.
DE Protein PRO326 cDNA clone DNA37140-1234.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1093
ID AA252208 standard; cDNA; 4053 BP.
DE Human PRO326 protein encoding cDNA, UNQ287.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1094
ID AAF72424 standard; cDNA; 4053 BP.
DE Human PRO326 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1095
ID AAC84422 standard; cDNA; 4053 BP.
DE Human PRO326 polypeptide encoding cDNA.
PN WO200075316-A1.
PD 14-DEC-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1096
ID AAS00163 standard; cDNA; 4053 BP.
DE Human cDNA clone DNA37140-1234 encoding PRO326 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1097
ID AAS21419 standard; cDNA; 4053 BP.
DE Human cDNA sequence encoding for PRO326 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1098
ID ACA60241 standard; cDNA; 4053 BP.
DE Human cDNA for secreted/transmembrane protein PRO326.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1099
ID ACD07641 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1100
ID ACA03778 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1101
ID ABX71689 standard; cDNA; 4053 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO326.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatch: 148
Indels: 146
RESULT 1102
ID ACH07021 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane polypeptide PRO326 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
```



Query Match: 12.40% Indels: 146  
RESULT 1119  
ID ADB15943 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1120  
ID ADA47729 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1121  
ID ADA18354 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1122  
ID ACD67031 standard; cDNA; 4053 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO326.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1123  
ID ADA67524 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1124  
ID ADB30531 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1125  
ID ADA85827 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1126  
ID ADA97039 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1127  
ID ADA79343 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1128  
ID ADA87482 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1129  
ID ADB16684 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1130  
ID ACD83192 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #52.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1131  
ID ADA16329 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1132  
ID ADA91776 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003083694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1133  
ID ADB14839 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1134  
ID ADB18800 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1135

ID ADA94015 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US200307722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1136

ID ADB19911 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1137

ID ADB13223 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1138

ID ACD98599 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1139

ID ADA74477 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1140

ID ADA42474 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1141

ID ADB24710 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1142

ID ADAB2234 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1143

ID ADA75197 standard; cDNA; 4053 BP.  
DE

DE Human PRO polynucleotide #176.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1144

ID ADA85275 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1145

ID ADA84723 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1146

ID ACD23370 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #52.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1147

ID ADB29979 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1148

ID ADA80507 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1149

ID ADA75749 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1150

ID ADA46974 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1151

ID ADB25270 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.

PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1152  
ID ADA93446 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1153  
ID ADB26796 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1154  
ID ADB31083 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1155  
ID ADA61011 standard; cDNA; 4053 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1156  
ID ADB24158 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1157  
ID ADA96487 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1158  
ID ADA81059 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1159  
ID ADA95935 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082759-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1160  
ID ADB26244 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1161  
ID ADB21729 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1162  
ID ADA77508 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1163  
ID ADB18248 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1164  
ID ADA86931 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1165  
ID ADA16753 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1166  
ID ADA13182 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1167  
ID ADA42050 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003082540-A1.  
PD 01-MAY-2003.



PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1168  
ID ADA88034 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1169  
ID ADA46422 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1170  
ID ADA17397 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
FN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1171  
ID ADA42900 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
FN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1172  
ID ADB28452 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
FN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1173  
ID ADB29004 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
FN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1174  
ID ADA76956 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1175  
ID ADA88586 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1176  
ID ADA97591 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1177  
ID ADB27348 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
FN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1178  
ID ADB22281 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1179  
ID ACD23732 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #52.  
FN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1180  
ID ADA66972 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1181  
ID ADB22833 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1182  
ID ADB23606 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.  
FN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1183  
ID ADA92328 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1184  
ID ADA88586 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

RESULT 1184  
ID ADB15391 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1185  
ID ADB38643 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1186  
ID ADB38091 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1187  
ID ADB66563 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1188  
ID ADB9643 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1189  
ID ADB77819 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1190  
ID ADB39476 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1191  
ID ADB39476 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1192  
ID ADB36124 standard; cDNA; 4053 BP.

ID ADB74955 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1193  
ID ADB47099 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1194  
ID ADB86706 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1195  
ID ADB77311 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1196  
ID ADB34468 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1197  
ID ADB35572 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1198  
ID ADB39316 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1199  
ID ADB35020 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide SEQ ID NO 351.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
RESULT 1200  
ID ADB36124 standard; cDNA; 4053 BP.

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DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1201
ID ADB46519 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1202
ID ADC28601 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1203
ID ADC39801 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1204
ID ADC40315 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1205
ID ADC19139 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1206
ID ADC34439 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1207
ID ADC29494 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1208
ID ADC29025 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003087365-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1209
ID ADC40910 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1210
ID ADC19567 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1211
ID ADC34015 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1212
ID ADC13085 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1213
ID ADC50392 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1214
ID ADC71939 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1215
ID ADC59918 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1216
ID ADC52925 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087365-A1.
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PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1217  
ID ADC57279 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID351.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1218  
ID ADC60470 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1219  
ID ADC50945 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1220  
ID ADC65472 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1221  
ID ADC54570 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID351.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1222  
ID ADC53531 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID351.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1223  
ID ADC59054 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID351.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1224  
ID ADC55932 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID351.  
PN US2003087360-A1.  
PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1225  
ID ADC58502 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID351.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1226  
ID ADC12537 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1227  
ID ADD03176 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1228  
ID ADC90168 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1229  
ID ADC69587 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1230  
ID ADC48476 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1231  
ID ADD10005 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match: 12.40%  
RESULT 1232  
ID ADD04580 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1233  
ID ADC80536 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1234  
ID ADD11043 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1235  
ID ADC47924 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1236  
ID ADD05092 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1237  
ID ADC79984 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1238  
ID ADD09453 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1239  
ID ADD04098 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1240  
ID ADD03674 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54

Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1241  
ID ADD41166 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1242  
ID ADD52305 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1243  
ID ADD53045 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1244  
ID ADD53597 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1245  
ID ADD51753 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1246  
ID ADD02552 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1247  
ID ADD01986 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1248  
ID ADD54168 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148

Query Match: 12.40% Indels: 146  
RESULT 1249  
ID ADD92485 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1250  
ID ADE03995 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1251  
ID ADE03995 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1252  
ID ADE32292 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1253  
ID ADE22224 standard; cDNA; 4053 BP.  
DE CDNA encoding human PRO polypeptide #176.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1254  
ID ADD79448 standard; cDNA; 4053 BP.  
DE CDNA encoding human PRO polypeptide #176.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1255  
ID ADE41984 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1256  
ID ADE17801 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:

RESULT 1257  
ID ADD91933 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1258  
ID ADE33396 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1259  
ID ADE33948 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1260  
ID ADD80000 standard; cDNA; 4053 BP.  
DE CDNA encoding human PRO polypeptide #176.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1261  
ID ADD93037 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1262  
ID ADE19457 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1263  
ID ADE34926 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1264  
ID ADE18905 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatch: 148  
Indels: 146  
Query Match:  
RESULT 1265

ID AD843101 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1266  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADD95890 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1267  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID AD822776 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1268  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADD78894 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1269  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID AD832844 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1270  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID AD842536 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1271  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADD80552 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1272  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADD89580 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1273  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADE40864 standard; cDNA; 4053 BP.  
DE

DE Human PRO polynucleotide #176.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1274  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID AD804663 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1275  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADE92792 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1276  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADG21501 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1277  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADG23142 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1278  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADF97477 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1279  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADG80541 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1280  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADG79989 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1281  
Conservative: 54  
Mismatches: 148  
Indels: 146

ID ADH59409 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.

PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1282  
ID ADH55281 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1283  
ID ADH55833 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1284  
ID ADH31818 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1285  
ID ADH4052 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1286  
ID ADH65001 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1287  
ID ADH63500 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1288  
ID ADH81914 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1289  
ID ADH81362 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207377-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1290  
ID ACA59137 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #52.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1291  
ID ACD24028 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1292  
ID ACA58534 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #52.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1293  
ID ACA67169 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1294  
ID ADJ26456 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1295  
ID ADM82531 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1296  
ID ADN15930 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
RESULT 1297  
ID ADN16559 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003087385-A1.  
PD 08-MAY-2003.



PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1298  
ID ADN15378 standard; cDNA; 4053 BP.  
DE Human secreted and transmembrane protein PRO326 cDNA.  
FN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1299  
ID ADN14926 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1300  
ID ADC81088 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
FN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1301  
ID ADE79371 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
FN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1302  
ID ADD76536 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1303  
ID ADD87900 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1304  
ID ADD86304 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1305  
ID ADE79795 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
FN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1306  
ID ADE75752 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1307  
ID ADE73471 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
FN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1308  
ID ADE23328 standard; cDNA; 4053 BP.  
DE CDNA encoding human PRO polypeptide #176.  
FN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1309  
ID ADE23880 standard; cDNA; 4053 BP.  
DE CDNA encoding human PRO polypeptide #176.  
FN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1310  
ID ADE24523 standard; cDNA; 4053 BP.  
DE CDNA encoding human PRO polypeptide #176.  
FN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1311  
ID ADD87348 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1312  
ID ADE89214 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
FN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1313  
ID ADE74006 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
FN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%

Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1314  
ID ADEL8353 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1315  
ID ADE88662 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1316  
ID ADE99560 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1317  
ID ADE94682 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1318  
ID ADE91093 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1319  
ID ADE95234 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1320  
ID ADE93344 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1321  
ID ADE34925 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1322  
ID ADE98679 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1323  
ID ADE92240 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1324  
ID ADE90541 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1325  
ID ADE91688 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1326  
ID ADE99106 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1327  
ID ADG40576 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1328  
ID ADF73970 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1329  
ID ADG02267 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.

Query Match: 12.40% Indels: 146  
RESULT 1322  
ID ADE98679 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1323  
ID ADE92240 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1324  
ID ADE90541 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1325  
ID ADE91688 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1326  
ID ADE99106 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1327  
ID ADG40576 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1328  
ID ADF73970 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1329  
ID ADG02267 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.

PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1330  
ID ADG22053 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1331  
ID ADG20123 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1332  
ID ADF98029 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1333  
ID ADG24246 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1334  
ID ADF98600 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1335  
ID ADG03431 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1336  
ID ADF99152 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1337  
ID ADG16737 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003207359-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1338  
ID ADG05196 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1339  
ID ADG19463 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1340  
ID ADF73546 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1341  
ID ADG13300 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1342  
ID ADG08357 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1343  
ID ADG15527 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1344  
ID ADF96925 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
Query Match:  
RESULT 1345  
ID ADG06110 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207374-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1346  
ID ADG23694 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1347  
ID ADG03983 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1348  
ID ADG24884 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1349  
ID ADG07181 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1350  
ID ADG07733 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1351  
ID ADG55228 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1352  
ID ADG60892 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1353  
ID ADG61996 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1354  
ID ADG92389 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1355  
ID ADG82197 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1356  
ID ADG57436 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1357  
ID ADG56884 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1358  
ID ADG55780 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1359  
ID ADG58540 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1360  
ID ADG70906 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1361  
ID ADG92816 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1362  
ID ADG57436 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1362  
ID ADG57988 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1363  
ID ADG53572 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1364  
ID ADG71458 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1365  
ID ADG81645 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1366  
ID ADH30607 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1367  
ID ADH11974 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1368  
ID ADG52396 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1369  
ID ADG54124 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146

RESULT 1370  
ID ADG81093 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1371  
ID ADG56332 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1372  
ID ADH12598 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1373  
ID ADG61444 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1374  
ID ADH28531 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1375  
ID ADG54676 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1376  
ID ADG59716 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1377  
ID ADH20605 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146  
RESULT 1378  
ID ADH20605 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73% Mismatches: 54  
Query Match: 12.40% Indels: 146

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ID ADH07460 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1379
ID ADH60005 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1380
ID ADH07033 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1381
ID ADH1140 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1382
ID ADH18775 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1383
ID ADH37754 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1384
ID ADG09883 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1385
ID ADH97554 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1386
ID ADH15354 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1387
ID ADG09231 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1388
ID ADH65922 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1389
ID ADH14686 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1390
ID ADH60665 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1391
ID ADH18281 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1392
ID ADJ99722 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
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PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1393  
ID ADL08915 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1394  
ID ADM25256 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1395  
ID ADJ63562 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1396  
ID ADM30006 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1397  
ID ADJ77457 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #176.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1398  
ID ADJ65579 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1399  
ID ADM27715 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1400  
ID ADM42439 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2004058424-A1.

PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1401  
ID ADO06328 standard; cDNA; 4053 BP.  
DE Human PRO polynucleotide #54.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1402  
ID ADM28301 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1403  
ID ADR11180 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1404  
ID ADR18089 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANG/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146  
RESULT 1405  
ID ADI95783 standard; cDNA; 4053 BP.  
DE cDNA encoding human PRO polypeptide #176.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03%  
Best Local Similarity: 20.73%  
Query Match: 12.40%  
Conservative: 54  
Mismatches: 148  
Indels: 146

RESULT 1406  
ID AD196335 standard; cDNA; 4053 BP.  
DE Novel human secreted and transmembrane protein PRO326 cDNA.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1407  
ID AD703765 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane protein cDNA, #56.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1408  
ID AD574728 standard; cDNA; 4053 BP.  
DE Human secreted/transmembrane cDNA #56.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DSN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Percent Similarity: 33.03% Conservative: 54  
Best Local Similarity: 20.73% Mismatches: 148  
Query Match: 12.40% Indels: 146  
RESULT 1409  
ID ABA06424 standard; cDNA; 2667 BP.  
DE Human cDNA SEQ ID NO: 90.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 37.92% Conservative: 34  
Best Local Similarity: 25.28% Mismatches: 123  
Query Match: 12.38% Indels: 45  
RESULT 1410  
ID ABV83761 standard; cDNA; 2667 BP.  
DE Human polynucleotide SEQ ID NO 90.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Percent Similarity: 37.92% Conservative: 34  
Best Local Similarity: 25.28% Mismatches: 123  
Query Match: 12.38% Indels: 45  
RESULT 1411  
ID ABX34664 standard; cDNA; 1213 BP.  
DE Human mddt cDNA SEQ ID 225.

PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 38.94% Conservative: 38  
Best Local Similarity: 26.40% Mismatches: 123  
Query Match: 12.35% Indels: 62  
RESULT 1412  
ID AAZ33346 standard; cDNA; 1417 BP.  
DE Human secreted protein clone cw1000\_2 nucleotide sequence SEQ ID NO:61.  
PN WO9957132-A1.  
PD 11-NOV-1999.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 42.25% Conservative: 61  
Best Local Similarity: 25.07% Mismatches: 153  
Query Match: 12.35% Indels: 52  
RESULT 1413  
ID ADP28012 standard; cDNA; 3540 BP.  
DE Long form full-length IGSF9 protein encoding cDNA.  
PN WO2004066933-A2.  
PD 12-AUG-2004.  
PA (MCLA/) MCLACHLAN K.  
PA (GLAS/) GLASER S.  
PA (PEAC/) PEACH R J.  
PA (ROWE/) ROWE I.  
Percent Similarity: 39.48% Conservative: 51  
Best Local Similarity: 24.78% Mismatches: 144  
Query Match: 12.35% Indels: 66  
RESULT 1414  
ID ADP28247 standard; DNA; 3018 BP.  
DE Human secreted protein encoding sequence SEQ ID #245.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 40.81% Conservative: 49  
Best Local Similarity: 25.55% Mismatches: 142  
Query Match: 12.29% Indels: 48  
RESULT 1415  
ID ADP28237 standard; DNA; 3018 BP.  
DE Human secreted protein encoding sequence SEQ ID #235.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 40.81% Conservative: 49  
Best Local Similarity: 25.55% Mismatches: 142  
Query Match: 12.29% Indels: 48  
RESULT 1416  
ID ADH72193 standard; DNA; 3333 BP.  
DE Human gene of the invention NOV51d SEQ ID NO:1089.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 39.25% Conservative: 40  
Best Local Similarity: 24.15% Mismatches: 111  
Query Match: 12.29% Indels: 50  
RESULT 1417  
ID ABL23498 standard; DNA; 7171 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21967.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.66% Conservative: 43  
Best Local Similarity: 24.05% Mismatches: 115  
Query Match: 12.29% Indels: 101  
RESULT 1418  
ID AAA43911 standard; cDNA; 971 BP.  
DE Human secreted expressed sequence tag SEQ ID NO:486.  
PN WO200021991-A1.  
PD 20-APR-2000.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 42.34% Conservative: 53  
Best Local Similarity: 26.43% Mismatches: 128  
Query Match: 12.24% Indels: 65  
RESULT 1419



ID AAS86820 standard; cDNA; 2948 BP.  
DE DNA encoding novel human diagnostic protein #22624.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.77%  
Best Local Similarity: 25.75%  
Query Match: 12.24%  
Indels: 38  
RESULT 1420  
ID AAV31988 standard; cDNA; 6413 BP.  
DE Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.  
FN WO9817795-A1.  
PD 30-APR-1998.  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
Percent Similarity: 40.25%  
Best Local Similarity: 28.63%  
Query Match: 12.24%  
Indels: 22  
RESULT 1421  
ID AAV31981 standard; cDNA; 6604 BP.  
DE Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.  
FN WO9817795-A1.  
PD 30-APR-1998.  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
Percent Similarity: 40.25%  
Best Local Similarity: 28.63%  
Query Match: 12.24%  
Indels: 22  
RESULT 1422  
ID ADK71086 standard; DNA; 6649 BP.  
DE Human MP21 polypeptide encoding DNA.  
FN WO2004015073-A2.  
PD 19-FEB-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 40.25%  
Best Local Similarity: 28.63%  
Query Match: 12.24%  
Indels: 22  
RESULT 1423  
ID ADR41293 standard; cDNA; 1153 BP.  
DE Human CD-like molecule HATCZ07 cDNA, SEQ ID NO:92.  
FN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1424  
ID AAS80677 standard; cDNA; 1329 BP.  
DE Human secreted protein #11 nucleotide sequence SEQ ID #137.  
FN WO200029435-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1425  
ID ADA27145 standard; cDNA; 1329 BP.  
DE Human novel secreted protein from gene 11 cDNA #3.  
FN US200305231-A1.  
PD 20-MAR-2003.  
PA (NIJ/) NI J.  
PA (YOUN/) YOUNG P E.  
PA (KENV/) KENNY J J.  
PA (OLSE/) OLSEN H S.  
PA (MOOR/) MOORE P A.  
PA (WEI/) WEI Y.  
PA (GREE/) GREENE J M.  
PA (RUBE/) RUBEN S M.  
PA (LIUD/) LIU D.  
PA (CROC/) CROCKER P R.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1426  
ID ADE86686 standard; cDNA; 1329 BP.

DE Novel human secreted protein #11 associated cDNA #1.  
FN US2003129685-A1.  
PD 10-JUL-2003.  
PA (NIJ/) NI J.  
PA (YOUN/) YOUNG P E.  
PA (KENV/) KENNY J J.  
PA (OLSE/) OLSEN H S.  
PA (MOOR/) MOORE P A.  
PA (WEI/) WEI Y.  
PA (GREE/) GREENE J M.  
PA (RUBE/) RUBEN S M.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1427  
ID AAX80055 standard; cDNA; 1413 BP.  
DE Human PRO355 nucleotide sequence.  
FN WO9928462-A2.  
PD 10-JUN-1999.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1428  
ID AAA49563 standard; cDNA; 1413 BP.  
DE Human PRO355 cDNA.  
FN WO200032776-A2.  
PD 08-JUN-2000.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1429  
ID AAS45941 standard; cDNA; 1413 BP.  
DE Human DNA encoding PRO polypeptide sequence #17.  
FN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1430  
ID ACA89391 standard; cDNA; 1413 BP.  
DE cDNA encoding human PRO polypeptide #17.  
FN US2003036141-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1431  
ID ACA73401 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
FN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1432  
ID ACA05716 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
FN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 43.22%  
Best Local Similarity: 26.18%  
Query Match: 12.21%  
Indels: 45  
RESULT 1433  
ID ACA66550 standard; cDNA; 1413 BP.  
DE cDNA encoding human PRO protein #17.  
FN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.

Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1434  
ID ACF20125 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1435  
ID ACF19511 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1436  
ID ACD21799 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1437  
ID ACF12964 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1438  
ID ACD25067 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1439  
ID ACF00116 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1440  
ID ABX96814 standard; cDNA; 1413 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO355.  
PN US2002173463-A1.  
PD 21-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1441  
ID ACA72173 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1442  
ID ACD04697 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003032101-A1.

PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1443  
ID ACD18158 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1444  
ID ACD08165 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1445  
ID ABX78468 standard; cDNA; 1413 BP.  
DE DNA encoding Novel human secreted protein PRO355.  
PN US2002150976-A1.  
PD 17-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1446  
ID ACB88599 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1447  
ID ACA70041 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1448  
ID ACD1263 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1449  
ID ACC74178 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1450  
ID ACD15806 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1451  
ID ACD25374 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003036118-A1.

PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1452  
ID ACD17951 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1453  
ID ACC88138 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1454  
ID ACD21492 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1455  
ID ACD18559 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1456  
ID ABX77102 standard; cDNA; 1413 BP.  
DE cDNA encoding human PRO355 protein.  
PN US2002142958-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1457  
ID ABX98169 standard; cDNA; 1413 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 33.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1458  
ID ACD13920 standard; cDNA; 1413 BP.  
DE Human PRO polynucleotide #17.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1459  
ID ACD09700 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1460  
ID ACC88445 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.

PN US2003027266-A1.  
PD 06-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1461  
ID ACD21185 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1462  
ID ABX75557 standard; cDNA; 1413 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO355.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1463  
ID ABX97760 standard; cDNA; 1413 BP.  
DE Human PRO polynucleotide #17.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1464  
ID ACA97236 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1465  
ID ACA57699 standard; cDNA; 1413 BP.  
DE Human PRO355 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1466  
ID ACD14227 standard; cDNA; 1413 BP.  
DE Human PRO polynucleotide #17.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1467  
ID ACC91010 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1468  
ID ACC89752 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1469  
ID ACD06949 standard; cDNA; 1413 BP.

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DE Human PRO polynucleotide #17.
PN US2003008353-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1470
ID ACA67400 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003017542-A1.
PD 23-JAN-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1471
ID ACC81455 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032137-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1472
ID ACC89059 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027369-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1473
ID ACC86415 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027268-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1474
ID ACC89673 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027274-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1475
ID ACC92852 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1476
ID ACA72480 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003022295-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1477
ID ACA88998 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003022297-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1478
ID ACA89677 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1479
ID ACA96877 standard; cDNA; 1413 BP.
DE Human secreted and transmembrane protein PRO355 cDNA.
PN US2003032105-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1480
ID ACA90873 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1481
ID ACA70655 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003032111-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1482
ID ACA95165 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1483
ID ACC86108 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027263-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1484
ID ACC89980 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027271-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1485
ID ACD12588 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036125-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1486
ID ACF19818 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003040068-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1487
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ID ABX75933 standard; cDNA; 1413 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO355.  
PN US2002132981-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1488  
ID ABX76762 standard; cDNA; 1413 BP.  
DE Human PRO polynucleotide #17.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1489  
ID ACA73094 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1490  
ID ACA68637 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1491  
ID ACA74481 standard; cDNA; 1413 BP.  
DE cDNA encoding human PRO polypeptide #17.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1492  
ID ACA70348 standard; cDNA; 1413 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #17.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1493  
ID ACD14534 standard; cDNA; 1413 BP.  
DE Human PRO polynucleotide #17.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1494  
ID ABX89644 standard; cDNA; 1413 BP.  
DE cDNA encoding novel secreted and transmembrane protein PRO355.  
PN US2002168715-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1495  
ID ACA68206 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45

RESULT 1496  
ID ABX98671 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1497  
ID ACC81148 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1498  
ID ACA95472 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1499  
ID ACD04390 standard; cDNA; 1413 BP.  
DE Novel human secreted and transmembrane protein PRO355 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45  
RESULT 1500  
ID ACC87831 standard; cDNA; 1413 BP.  
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 43.22% Conservative: 54  
Best Local Similarity: 26.18% Mismatches: 135  
Query Match: 12.21% Indels: 45

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 30, 2005, 07:24:31 ; Search time 3856 Seconds  
(without alignments)  
3395.775 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKHNSISWAIFTGL.....RRAGCVWLLPLVLHLLKF 344

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool/US10017084/runat\_28102005\_112601\_9167/app\_query\_fasta\_1.519  
-DB=EST\_QPWT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10017084 -CGN 1.1 4352 @runat\_28102005\_112601\_9167 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hcc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1780	98.6	1808	3	AK045973 Mus muscu
2	1780	98.6	1808	3	AK046377 Mus muscu
3	1506	83.4	874	9	AY406347 Homo sapi
4	1488	82.4	874	9	AY406349 Mus muscu
5	1324	73.3	773	9	AY406348 Pan trogl
6	1321	73.1	1450	7	CO635648 Contig266
7	1254	69.4	765	6	CD354474 UI-M-GMO-
8	1199.5	66.4	856	5	BU155617 AGENCOURT
9	1167	64.6	1039	2	BE798585 601581610

10	1117.5	61.9	748	7	CN362539
11	1112	61.6	890	6	CD327172
12	1094.5	60.6	759	7	CF737474
13	1062.5	58.8	1027	1	AL533026
14	1062.5	58.8	2512	3	CR602526
15	1047	58.0	740	5	BU368328
16	1042	57.7	840	5	BU320256
17	1005.5	55.7	849	4	BI755360
18	982.5	54.4	865	4	BI66583
19	973	53.9	601	6	CB582386
20	952	52.7	600	7	CR548212
21	932.5	51.6	1017	9	AY406971
22	929	51.4	793	5	BU365385
23	926.5	51.3	1017	9	AY406973
24	926	51.3	545	2	BE263639
25	925.5	51.2	979	4	BG261691
26	920	50.9	737	7	CN533076
27	916.5	50.7	2768	3	AK030681
28	912	50.5	732	4	BI551784
29	910	50.4	553	2	BE864555
30	908.5	50.3	1015	9	AY406972
31	907	50.2	524	2	BE014142
32	902.5	50.0	859	6	CD325278
33	900	49.8	636	7	CR540711
34	894	49.5	2467	3	AK044845
35	890	49.3	784	4	BI549918
36	881	48.8	768	1	AU080629
37	875	48.4	754	4	BI550038
38	869	48.1	580	4	BI548566
39	868	48.1	680	7	CR751151
40	862.5	47.8	661	4	BM009450
41	862.5	47.8	953	4	BM423716
42	858.5	47.5	1033	4	BM807426
43	855.5	47.4	1083	4	BM809227
44	843.5	46.7	2330	3	BC080168
45	830	46.0	739	5	BU277649
46	818	45.3	728	6	CD353574
47	814.5	45.1	1138	4	BM556708
48	814	45.1	804	7	CN232247
49	811.5	44.9	557	4	BM256660
50	805	44.6	2096	3	AK035218
51	801	44.4	705	4	BG704152
52	799	44.2	1953	3	AK030503
53	795	44.0	660	6	BY723873
54	793.5	43.9	759	7	CN094277
55	791.5	43.8	764	5	BM945665
56	781.5	43.3	780	7	CK131381
57	774.5	42.9	724	7	CK312152
58	772.5	42.8	849	6	CA472810
59	771.5	42.7	533	4	BI341675
60	770	42.6	671	2	BB644996
61	767.5	42.5	582	5	BP194945
62	763	42.2	437	6	CB724811
63	761.5	42.2	858	6	CD325821
64	761	42.1	663	4	BM724307
65	759	42.0	2534	3	AK039193
66	748	41.4	690	7	CN233126
67	743	41.1	613	7	CR540607
68	742	41.1	827	6	CA306798
69	730	40.4	633	4	BG706987
70	727	40.3	677	5	BQ444788
71	726.5	40.2	1304	5	BM911516
72	709	39.3	815	5	BU230452
73	707.5	39.2	819	5	BU750937
74	707.5	39.2	823	5	BU750936
75	706	39.1	754	4	BI598759
76	705	39.0	934	7	CN015939
77	703.5	39.0	778	7	CN078143
78	697	38.6	683	2	BB640070
79	697	38.6	3166	3	AK042854
80	695	38.5	470	7	CR537991
81	688	38.1	695	7	CN228731
82	688	38.1	754	7	C0043662

83	687.5	38.1	2798	3	AK028345	Mus muscu	156	498	27.6	611	6	CA355517	CA355517 627428 NC
84	685.5	38.0	602	2	BB611718	BB611718	157	498	27.6	914	5	EX843874	EX843874 BX843874
85	682	37.8	870	5	BU515609	AGENCOURT	158	497	27.5	768	5	EX868437	EX868437 BX868437
86	672	37.2	534	4	BM686717	UI-E-C00-	C 159	492.5	27.3	753	1	AI589824	AI589824 tm74909.x
87	671	37.2	643	5	BU390882	603807132	160	490	27.1	599	7	CN229507	CN229507 RJB072D02
88	671	37.2	806	1	AU051132	AU051132	161	488.5	27.0	835	5	EX881962	EX881962 BX881962
89	670.5	37.1	660	7	CR543517	DKF2p459N	C 162	486	26.9	290	7	F05894	F05894 HSC0PH101.n
90	666.5	36.9	796	7	CO399311	AGENCOURT	C 163	485	26.9	578	2	BE121132	BE121132 UI-R-CA0-
91	666	36.9	764	4	BI752729	603028343	164	484	26.8	456	6	CD803885	CD803885 UI-M-GVO-
92	665	36.8	563	6	CB296574	12822045	165	483	26.7	347	7	CN094278	CN094278 EC2BBA3CA
93	661	36.6	548	2	BE015245	127482 MA	166	483	26.7	755	5	EX913106	EX913106 BX913106
94	654	36.2	880	6	CD303536	AGENCOURT	167	480.5	26.6	664	3	CN362538	CN362538 170006001
95	651	36.0	704	7	CN228803	RJB061B04	168	480	26.6	795	1	AU080106	AU080106 AU080106
96	644.5	35.7	640	7	CR545244	DKF2p459F	169	478	26.5	566	7	CF977262	CF977262 2-84-B04.
97	637.5	35.3	496	5	BP201259	BP201259	170	477	26.4	478	5	BY245406	BY245406 BY245406
98	632.5	35.0	621	5	EX312928	EX312928	171	476	26.4	661	6	CA452139	CA452139 UI-M-P20-
99	632.5	35.0	1148	4	BM466102	AGENCOURT	172	475.5	26.3	392	2	BE651010	BE651010 UI-M-BH3-
100	632	35.0	688	2	BB646531	BB646531	173	475	26.3	646	6	CA334396	CA334396 NISC 1808
101	629	34.8	674	6	CD767791	AGENCOURT	174	474.5	26.3	953	5	BU116264	BU116264 603139651
102	619.5	34.3	786	7	CO811192	AGENCOURT	175	473	26.2	284	7	CR543721	CR543721 DKF2p459H
103	616	34.1	867	6	CD300857	AGENCOURT	176	468.5	25.9	703	7	CF530869	CF530869 UI-M-GH0-
104	614.5	34.0	511	5	EX493152	DKF2p781G	C 177	468.5	25.9	772	7	CK776016	CK776016 967158 MA
105	613	33.9	513	5	BX279850	BX279850	178	468	25.9	936	5	BO227365	BO227365 AGENCOURT
106	612.5	33.9	858	7	CO914076	AGENCOURT	179	467.5	25.9	617	6	BY730405	BY730405 BY730405
107	607.5	33.6	492	2	AN967001	EST379075	180	467	25.9	390	4	BM719375	BM719375 UI-E-EJ1-
108	607	33.6	587	7	CN088583	EC2BBA30B	181	467	25.9	390	5	BM719757	BM719757 UI-E-EJ1-
109	604.5	33.5	639	7	CV030584	9878 Full	182	467	25.9	390	5	BM931279	BM931279 UI-E-EJ1-
110	603	33.4	656	7	CK619540	mk25d06.y	C 183	467	25.9	394	4	BM684112	BM684112 UI-E-EJ1-
111	591	32.7	522	4	BI553032	603193672	C 184	467	25.9	394	4	BM684852	BM684852 UI-E-EJ1-
C 112	591	32.7	528	5	BU624639	UI-H-FG1-	C 185	467	25.9	394	5	BQ184395	BQ184395 UI-E-EJ1-
C 113	590	32.7	672	6	CA444805	UI-H-DH1-	C 186	467	25.9	394	5	BQ184512	BQ184512 UI-E-EJ1-
114	590	32.7	926	6	CD325412	AGENCOURT	C 187	467	25.9	394	7	CK300895	CK300895 UI-E-EJ1-
115	589	32.6	697	6	CD217649	pgrln.pk0	C 188	467	25.9	403	4	BM684212	BM684212 UI-E-EJ1-
C 116	589	32.6	697	5	BQ021243	UI-H-DH1-	C 189	467	25.9	608	5	BQ189888	BQ189888 UI-E-EJ1-
117	577	31.9	652	7	CO708144	EC2BBA14C	190	467	25.9	700	5	BQ189788	BQ189788 UI-E-EJ1-
118	575	31.8	567	2	BF078551	228917 MA	191	467	25.9	734	5	BQ187606	BQ187606 UI-E-EJ1-
119	569.5	31.5	1084	6	CD255729	AGENCOURT	192	466.5	25.8	884	5	BU323269	BU323269 603405983
120	569	31.5	611	7	CO705612	EC2BBA10C	C 193	463.5	25.7	564	7	CO602836	CO602836 DGB-24911
121	567	31.4	655	4	BI548049	603196558	194	463	25.6	666	5	BM951674	BM951674 UI-M-EG0-
122	565.5	31.3	528	2	BB856778	BB856778	C 195	461	25.5	795	7	CO395735	CO395735 AGENCOURT
C 123	564.5	31.3	896	5	BQ890272	AGENCOURT	C 196	460	25.5	572	2	BF407747	BF407747 UI-R-BJ2-
125	561.5	31.1	519	7	CV038761	4136000 B	C 197	459	25.4	282	7	R75391	R75391 MDB0556R MO
126	561	31.1	726	5	BX912600	BX912600	198	459	25.4	858	2	BF676478	BF676478 602086277
C 127	560.5	31.0	719	7	CK465166	936244 MA	C 200	455	25.2	456	1	AI369684	AI369684 QY71903.x
128	555.5	31.0	572	6	CB265380	1004285 H	C 201	453.5	25.1	651	6	BY726997	BY726997 BY726997
C 129	559	31.0	2296	3	CR592222	full-leng	C 202	448	24.8	257	2	AW327110	AW327110 20640 MAR
C 130	558	30.9	656	6	CA307492	UI-H-FT1-	C 203	448	24.8	909	5	BU132565	BU132565 603120307
131	554.5	30.7	625	2	BB643056	BB643056	C 204	445.5	24.7	637	6	CB528708	CB528708 UI-H-FT2-
C 132	553	30.6	636	7	CK843444	UI-R-BJ2-	C 205	444	24.6	894	6	CB199088	CB199088 AGENCOURT
133	552.5	30.6	670	7	CN083622	CN083622	C 206	443.5	24.6	791	7	CK308721	CK308721 SB02047A2
134	548	30.3	862	7	CK397022	AGENCOURT	C 207	441.5	24.4	497	7	CV036959	CV036959 4134532 B
135	545	30.2	593	7	CR545391	DKF2p459M	C 208	441	24.4	801	5	BU357013	BU357013 603475462
136	544	30.1	660	2	BB633037	BB633037	C 209	440.5	24.4	700	7	CN458398	CN458398 UI-M-HN0-
137	543.5	30.1	640	7	CO351229	DR AOV FL	C 210	440	24.4	445	5	BY269882	BY269882 BY269882
138	543.5	30.1	647	7	CV030870	10123 Full	C 211	433.5	24.0	584	5	BP257486	BP257486 BP257486
139	541.5	30.0	415	7	R18841	Y922906.r1	C 212	432.5	23.9	892	5	BP462753	BP462753 BP462753
C 140	536	29.7	497	2	BB854833	BB854833	C 213	432	23.9	457	5	BY245728	BY245728 BY249728
141	535.5	29.7	906	5	BU186468	AGENCOURT	C 214	427.5	23.7	580	7	CN089827	CN089827 EC2BBA32B
142	532.5	29.5	825	5	BP166655	BP166655	C 215	426	23.6	544	5	BU735309	BU735309 UI-E-DW0-
143	531.5	29.4	867	7	CO543917	LYRST116	C 216	426	23.6	544	6	CA439326	CA439326 UI-H-DT1-
C 144	529	29.3	329	7	F06205	F06205 HSC10F041.n	C 217	423	23.4	481	5	BY256150	BY256150 BY256150
145	525	29.1	593	7	CK845949	968393 MA	C 218	416.5	23.1	496	7	CK693129	CK693129 ZF101-P00
146	523.5	29.0	923	1	AL583491	AL583491	C 219	413	22.9	494	1	AA548396	AA548396 nj14e04.8
147	518	28.7	565	2	BB663866	147903 MA	C 220	411.5	22.8	617	4	BU622933	BU622933 BU622933
148	512.5	28.4	535	9	AY409767	Homo sapi	C 221	407.5	22.6	778	7	CK315507	CK315507 SB02026A1
149	511	28.3	764	6	CA350929	621861 NC	C 222	407.5	22.6	788	4	BI017621	BI017621 603057906
150	510	28.2	579	2	BB644523	BB644523	C 223	402	22.3	277	4	BI011319	BI011319 QV2-EN009
151	509.5	28.2	773	4	BG208674	RST28306	C 224	401.5	22.2	600	6	CA526928	CA526928 8023-83 M
152	508.5	28.2	535	9	AY409769	Mus muscu	C 225	396.5	22.0	862	5	BP462754	BP462754 BP462754
153	508	28.1	739	7	CK679857	ZF101-P00	C 226	394	21.8	598	1	AI815935	AI815935 au43902.x
C 154	507	28.1	659	2	AW149545	xf39c10.x	C 227	390.5	21.6	771	7	CN528825	CN528825 UI-N-HQ0-
155	506.5	28.0	703	5	BU117309	603138889	C 228	390	21.6	465	1	AI934791	AI934791 wp89e04.x



229 389.5 21.6 878 5 BP165624 BP165624  
230 389 21.5 450 5 BP263302 BP263302  
231 388 21.5 294 7 W15256 zc16h07.s1  
232 388 21.5 357 7 BP303236 BP303236  
233 385 21.3 673 7 CR736885 CR736885  
234 384.5 21.3 444 1 AA682970 ae89a04.s  
235 380.5 21.1 775 4 B1199955 602761121  
236 379.5 21.0 660 5 BP337636 BP337636  
237 377.5 20.9 833 5 BP164129 BP164129  
238 376.5 20.8 535 9 AY409768 Pan trogl  
239 376 20.8 470 1 A1580850 ta33e06.x  
240 373.5 20.7 478 6 CA885050 B0115808-  
241 372 20.6 511 1 A1415689 mc70a03.x  
242 371.5 20.6 723 9 AG035406 Pan trogl  
243 370 20.5 863 6 CA475514 AGENCOURT  
244 365.5 20.2 809 2 BP304194 601887043  
245 364 20.2 268 1 AA296886 ES7112650  
246 363.5 20.1 801 5 BX852740 BX852740  
247 363 20.1 519 1 AA828266 od3e04.s  
248 362 20.0 229 1 AA450172 zx42d09.r  
249 358 19.8 855 5 BP158085 BP158085  
250 357.5 19.8 483 7 CR536826 DKZp459J  
251 355.5 19.7 368 2 BP350775 OVO-H7036  
252 355 19.7 348 7 R55964 Y989e11.r1  
253 355 19.7 431 5 BP276402 BP276402  
254 353 19.5 711 5 BU363662 603790080  
255 352.5 19.5 729 2 BB585976 BB585976  
256 351 19.4 429 5 BP272572 BP272572  
257 350 19.4 504 5 BX281785 BX281785  
258 348.5 19.3 868 5 BQ672092 AGENCOURT  
259 342.5 19.0 960 5 BQ933325 AGENCOURT  
260 341 18.9 525 1 AL919221 AL919221  
261 339.5 18.8 825 4 BG814603 dafe6d77  
262 338.5 18.7 514 4 BP168056 BP168056  
263 338 18.7 807 5 BP168056 BP168056  
264 331.5 18.4 801 7 CK303983 SB02022A1  
265 331 18.3 594 5 BU400899 603481850  
266 330 18.3 410 5 BP276506 BP276506  
267 329 18.2 651 6 CB557691 AMGNNUC:N  
268 327.5 18.1 458 7 CO667956 DK33-31f8  
269 323.5 17.9 562 5 BU381982 603582664  
270 320.5 17.7 470 5 BX954423 DKZp781K  
271 320.5 17.7 613 7 CF892168 A0106807-  
272 320 17.7 579 7 CN089828 CN089828  
273 318.5 17.6 446 7 CO352257 GR AOV SU  
274 315 17.4 422 1 A1288864 qn24f12.x  
275 314 17.4 845 4 BM042630 603615963  
276 312.5 17.3 641 2 AW379374 CM2-HT024  
277 312 17.3 514 1 A1285235 qk59h04.x  
278 311 17.2 378 2 BP601149 266043 MA  
279 311 17.2 489 6 CB726015 AMGNNUC:N  
280 310.5 17.2 527 5 BP243052 BP243052  
281 310.5 17.2 552 4 B1337752 361275 MA  
282 310.5 17.2 789 7 CR531801 CR531801  
283 310 17.2 359 2 BE156390 QVO-HT036  
284 310 17.2 415 5 BP263876 BP263876  
285 310 17.2 461 2 BF463934 UI-M-CG0P  
286 308 17.1 694 7 CK699353 ZF101-P00  
287 307.5 17.0 705 7 CN108877 EC3CAA32D  
288 307 17.0 178 6 CB118055 K-ESTU164  
289 306.5 17.0 730 5 BX610460 BX610460  
290 306.5 17.0 720 7 CR526028 CR526028  
291 304 16.8 528 2 AW490008 UI-M-BH3-  
292 303.5 16.8 790 5 BP141505 BP141505  
293 302.5 16.7 394 9 AY400233 Homo sapi  
294 302.5 16.7 394 9 AY400233 Pan trogl  
295 300.5 16.6 481 5 BP247646 BP247646  
296 300 16.6 377 7 CF977263 2-98-A10  
297 300 16.6 646 5 BW346790 BW346790  
298 298 16.5 372 6 BV768835 BV768835  
299 298 16.5 386 5 BP263646 BP263646  
300 297 16.4 708 7 CK661144 LP20336.5  
301 296.5 16.4 382 9 AY400235 Mus muscu

302 296.5 16.4 417 6 CA884109 CA884109  
303 295 16.3 994 6 CD325921 AGENCOURT  
304 294.5 16.3 451 1 AA933871 O191d04.s  
305 293 16.2 220 7 H16176 Ym21q09.r1  
306 293 16.2 665 9 BX243020 Danio rer  
307 293 16.2 761 6 CD755145 AGENCOURT  
308 291.5 16.1 899 5 BU134624 603119839  
309 291 16.1 402 5 BY289266 BY289266  
310 290.5 16.1 733 7 CO619752 DG9-1d13  
311 290 16.1 585 7 CO628980 DG9-3m14  
312 289.5 16.0 726 5 BU395513 603404749  
313 288.5 16.0 411 5 BY288341 BY288341  
314 288 15.9 422 4 B1390270 P9plc.pk0  
315 285 15.8 691 7 CK661190 LP20417.5  
316 285 15.8 693 7 CK657729 LP24251.5  
317 283 15.7 386 6 CB806970 AMGNNUC:N  
318 283 15.7 488 5 BX477962 DKZp686N  
319 282.5 15.6 2193 9 AY418859 Mus muscu  
320 282.5 15.6 2709 3 AK082621 AK082621  
321 282.5 15.6 2713 3 AK051197 AK051197  
322 278.5 15.4 473 5 BY261511 BY261511  
323 278 15.4 2190 9 AY418858 Pan trogl  
324 276 15.3 2190 9 AY418857 Homo sapi  
325 275 15.2 583 6 CA353359 CA353359  
326 273.5 15.1 314 7 CN075611 CN075611  
327 271.5 15.0 316 1 A1884993 A1884993  
328 269.5 14.9 452 1 A1262821 A1262821  
329 269.5 14.9 656 2 BB617916 BB617916  
330 268 14.8 402 2 AW522667 UI-R-B00-  
331 268 14.8 3089 3 BC062942 BC062942  
332 267.5 14.8 392 5 BY267956 BY267956  
333 265.5 14.7 421 5 BY275639 BY275639  
334 263 14.6 2397 3 AK033973 AK033973  
335 263 14.6 2509 3 AK046800 AK046800  
336 263 14.6 3880 3 AK043760 AK043760  
337 263 14.6 3892 3 AK038842 AK038842  
338 260 14.4 412 5 BY274659 BY274659  
339 257.5 14.3 401 5 BY266910 BY266910  
340 257.5 14.3 3315 3 HSM805302 HSM805302  
341 257 14.2 1080 5 BM916998 AGENCOURT  
342 256 14.2 336 5 BY134531 BY134531  
343 254.5 14.1 763 1 A1427225 A1427225  
344 253 14.0 456 5 BY249027 BY249027  
345 253 14.0 760 6 CD636199 CD636199  
346 253 14.0 929 5 BX409828 BX409828  
347 251.5 13.9 700 6 CD636207 CD636207  
348 251.5 13.9 815 1 AU079716 AU079716  
349 251 13.9 332 2 BE826737 BE826737  
350 251 13.9 374 2 BE826640 BE826640  
351 251 13.9 734 7 CF735216 CF735216  
352 250 13.8 751 7 CF746910 UI-M-HB0-  
353 250 13.8 797 7 CF746875 UI-M-HB0-  
354 248.5 13.8 649 6 CD636249 CD636249  
355 248.5 13.8 783 6 CD636239 CD636239  
356 248.5 13.6 785 6 CD636241 6038385J  
357 246.5 13.6 5626 3 CR749495 CR749495  
358 246 13.6 385 5 BY275013 BY275013  
359 246 13.6 737 4 BM679797 UI-B-EJ0-  
360 246 13.6 780 5 BU559185 BU559185  
361 246 13.6 3198 9 AY416712 Homo sapi  
362 245.5 13.6 724 6 CD636193 CD636193  
363 245.5 13.6 753 6 CD636243 CD636243  
364 244.5 13.5 1871 3 BC029119 Homo sapi  
365 243.5 13.5 649 6 CD636211 60311058J  
366 243.5 13.5 690 6 CD636247 6038477J  
367 243.5 13.5 1946 3 BC028193 BC028193  
368 242.5 13.4 354 2 BE826697 BE826697  
369 242 13.4 668 6 CD636194 CD636194  
370 241.5 13.4 632 6 CD636203 CD636203  
371 241 13.3 733 9 BX190380 Danio rer  
372 240.5 13.3 629 6 CD636245 6038469J  
373 239.5 13.3 656 2 BB645027 BB645027  
374 238.5 13.2 374 5 BY294857 BY294857

c 375 238.5 13.2 377 2 BF358688 QV1-ET000  
376 238.5 13.2 378 6 CD636251 56038493J  
377 237.5 13.2 3133 9 AY416714 Mus muscu  
378 237.5 13.2 3179 3 AK028527  
379 237.5 13.2 3948 3 AK036116 Mus muscu  
380 236.5 13.1 646 4 B1393264 p9pln.pk0  
381 236 13.1 529 6 CD284927 G39161.77  
382 235 13.0 479 2 AW524531 UI-R-B00-  
383 235 13.0 711 7 CO669353 DG33-50b1  
384 233 12.9 582 7 CO626674 DG9-278a2  
385 232 12.8 747 7 CF743366 UI-M-GV0-  
386 232 12.8 758 6 CB525885 UI-M-FY0-  
387 231.5 12.8 3057 9 AY417678 Homo sapi  
388 231.5 12.8 4327 3 BC033255 Homo sapi  
389 231 12.8 3392 3 BC036338 Homo sapi  
390 231 12.8 3480 9 AY418997 Homo sapi  
391 230 12.7 339 2 BB826667 QV1-EN004  
392 230 12.7 872 5 BU411493 G02954338  
393 229.5 12.7 705 6 CD636208 56031050H  
394 229 12.7 782 8 A2731274 RPCI-24-1  
395 228.5 12.7 442 7 CN081576 EC2BBA19C  
396 228.5 12.7 897 7 CN161781  
397 228.5 12.7 2530 3 AK018522 Mus muscu  
398 228 12.6 194 4 B1337742  
399 228 12.6 816 5 BU385923 603858616  
400 228 12.6 3468 3 AK052972 Mus muscu  
401 227 12.6 3988 3 BC034594 Mus muscu  
402 227 12.6 4131 3 AK078536 Mus muscu  
403 226.5 12.5 550 2 B5012499 121990 MA  
404 226.5 12.5 763 4 BG519515 602577790  
405 226 12.5 368 7 CN086072 EC2BBA26C  
406 224.5 12.4 3050 9 AY417680 Mus muscu  
407 224 12.4 652 7 CV462964 CS\_hyp\_49  
408 224 12.4 4187 3 AK053044 CS\_hyp\_49  
409 223 12.3 336 4 BG199531 RST18822  
410 223 12.3 433 1 AL921475 RS121475  
411 223 12.3 494 4 B1515616 BB160019B  
412 223 12.3 544 4 B1515545 BB160019B  
413 223 12.3 3540 9 AY418995 Homo sapi  
414 222 12.3 723 5 BU704037 UI-M-F00-  
415 222 12.3 932 5 BX409829 BX409829  
416 221.5 12.3 1118 3 AK013775 Mus muscu  
417 220.5 12.2 1372 3 AK053839 Mus muscu  
418 220.5 12.2 2126 3 AK013911 Mus muscu  
419 220 12.2 754 6 C3448116 UI-H-ED1-  
420 220 12.2 770 2 AW117456 xds2a06.x  
421 220 12.2 2664 3 AK043379 Mus muscu  
422 219.5 12.2 3345 9 AY403614 Homo sapi  
423 219 12.1 821 5 BU389844 603511165  
424 218.5 12.1 916 5 BO672140 AGENCOURT  
425 218 12.1 712 5 BU212380 603952444  
426 218 12.1 2874 3 AK036262 Mus muscu  
427 217.5 12.0 586 4 BM696801 UI-E-DW0-  
428 217.5 12.0 866 5 BQ923836 AGENCOURT  
429 217 12.0 780 5 BX917601 BX917601  
430 216.5 12.0 375 5 BY292584 BY292584  
431 216.5 12.0 473 7 CO280999 EK155707  
432 215.5 11.9 657 2 B8618284 BB618284  
433 215.5 11.9 1311 3 CR731011 Tetraodon  
434 214.5 11.9 734 6 CB448011 702065 MA  
435 214.5 11.9 742 7 CO395507 AGENCOURT  
436 214 11.8 711 1 AU004083 AU004083  
437 214 11.8 724 7 CO561566 AGENCOURT  
438 214 11.8 813 4 B1651587 603298063  
439 214 11.8 1280 3 CR648110 Tetraodon  
440 214 11.8 2464 3 AK043507 Mus muscu  
441 214 11.8 2535 3 BC012380 Homo sapi  
442 214 11.8 2553 3 BC046975 Mus muscu  
443 213.5 11.8 701 5 BW223428 BW223428  
444 213.5 11.8 1306 3 CR605082 full-1eng  
445 213.5 11.8 1315 3 CR733537 Tetraodon  
446 213 11.8 558 7 CR875240 GSP136467  
447 213 11.8 593 5 BX499713 DKF2p779M

448 213 11.8 669 6 CB246171 UI-M-F00-  
c 449 213 737 5 BX915880 BX915880  
450 213 761 5 BU355132 BU355132  
451 213 1288 3 CR728377 Tetraodon  
452 213 1304 3 CR644432 Tetraodon  
453 213 3219 3 AK041230 Mus muscu  
454 213 3518 3 BC036088 Homo sapi  
455 212 1253 3 CR636279 Tetraodon  
456 212 1270 3 CR637013 Tetraodon  
457 211.5 710 6 CA349374 619770 NC  
458 211.5 768 6 CD636212 56031066H  
459 211.5 3342 9 AY403616 Mus muscu  
460 211.5 4015 3 AK028770 Mus muscu  
461 211.5 4429 3 AK028889 Mus muscu  
462 211 687 4 B1827613 603073581  
c 463 211 723 5 BX923781 BX923781  
464 211 1623 3 AK038917 Mus muscu  
465 211 4113 3 AK053077 Mus muscu  
466 210 11.6 540 9 CD573801 CH240\_450  
467 209.5 11.6 588 6 CD636204 56030593H  
468 209 870 4 B1913885 603183295  
469 209 3037 4 AK052440 Mus muscu  
470 208.5 492 4 B1359722 384371 MA  
471 208.5 562 5 BX952176 DKF2p781K  
472 208.5 694 7 CF125589 UI-HF-B10  
473 208 700 2 BB652926 BB652926  
c 474 208 712 6 CD620699 56100889J  
475 208 990 9 AY418721 Mus muscu  
476 207.5 11.5 1290 3 CR649578 Tetraodon  
477 207.5 11.5 2104 3 AK033487 Mus muscu  
478 207.5 4441 3 AK081990 Mus muscu  
479 207 842 6 CA317300 UI-M-FW0-  
480 206.5 685 4 B37000543 B37000543  
481 206.5 779 6 CA511514 UI-R-FJ0-  
c 482 206.5 904 6 CB756103 AGENCOURT  
c 483 206 11.4 778 6 CD620690 56100765H  
484 206 11.4 1516 6 CR727897 Tetraodon  
485 205.5 11.4 783 7 CF540537 UI-M-GV0-  
486 205.5 11.4 2017 3 AK042488 Mus muscu  
487 205 729 7 CN533735 UI-M-H00-  
488 205 990 9 AY418719 Homo sapi  
489 205 11.4 1228 3 CR648907 Tetraodon  
490 204.5 701 5 BX669319 BX669319  
c 491 204.5 893 5 BU523040 AGENCOURT  
492 204.5 1237 3 CR641398 Tetraodon  
493 204 843 5 BX854499 BX854499  
c 494 203.5 613 6 CD636184 56020447H  
495 203.5 3642 3 AK084609 Mus muscu  
c 496 203 334 1 A1422503 tfl1e04.x  
497 202.5 651 7 CK831552 4055165 B  
498 202.5 687 5 BP461989 BP461989  
499 202 810 5 BU338342 BU338342  
c 500 202 846 5 BQ423040 AGENCOURT  
501 202 867 7 CN163166 952638 MA  
502 201 3123 3 AK049284 Mus muscu  
c 503 201 467 4 B1134406 UI-M-BH3-  
504 201.5 701 7 CO422929 GGEZHT102  
505 201.5 1304 3 CR639237 Tetraodon  
506 201.5 1548 3 CR728005 Tetraodon  
507 201 865 7 CK401822 AUF\_Ifint  
508 201 1788 9 AY411536 Mus muscu  
509 200.5 525 6 CB720159 AMGNNUC.N  
510 200.5 541 6 CD803660 UI-M-GV0-  
511 200.5 935 5 BQ893857 AGENCOURT  
512 200 550 6 CD636197 56030950J  
513 200 703 7 CV434528 CS\_hyp\_36  
c 514 200 1062 5 BX343871 BX343871  
515 199.5 783 7 CN055172 Salamande  
516 199.5 1025 7 CR754135 CR754135  
c 517 199.5 1074 7 CR754275 CR754275  
518 199.5 11.0 1267 3 CR634286 Tetraodon  
519 199 816 1 AU117395 AU117395  
520 199 954 1 AL551492 AL551492

521	199	11.0	2236	3	BC030834	Homo sapi	594	190.5	10.5	779	5	BU419715	603953627
522	199	11.0	2705	3	AK090377	Mus muscu	595	190.5	10.5	797	7	CK311806	BQ2010A1
523	199	11.0	4068	9	AY046427	Mus muscu	596	190.5	10.5	924	5	BQ882851	AGENCOURT
524	198.5	11.0	618	6	CD363200	56030966H	597	190.5	10.5	1499	3	CR636336	Tetraodon
525	198.5	11.0	732	7	CN381875	170005328	598	190	10.5	514	5	EX111689	EX111689
526	198.5	11.0	796	6	CD626697	56100881J	599	190	10.5	769	5	EX857871	EX857871
527	198.5	11.0	4919	3	BC040674	Homo sapi	600	190	10.5	1463	8	CC288776	CH261-170
528	198	11.0	625	4	BJ032692	BJ032692	c	601	189.5	714	7	CN460823	BU5-M-HB0-
529	198	11.0	728	7	CF728819	UI-M-HB0-	602	189.5	10.5	748	5	BU058289	UI-M-FOO-
530	198	11.0	838	7	CK028945	AGENCOURT	603	189.5	10.5	946	4	BI549835	603194572
531	198	11.0	1104	7	CR755975	CR755975	604	189.5	10.5	2211	9	AY418471	Pan trogl
532	197.5	10.9	534	7	CR950627	Ha_mx0_36	605	189.5	10.5	3057	9	AY417679	Pan trogl
533	197.5	10.9	766	6	CA326802	UI-M-FY0-	606	189	10.5	609	6	CA381472	660987 NC
534	197.5	10.9	795	7	CN532710	UI-M-FY0-	607	189	10.5	683	2	BB318882	BB318882
535	197.5	10.9	1145	7	CR754709	CR754709	608	189	10.5	706	6	CA324144	UI-M-FY0-
536	197	10.9	433	4	BG515406	dae04h10.	609	189	10.5	710	7	CK638303	UI-M-HO0-
537	197	10.9	474	2	BG682022	BB682022	610	189	10.5	938	5	EX708988	EX708988
538	197	10.9	631	4	BM426245	pgf2n.pk0	611	188.5	10.4	603	1	AL679324	AL679324
539	197	10.9	781	6	CD626693	56100781J	612	188.5	10.4	663	5	BU708530	UI-M-FY0-
540	196.5	10.9	582	5	BP355301	BP355301	613	188.5	10.4	720	3	CR644200	Tetraodon
541	196.5	10.9	686	6	CA372777	646750 NC	614	188.5	10.4	773	6	CD348004	CD348004
542	196.5	10.9	812	5	B0180027	UI-M-EW0-	615	188.5	10.4	839	4	BI851286	603377864
543	196.5	10.9	923	5	BUI140452	603135370	616	188.5	10.4	922	4	BM802337	AGENCOURT
544	196.5	10.9	1272	3	CR731454	Tetraodon	617	188.5	10.4	4185	3	AK083540	Mus muscu
545	196.5	10.9	3647	3	BC046957	Mus muscu	618	188	10.4	313	2	AW430704	70599 MAR
546	196	10.9	895	7	CR761982	ID0AAA3BG	619	188	10.4	558	6	CB448500	702638 MA
547	196	10.9	925	4	BG413088	602446318	620	188	10.4	722	7	CN530508	UI-M-HO0-
548	196	10.9	987	6	CD507156	CD483-C12	c	621	188	833	6	CD636250	56038493H
549	196	10.9	4068	9	AY046425	Homo sapi	622	188	10.4	1121	7	CR755403	CR755403
550	195.5	10.8	576	1	AL699151	DKFZp886E	623	187.5	10.4	582	5	BP355339	BP355339
551	195.5	10.8	632	7	CO432230	UI-M-HX0-	c	624	187.5	652	8	BH269030	CH230-66P
552	195.5	10.8	675	7	CR060015	Salamande	625	187.5	10.4	655	1	AI980307	pat.pk002
553	195.5	10.8	787	6	CD802924	UI-M-GV0-	626	187.5	10.4	759	7	CN430206	CK430206
554	195.5	10.8	857	6	CD520168	UI-M-GV0-	627	187.5	10.4	784	7	CK478969	AGENCOURT
555	195.5	10.8	1261	3	CR640626	Tetraodon	628	187	10.4	497	5	EX515241	EX515241
556	195.5	10.8	1263	3	CR647139	Tetraodon	629	187	10.4	616	7	CN532902	UI-M-HO0-
557	195	10.8	617	5	BQ555199	H4032G01-	630	187	10.4	766	2	BE213159	IPbtrn0200
558	195	10.8	666	7	CR832582	AGENCOURT	c	631	187	837	7	CF345598	AGENCOURT
559	194.5	10.8	455	7	CO337067	EN13754.5	632	187	10.4	3531	3	AK035110	Mus muscu
560	194.5	10.8	632	7	CR689464	ZF101-P00	633	187	10.4	3821	3	AK085461	Mus muscu
561	194.5	10.8	730	6	CA357629	630022 NC	634	186.5	10.3	664	7	BJ732469	BJ732469
562	194.5	10.8	763	6	CR519682	UI-M-GH0-	635	186.5	10.3	835	7	CK847657	970316 MA
563	194.5	10.8	852	7	CR422792	CD422792	636	186.5	10.3	923	3	BU326524	603489483
564	194	10.7	523	4	BI512632	BB160009B	637	186.5	10.3	1230	3	CR641410	Tetraodon
565	194	10.7	896	6	CD514588	AGENCOURT	638	186	10.3	644	6	CB518611	UI-M-GH0-
566	194	10.7	3424	3	AK044694	Mus muscu	639	186	10.3	648	5	BM935487	UI-M-BH3-
567	193.5	10.7	4178	6	CD352315	UI-M-GV0-	640	186	10.3	727	7	CO431177	UI-M-HX0-
568	193.5	10.7	226	1	AA776056	ae79a07.s	641	186	10.3	752	7	CF741342	UI-M-GH0-
569	193	10.7	710	7	CR225540	WLA073F11	642	186	10.3	788	7	CF737289	UI-M-HD0-
570	193	10.7	808	5	BU746846	CH3#007 D	643	186	10.3	791	7	CO557024	AGENCOURT
571	193	10.7	614	6	CD636183	56020347J	644	186	10.3	883	7	CN985580	CN985580
572	192.5	10.7	944	5	B0681009	AGENCOURT	645	186	10.3	1146	7	CR755551	CR755551
573	192.5	10.7	945	9	CN504AD2	UI-M-FY0-	646	186	10.3	1791	9	AY411534	AY411534
574	192.5	10.7	1259	3	CR636055	Tetraodon	647	185.5	10.3	636	5	BU363294	603585969
575	192.5	10.7	2283	9	AY418472	Mus muscu	648	185.5	10.3	761	6	CA384559	665213 NC
576	192.5	10.7	4329	3	AK040765	Mus muscu	649	185.5	10.3	987	2	BF579256	602093426
577	192.5	10.7	534	7	CR556169	DKFZp459D	650	185.5	10.3	1215	9	AY421473	Homo sapi
578	192	10.6	730	7	CO508029	GGEZEB103	651	185.5	10.3	2299	9	AY418470	Homo sapi
579	192	10.6	730	7	CO508029	GGEZEB103	652	185	10.2	736	1	AA439246	LD13756.5
580	192	10.6	839	6	CD578410	UI-M-FY0-	653	185	10.2	951	5	BQ680360	AGENCOURT
581	192	10.6	877	5	BU322077	603850177	654	185	10.2	990	9	AY418720	Pan trogl
582	192	10.6	2132	6	AY045734	Homo sapi	655	185	10.2	3638	3	AK045373	Mus muscu
583	192	10.6	4068	9	AY046426	Pan trogl	656	184.5	10.2	644	5	BQ561052	H4068A05-
584	191.5	10.6	581	8	BH269028	CH230-66P	657	184.5	10.2	700	4	BM623297	170006874
585	191.5	10.6	702	7	CR359049	170004245	658	184.5	10.2	1497	3	AK053039	Mus muscu
586	191.5	10.6	779	8	BH292378	CH230-44D	659	184	10.2	565	4	BG732685	333483 MA
587	191.5	10.6	1291	3	CR641448	Tetraodon	660	184	10.2	662	4	BM624477	170006874
588	191.5	10.6	3157	9	AY403615	Pan trogl	661	184	10.2	669	7	CF745309	UI-M-GV0-
589	191	10.6	613	4	BM487940	pgm2n.pk0	662	184	10.2	670	4	BM117149	imageqc 5
590	191	10.6	754	7	CF530715	UI-M-FY0-	663	184	10.2	791	7	CO572836	AGENCOURT
591	191	10.6	1055	4	BM551034	AGENCOURT	c	664	184	838	6	CD636246	6036477H
592	190.5	10.5	643	6	CA385573	666709 NC	665	184	10.2	865	5	EX725298	EX725298
593	190.5	10.5	649	7	CO505951	GGEZEB103	666	184	10.2	940	7	CK871065	AGENCOURT



813	174.5	9.7	847	7	CF374272	AGENCOURT	886	170.5	9.4	585	5	BP377151	BP377151
814	174.5	9.7	875	5	EX403262	EX403262	887	170.5	9.4	588	6	CB585172	AMGNNUC:N
815	174	9.6	285	7	BN209637	4115576 B	888	170.5	9.4	600	4	BG806560	2032-50 M
816	174	9.6	581	5	BP217876	BP217876	889	170.5	9.4	600	5	BU920372	.6053-62
817	174	9.6	625	1	AU134398	AU134398	890	170.5	9.4	614	6	CD351134	UI-M-FY0-
818	174	9.6	669	5	EX670963	EX670963	891	170.5	9.4	746	6	CD636196	56030950H
819	174	9.6	736	8	AX2989621	2M0273104	892	170.5	9.4	778	2	BF305263	601892727
820	174	9.6	940	7	CK865164	AGENCOURT	893	170.5	9.4	816	7	CF220046	AGENCOURT
821	174	9.6	2756	3	AK038385	Mus muscu	894	170.5	9.4	892	5	BU135652	603124302
822	174	9.6	3075	3	AK034142	Mus muscu	895	170.5	9.4	893	7	CN507252	AGENCOURT
823	174	9.6	4152	3	AK079332	Mus muscu	896	170.5	9.4	999	4	BM561628	AGENCOURT
824	173.5	9.6	569	6	CB616002	AMGNNUC:N	897	170	9.4	561	7	CN991327	67958-125
825	173.5	9.6	629	7	CF364674	834668 MA	898	170	9.4	723	9	CG784243	PHCRC-GT-
826	173.5	9.6	634	6	CB577096	AMGNNUC:N	899	170	9.4	748	6	CD620698	56100889H
827	173.5	9.6	888	7	CK424119	AUF IpSto	900	170	9.4	776	7	CN171251	AGENCOURT
828	173.5	9.6	2240	9	AY418469	Mus muscu	901	170	9.4	825	7	CF222141	AGENCOURT
829	173	9.6	527	1	AA741334	Ob30f08-s	902	170	9.4	827	7	CR445411	CR445411
830	173	9.6	619	6	CD636182	56020347H	903	170	9.4	836	7	CF147692	AGENCOURT
831	173	9.6	642	4	BM310781	ig48d12.Y	904	170	9.4	856	7	CF237672	AGENCOURT
832	173	9.6	765	7	CN535749	UI-M-HS0-	905	169.5	9.4	499	2	BF151777	uz20c07.Y
833	173	9.6	812	7	CO426708	UI-M-HU0-	906	169.5	9.4	563	7	CF534807	UI-M-GH0-
834	173	9.6	935	7	CK870930	AGENCOURT	907	169.5	9.4	581	5	BP195803	BP195803
835	173	9.6	1088	7	CK030075	AGENCOURT	908	169.5	9.4	662	2	BB665541	BB665541
836	173	9.6	2976	3	HL366554	Homo sapi	909	169.5	9.4	708	6	CB423451	596888 MA
837	172.5	9.6	452	7	CN359001	170005322	910	169.5	9.4	752	7	CF729863	UI-M-HB0-
838	172.5	9.6	643	7	CF895017	A0142H05-	911	169.5	9.4	755	4	BJ723979	BJ723979
839	172.5	9.6	646	4	BM576695	170006871	912	169.5	9.4	759	7	CK871118	AGENCOURT
840	172.5	9.6	685	7	CF790517	DFZ2p459K	913	169.5	9.4	760	6	CA513275	UI-R-FJ0-
841	172.5	9.6	761	6	CD636201	56030966J	914	169.5	9.4	803	1	AU131954	AU131954
842	172.5	9.6	782	7	CK807818	AGENCOURT	915	169.5	9.4	804	7	CK869114	AGENCOURT
843	172.5	9.6	808	5	BX771524	BX771524	916	169.5	9.4	832	9	BN238729	Danio rer
844	172.5	9.6	814	6	CD758575	AGENCOURT	917	169.5	9.4	843	7	CN157026	944474 MA
845	172.5	9.6	842	7	CK597432	AGENCOURT	918	169.5	9.4	1097	1	AL561703	ILLUMIGEN
846	172.5	9.6	889	7	CF375649	AGENCOURT	919	169.5	9.4	1106	1	AL561703	AL561703
847	172.5	9.6	892	1	AU079295	AU079295	920	169.5	9.4	3230	3	AK011916	Mus muscu
848	172.5	9.6	930	5	BQ950644	AGENCOURT	921	169	9.4	547	7	CK656925	3017HFX2
849	172.5	9.6	933	7	CK867774	AGENCOURT	922	169	9.4	582	5	BP194396	BP194396
850	172.5	9.6	2784	3	AK052040	Mus muscu	923	169	9.4	595	1	AI722009	fd18c09.Y
851	172	9.5	616	1	A1924653	wn57h07.x	924	169	9.4	604	2	AW025115	wu71h04.X
852	172	9.5	728	7	CN530285	UI-M-HQ0-	925	169	9.4	658	4	BJ011427	BJ011427
853	172	9.5	800	4	BG293215	602390177	926	169	9.4	702	5	BM098413	BM098413
854	172	9.5	802	7	CK777862	965008 MA	927	169	9.4	740	7	CF744590	UI-M-GV0-
855	172	9.5	811	5	BX761240	BX761240	928	169	9.4	767	6	CA345552	676226 NC
856	172	9.5	818	7	CN977731	28379-125	929	169	9.4	799	7	CR409324	CR409324
857	172	9.5	840	1	AL524519	AL524519	930	169	9.4	805	5	BQ745652	UI-M-EW0-
858	171.5	9.5	567	5	BP370399	BP370399	931	169	9.4	886	6	CD172256	AGENCOURT
859	171.5	9.5	568	6	CD674218	fs08a04.Y	932	169	9.4	888	7	CK409633	AUF Iflvr
860	171.5	9.5	579	7	CN359288	170005999	933	169	9.4	1143	6	CD503634	CD503634
861	171.5	9.5	580	5	BP210849	BP210849	934	169	9.4	1735	2	AW888221	MDRA5 Hum
862	171.5	9.5	582	5	BP194652	BP194652	935	169	9.4	3553	3	AK081793	AK081793
863	171.5	9.5	583	5	BP359006	BP359006	936	168.5	9.3	528	6	CB719651	AMGNNUC:N
864	171.5	9.5	583	7	CN359285	170005326	937	168.5	9.3	539	1	AL918370	AL918370
865	171.5	9.5	587	5	BQ270237	ik08a10.Y	938	168.5	9.3	543	1	AU207958	AU207958
866	171.5	9.5	590	5	BP309421	BP309421	939	168.5	9.3	579	6	CB607385	AMGNNUC:N
867	171.5	9.5	603	5	BU789381	1040b04.Y	940	168.5	9.3	606	7	CV040428	CV040428
868	171.5	9.5	603	5	BX316915	BX316915	941	168.5	9.3	671	7	CO389127	AGENCOURT
869	171.5	9.5	688	6	CD296956	Str-Pu691.	942	168.5	9.3	673	6	CB248224	UI-M-F10-
870	171.5	9.5	685	7	CK544312	rswhb0.01	943	168.5	9.3	2645	3	BC038036	Mus muscu
871	171.5	9.5	686	7	CO505010	GGZER103	944	168.5	9.3	4199	3	AK030591	AK030591
872	171.5	9.5	726	6	CD636205	56030983J	945	168	9.3	535	2	AW786664	120025 MA
873	171.5	9.5	757	4	BG819912	602782004	946	168	9.3	571	4	BM272758	ig999a06.Y
874	171.5	9.5	786	2	BB306404	601103309	947	168	9.3	581	5	BP194328	BP194328
875	171.5	9.5	801	6	CD636213	56031066J	948	168	9.3	639	6	CA328483	CA328483
876	171.5	9.5	806	6	CD636192	56030942H	949	168	9.3	762	7	CO245579	AGENCOURT
877	171.5	9.5	816	6	CD636238	56038369H	950	168	9.3	774	5	BU205766	603102289
878	171.5	9.5	1749	3	CK643698	Tetraodon	951	168	9.3	804	7	CR414090	CR414090
879	171	9.5	583	5	BP219778	BP219778	952	168	9.3	873	7	CF251316	esa023-e1
880	171	9.5	684	5	BU625289	UI-H-FG1-	953	168	9.3	921	5	BU520481	AGENCOURT
881	171	9.5	816	7	CF220776	AGENCOURT	954	167.5	9.3	573	1	AI685262	wa75e11.x
882	171	9.5	1386	3	CK608576	full-lenq	955	167.5	9.3	725	7	CK691938	2F101-P00
883	171	9.5	1653	3	BC024164	Homo sapi	956	167.5	9.3	736	7	CK367468	AGENCOURT
884	170.5	9.4	484	5	BX099260	BX099260	957	167.5	9.3	786	5	BU382983	603582371
885	170.5	9.4	526	7	CN677790	E0102B04-	958	167.5	9.3	798	7	CK481268	AGENCOURT

959	167.5	9.3	817	4	BG9112522	BG9112522 602806620	1032	164	9.1	1164	3	AK008187	AK008187 Mus muscu
960	167.5	9.3	831	5	BU491858	BU491858 604131047	1033	164	9.1	1639	3	AK032833	AK032833 Mus muscu
961	167.5	9.3	930	7	CK407450	CK407450 AUF Iflvr	1034	164	9.1	1701	3	AK013156	AK013156 Mus muscu
962	167.5	9.3	981	5	BG964910	BG964910 AGENCOURT	1035	164	9.1	1930	3	AK003326	AK003326 Mus muscu
963	167.5	9.3	1469	3	AK044527	AK044527 Mus muscu	1036	164	9.1	2814	3	CR593108	CR593108 full-leng
964	167	9.2	514	6	CB716703	CB716703 AMGNNUC:N	1037	163.5	9.1	469	2	AW414520	AW414520 48011 MAR
965	167	9.2	608	6	CB636186	CB636186 56020455H	1038	163.5	9.1	584	6	CB586237	CB586237 AMGNNUC:M
966	167	9.2	616	7	CN164688	CN164688 995050 MA	1039	163.5	9.1	667	4	B1654678	B1654678 603285596
967	167	9.2	696	1	A1542894	A1542894 SD09407.5	1040	163.5	9.1	672	7	CN537405	CN537405 UI-M-HS0-
968	167	9.2	707	7	CK869511	CK869511 AGENCOURT	1041	163.5	9.1	693	2	BB525933	BB525933 BB525933
969	167	9.2	726	5	BU446195	BU446195 603766375	1042	163.5	9.1	705	4	B1662853	B1662853 603286287
970	167	9.2	912	7	CK870512	CK870512 AGENCOURT	1043	163.5	9.1	711	7	CK951501	CK951501 4091020 B
971	167	9.2	1289	3	CR729255	CR729255 Tetraodon	1044	163.5	9.1	724	7	CF998350	CF998350 AGENCOURT
972	167	9.2	3628	3	AK031696	AK031696 Mus muscu	1045	163.5	9.1	750	7	CF996540	CF996540 AGENCOURT
973	166.5	9.2	583	5	BP321297	BP321297	1046	163.5	9.1	791	7	CK867184	CK867184 AGENCOURT
974	166.5	9.2	775	7	CF348727	CF348727 AGENCOURT	1047	163.5	9.1	794	7	CF996588	CF996588 AGENCOURT
975	166.5	9.2	779	1	AU125657	AU125657	1048	163.5	9.1	810	6	CA382308	CA382308 662081 NC
976	166.5	9.2	812	6	CB723208	CB723208 UI-M-GH0-	1049	163.5	9.1	855	4	B1554904	B1554904 603236202
977	166.5	9.2	822	6	CA510738	CA510738 UI-R-FJ0-	1050	163.5	9.1	889	7	CN501295	CN501295 AGENCOURT
978	166.5	9.2	928	5	BQ891778	BQ891778 AGENCOURT	1051	163.5	9.1	910	7	CF266068	CF266068 AGENCOURT
979	166	9.2	583	4	BG223754	BG223754 1M00018F0	1052	163.5	9.1	923	7	CN322132	CN322132 AGENCOURT
980	166	9.2	647	7	CK781448	CK781448 UI-M-GV0-	1053	163.5	9.1	934	7	CK868656	CK868656 AGENCOURT
981	166	9.2	656	7	CK659672	CK659672 LPI7591.5	1054	163.5	9.1	951	7	CK866211	CK866211 AGENCOURT
982	166	9.2	680	7	CF899461	CF899461 A0303E02-	1055	163.5	9.1	1776	3	AK010153	AK010153 Mus muscu
983	166	9.2	740	4	BJ720179	BJ720179	1056	163.5	9.1	3248	3	AK004821	AK004821 Mus muscu
984	166	9.2	796	6	CD653854	CD653854 AGENCOURT	1057	163.5	9.1	3590	3	AK028479	AK028479 Mus muscu
985	166	9.2	805	4	BG117787	BG117787 602350472	1058	163	9.0	444	9	AY402969	AY402969 Homo sapi
986	166	9.2	805	7	CF785901	CF785901 AGENCOURT	1059	163	9.0	444	9	AY402970	AY402970 Pan trogl
987	166	9.2	910	5	BX324896	BX324896 BX324896	1060	163	9.0	444	9	AY402971	AY402971 Mus muscu
988	165.5	9.2	420	6	CB798880	CB798880 AMGNNUC:N	1061	163	9.0	548	7	CO323280	CO323280 EKJ90105.
989	165.5	9.2	517	6	CD290273	CD290273 St-Pu538.	1062	163	9.0	557	7	CK541739	CK541739 rswb0.00
990	165.5	9.2	589	1	AA606149	AA606149 fa16d03.8	1063	163	9.0	569	4	BM090970	BM090970 i918e09.x
991	165.5	9.2	634	6	CD803622	CD803622 UI-M-GV0-	1064	163	9.0	635	1	AL878745	AL878745 AL878745
992	165.5	9.2	654	7	CF744226	CF744226 UI-M-GV0-	1065	163	9.0	635	5	BX276614	BX276614 BX276614
993	165.5	9.2	699	6	CD802719	CD802719 UI-M-GV0-	1066	163	9.0	658	5	BX260070	BX260070 BX260070
994	165.5	9.2	793	7	CK870310	CK870310 AGENCOURT	1067	163	9.0	661	1	AL872179	AL872179 AL872179
995	165.5	9.2	797	7	CK636666	CK636666 UI-M-HN0-	1068	163	9.0	730	5	BU709173	BU709173 UI-M-EV0-
996	165.5	9.2	798	7	CK870327	CK870327 AGENCOURT	1069	163	9.0	744	4	BJ780707	BJ780707 BJ780707
997	165.5	9.2	886	5	BU528897	BU528897 AGENCOURT	1070	163	9.0	790	1	AU006391	AU006391 AU006391
998	165.5	9.2	939	5	BQ646105	BQ646105 AGENCOURT	1071	163	9.0	803	7	CK311931	CK311931 SB02010A2
999	165.5	9.2	1057	5	BX396408	BX396408 BX396408	1072	163	9.0	904	4	BG760809	BG760809 602717170
1000	165.5	9.2	1138	7	CK030399	CK030399 AGENCOURT	1073	163	9.0	935	4	BG923654	BG923654 602823392
1001	165	9.1	618	4	BI065024	BI065024 p6fin.pk0	1074	163	9.0	1181	3	CR722859	CR722859 Tetraodon
1002	165	9.1	624	1	AL968116	AL968116 AL968116	1075	163	9.0	1694	3	AK040711	AK040711 Mus muscu
1003	165	9.1	641	1	AL892168	AL892168 AL892168	1076	162.5	9.0	562	1	AV614571	AV614571 AV614571
1004	165	9.1	645	1	AL846277	AL846277 AL846277	1077	162.5	9.0	580	4	BG710895	BG710895 p6lin.pk0
1005	165	9.1	693	7	CK781175	CK781175 UI-M-GV0-	1078	162.5	9.0	590	7	CK824237	CK824237 I918e09.y
1006	165	9.1	700	5	BX331242	BX331242 BX331242	1079	162.5	9.0	601	1	AL703664	AL703664 DKF2p686A
1007	165	9.1	748	6	CD079492	CD079492 MA3-9999U	1080	162.5	9.0	685	7	CN537909	CN537909 UI-M-HS0-
1008	165	9.1	775	7	CN532584	CN532584 UI-M-HQ0-	1081	162.5	9.0	699	7	CF536456	CF536456 UI-M-HS0-
1009	165	9.1	780	7	CF539770	CF539770 UI-M-GV0-	1082	162.5	9.0	708	6	CA439206	CA439206 UI-H-D10-
1010	165	9.1	786	7	CF216645	CF216645 AGENCOURT	1083	162.5	9.0	728	5	BX499682	BX499682 DKF2p779H
1011	165	9.1	898	7	CF223675	CF223675 AGENCOURT	1084	162.5	9.0	755	7	CK018234	CK018234 AGENCOURT
1012	165	9.1	912	7	CN093676	CN093676 EC2BBA8CB	1085	162.5	9.0	763	4	BG921356	BG921356 602824217
1013	165	9.1	1137	6	CD507144	CD507144 CDA83-C06	1086	162.5	9.0	763	4	BI080254	BI080254 602876680
1014	164.5	9.1	559	5	BP370855	BP370855 BP370855	1087	162.5	9.0	779	6	CD636252	CD636252 56049016H
1015	164.5	9.1	561	7	CK618594	CK618594 mk14a07.y	1088	162.5	9.0	814	7	CO810649	CO810649 AGENCOURT
1016	164.5	9.1	604	5	BU102167	BU102167 PRODIGID	1089	162.5	9.0	856	6	BI130635	BI130635 603118991
1017	164.5	9.1	683	4	BI393255	BI393255 p6pin.pk0	1090	162.5	9.0	860	6	CB193630	CB193630 AGENCOURT
1018	164.5	9.1	743	6	CD494572	CD494572 CDA11-E10	1091	162.5	9.0	925	4	BI872091	BI872091 603396391
1019	164.5	9.1	836	8	BH044916	BH044916 RPT-24-3	1092	162.5	9.0	930	7	CK409630	CK409630 AUF Iflvr
1020	164.5	9.1	839	7	CO922821	CO922821 AGENCOURT	1093	162.5	9.0	933	5	BU856183	BU856183 AGENCOURT
1021	164.5	9.1	859	4	BI413783	BI413783 602987688	1094	162.5	9.0	3905	3	AK083069	AK083069 Mus muscu
1022	164	9.1	387	7	CO298825	CO298825 EKJ73933.	1095	162	9.0	455	4	BG358967	BG358967 BOVNS1-00
1023	164	9.1	599	8	AZ585520	AZ585520 1M030E18	1096	162	9.0	571	7	CK707773	CK707773 ZF201-P00
1024	164	9.1	627	7	CN983254	CN983254 51876.126	1097	162	9.0	625	5	BP277969	BP277969 BP277969
1025	164	9.1	644	6	CD3762018	CD3762018 UI-M-GO0-	1098	162	9.0	660	7	CF532017	CF532017 UI-M-FY0-
1026	164	9.1	651	6	CD806831	CD806831 UI-M-GW0-	1099	162	9.0	699	7	CF366889	CF366889 841594 MA
1027	164	9.1	720	6	CB520196	CB520196 UI-M-GT0-	1100	162	9.0	870	4	BI197164	BI197164 602756667
1028	164	9.1	767	4	BG570299	BG570299 602838903	1101	162	9.0	891	6	CB194073	CB194073 AGENCOURT
1029	164	9.1	883	8	BZ222298	BZ222298 CH230-324	1102	162	9.0	962	6	CD080179	CD080179 MA3-9999U
1030	164	9.1	924	5	BQ933843	BQ933843 AGENCOURT	1103	162	9.0	1056	5	BM925845	BM925845 AGENCOURT
1031	164	9.1	964	5	BQ715124	BQ715124 AGENCOURT	1104	161.5	8.9	581	5	BP346467	BP346467 BP346467

1105	161.5	8.9	583	5	BP347694	BP347694	1178	159.5	8.8	641	7	CK693848	CK693848	ZFI101-P00
c1106	161.5	8.9	622	2	BE864980	UI-M-BH1-	1179	159.5	8.8	699	4	BM728584	UI-E-EJ0-	BM728584
1107	161.5	8.9	679	7	CF900715	A0319A05-	c1180	159.5	8.8	717	5	BQ206762	UI-R-D21-	BQ206762
1108	161.5	8.9	694	7	CF792923	AGENCOURT	1181	159.5	8.8	801	7	CF182513	UI-M-EY0-	CF182513
c1109	161.5	8.9	708	5	EX881610	EX881610	1182	159.5	8.8	806	4	BI762516	603048638	BI762516
1110	161.5	8.9	723	4	EG974950	602844949	1183	159.5	8.8	808	4	BI833165	603090890	BI833165
1111	161.5	8.9	731	7	CN528054	UI-M-HQ0-	1184	159.5	8.8	832	2	BE563419	601335464	BE563419
1112	161.5	8.9	733	4	BG545860	602573145	1185	159.5	8.8	832	1	AU133135	AU133135	AU133135
1113	161.5	8.9	819	7	CK865025	AGENCOURT	1186	159.5	8.8	882	5	BK728325	BK728325	BK728325
1114	161.5	8.9	820	6	CD620694	56100873H	1187	159.5	8.8	938	7	CK866851	AGENCOURT	CK866851
1115	161.5	8.9	855	6	CS889827	AGENCOURT	1188	159.5	8.8	940	5	EX369835	EX369835	EX369835
1116	161.5	8.9	874	7	CQ733078	SILF02C04	1189	159.5	8.8	941	5	BU912943	AGENCOURT	BU912943
1117	161.5	8.9	878	5	BQ887533	AGENCOURT	1190	159.5	8.8	947	5	BQ644258	AGENCOURT	BQ644258
1118	161.5	8.9	910	5	BQ650842	AGENCOURT	1191	159.5	8.8	2748	3	AK036352	Mus muscu	AK036352
1119	161.5	8.9	979	4	BG420574	602448438	1192	159	8.8	259	2	BB607028	BB607028	BB607028
1120	161	8.9	489	2	BF705825	268993 MA	1193	159	8.8	451	1	AL119880	DKP2P761M	AL119880
1121	161	8.9	556	7	CR452315	CR452315	1194	159	8.8	557	6	CA563258	K0311H02-	CA563258
1122	161	8.9	581	4	BU070444	BU070444	1195	159	8.8	599	4	BU058708	BU058708	BU058708
1123	161	8.9	670	7	CN538094	UI-M-HS0-	1196	159	8.8	692	6	CB526667	UI-M-FY0-	CB526667
1124	161	8.9	673	7	CN366089	170005313	1197	159	8.8	719	6	CB724268	UI-M-FY0-	CB724268
1125	161	8.9	714	7	CN366080	170004243	1198	159	8.8	738	7	CR564541	CR564541	CR564541
1126	161	8.9	717	5	BU321343	603854520	1199	159	8.8	931	5	EX336244	EX336244	EX336244
1127	161	8.9	730	7	CN366076	170005331	1200	159	8.8	934	5	BU903988	AGENCOURT	BU903988
1128	161	8.9	732	7	CN304969	170005325	1201	159	8.8	1013	7	CN801753	ILLUMIGEN	CN801753
1129	161	8.9	738	4	BG864104	602797704	1202	159	8.8	1677	3	AK030635	Mus muscu	AK030635
1130	161	8.9	757	7	CN304990	170004240	1203	159	8.8	3687	3	AK076215	Mus muscu	AK076215
1131	161	8.9	766	5	EX869908	EX869908	1204	158.5	8.8	569	5	BP377634	BP377634	BP377634
1132	161	8.9	770	5	B0444091	UI-M-EX0-	1205	158.5	8.8	574	2	BP540423	602050188	BP540423
1133	161	8.9	879	6	CD557080	AGENCOURT	1206	158.5	8.8	582	5	BP208357	BP208357	BP208357
1134	161	8.9	887	7	CK408075	AUF_ILFVr	1207	158.5	8.8	583	5	BP357634	BP357634	BP357634
1135	161	8.9	901	7	CN319156	AGENCOURT	1208	158.5	8.8	586	5	BP254888	BP254888	BP254888
1136	161	8.9	902	7	CR442151	CR442151	1209	158.5	8.8	600	5	BU918743	5033-34 M	BU918743
1137	161	8.9	905	5	BU182251	AGENCOURT	1210	158.5	8.8	652	1	AL846235	AL846235	AL846235
1138	161	8.9	908	5	EX386931	EX386931	1211	158.5	8.8	760	6	CA319537	UI-M-FW0-	CA319537
1139	161	8.9	922	5	BQ894075	AGENCOURT	1212	158.5	8.8	828	7	CV077258	AGENCOURT	CV077258
1140	161	8.9	939	4	BH451147	AGENCOURT	1213	158.5	8.8	853	5	BQ719866	BQ719866	BQ719866
1141	161	8.9	1673	3	CR617412	full-leng	1214	158.5	8.8	906	5	BU916159	AGENCOURT	BU916159
1142	161	8.9	3533	3	BC057284	Hom sapi	c1215	158.5	8.8	964	9	CNS05CLJ	BX398530	BX398530
1143	160.5	8.9	460	1	AL155245	hmo40d12.r	1216	158.5	8.8	1057	5	EX398530	EX398530	EX398530
1144	160.5	8.9	486	7	CR746947	CR746947	1217	158.5	8.8	1154	6	CD503211	CD503211	CD503211
1145	160.5	8.9	530	2	BE226313	ia19a09.y	1218	158.5	8.8	1296	7	CF110468	Shultzomi	CF110468
1146	160.5	8.9	582	5	BP361289	BP361289	1219	158.5	8.8	1586	9	AY411535	Pan trogl	AY411535
1147	160.5	8.9	595	1	AV617433	AV617433	1220	158.5	8.8	3751	9	AY404031	Homo sapi	AY404031
1148	160.5	8.9	602	7	CF727943	CF727943	1221	158	8.7	382	6	CB809130	AMGNUG:C	CB809130
1149	160.5	8.9	606	5	BP505184	BP505184	1222	158	8.7	448	6	BY568324	BY568324	BY568324
1150	160.5	8.9	711	4	BG115636	602316760	1223	158	8.7	450	2	BF731087	ma81a06.	BF731087
1151	160.5	8.9	715	7	CN426680	170005321	1224	158	8.7	453	6	BY565338	BY565338	BY565338
1152	160.5	8.9	782	7	CK026234	AGENCOURT	1225	158	8.7	539	7	CN679683	E0127F05-	CN679683
1153	160.5	8.9	798	6	CD656120	AGENCOURT	1226	158	8.7	582	5	BP251115	BP251115	BP251115
1154	160.5	8.9	800	5	BU319927	603487913	1227	158	8.7	595	2	BE291062	601083890	BE291062
1155	160.5	8.9	884	4	BI771277	603054624	1228	158	8.7	614	1	AI809639	wf31g05.x	AI809639
1156	160.5	8.9	889	7	CF266344	AGENCOURT	1229	158	8.7	670	4	BG085642	BG085642	BG085642
1157	160.5	8.9	966	7	CF995094	AGENCOURT	1230	158	8.7	671	1	AL859372	AL859372	AL859372
1158	160.5	8.9	3146	3	AK084850	Mus muscu	1231	158	8.7	716	5	BU281132	603600750	BU281132
1159	160	8.9	456	7	CF796349	892593 NC	1232	158	8.7	716	6	CA376321	654651 NC	CA376321
1160	160	8.9	630	6	CA376096	654336 NC	1233	158	8.7	717	7	CF724990	UI-M-GZ0-	CF724990
1161	160	8.9	721	6	CA749345	UI-M-FY0-	1234	158	8.7	790	7	CK677667	603735879	CK677667
1162	160	8.9	727	7	CK457803	UI-M-HN0-	1235	158	8.7	818	5	BU306680	ZFI101-P00	BU306680
1163	160	8.9	740	7	CF533274	UI-M-FY0-	1236	158	8.7	822	7	CO870384	3017HF0N4	CO870384
1164	160	8.9	819	5	BX424510	BX424510	1237	158	8.7	827	4	BI463685	603207357	BI463685
1165	160	8.9	820	7	CO395177	AGENCOURT	1238	158	8.7	899	7	CK866029	AGENCOURT	CK866029
1166	160	8.9	824	5	BQ444246	UI-M-EX0-	1239	158	8.7	914	5	BQ898909	BQ898909	BQ898909
1167	160	8.9	824	7	CK470323	AGENCOURT	1240	158	8.7	936	5	BX853896	BX853896	BX853896
1168	160	8.9	865	1	AL134784	GHI2331.5	1241	157.5	8.7	582	5	BP250662	BP250662	BP250662
1169	160	8.9	1092	7	CN642662	ILLUMIGEN	1242	157.5	8.7	600	5	BU922970	7042-78 M	BU922970
1170	160	8.9	3811	3	AK031246	Mus muscu	1243	157.5	8.7	617	5	BQ359313	MR2-HN003	BQ359313
1171	159.5	8.8	383	1	AA401292	zv63g05.r	c1244	157.5	8.7	636	5	BU101548	PRODGLIGID	BU101548
1172	159.5	8.8	493	6	CD739385	4027892.1	1245	157.5	8.7	650	4	BM049915	603624395	BM049915
1173	159.5	8.8	538	2	BF022068	uy46d08.y	1246	157.5	8.7	664	4	BI373259	RE60514.5	BI373259
1174	159.5	8.8	582	5	BP315255	BP315255	1247	157.5	8.7	666	2	BE392233	601308119	BE392233
1175	159.5	8.8	600	5	BU101549	PRODGLIGID	1248	157.5	8.7	721	5	BQ769295	UI-M-FI0-	BQ769295
1176	159.5	8.8	615	4	BI067145	pgfin.pk0	1249	157.5	8.7	755	7	CK868145	AGENCOURT	CK868145
1177	159.5	8.8	629	1	AL657340	AL657340	1250	157.5	8.7	762	7	CK397238	AGENCOURT	CK397238

1251	157.5	8.7	776	7	CF737877	CF737877	UI-M-HDO-	1324	156	8.6	477	7	CN359280	CN359280	170005319
1252	157.5	8.7	796	5	BX923146	BX923146	BX923146	1325	156	8.6	596	1	AL599774	DKF7Q313M	
1253	157.5	8.7	818	8	CK868629	CK868629	AGENCOURT	1326	156	8.6	628	4	BJ685150	BJ685150	
1254	157.5	8.7	860	6	CD627471	56067512J		1327	156	8.6	653	7	CK003476	AGENCOURT	
1255	157.5	8.7	901	5	BQ8881261			1328	156	8.6	691	1	AV384111	AV384111	
1256	157.5	8.7	904	5	BQ685640	AGENCOURT		1329	156	8.6	729	4	BM621183	170006874	
1257	157.5	8.7	932	5	BX514323	BX514323	AGENCOURT	1330	156	8.6	740	7	CN531505	UI-M-HQO-	
1258	157.5	8.7	953	7	CK865103	AGENCOURT		1331	156	8.6	760	7	CN531514	UI-M-HQO-	
1259	157.5	8.7	953	7	CK865103	AGENCOURT		1332	156	8.6	767	2	AW175139	fi32f09.Y	
1260	157.5	8.7	958	2	BF795536			1333	156	8.6	775	6	CD080814	MA3-9999U	
1261	157.5	8.7	987	5	BX375028	BX375028		1334	156	8.6	780	5	BX444240	BX444240	
1262	157.5	8.7	1008	5	BX424991	BX424991		1335	156	8.6	784	6	CA350777	621665 NC	
1263	157.5	8.7	1046	4	BM552640	AGENCOURT		1336	156	8.6	795	7	CO248560	AGENCOURT	
1264	157.5	8.7	1072	7	CN643560	ILLUMIGEN		1337	156	8.6	810	7	CO799885	AGENCOURT	
1265	157.5	8.7	1488	3	CK608619	full-leng		1338	156	8.6	1096	7	CN642525	ILLUMIGEN	
1266	157.5	8.7	1594	3	CK617107	full-leng		1339	156	8.6	2036	3	AK089498	Mus muscu	
1267	157.5	8.7	1742	9	AY413879	Mus muscu		1340	156	8.6	2850	3	AK047868	Mus muscu	
1268	157.5	8.7	2090	3	AK003152	Mus muscu		1341	156	8.6	3312	3	AK004947	Mus muscu	
1269	157.5	8.7	2209	3	AK017447			1342	156	8.6	3449	9	AK041299	Mus muscu	
1270	157.5	8.7	2735	3	AK029024			1343	156	8.6	3559	9	AY404032	Pan trogl	
1271	157.5	8.7	3652	3	AK030851			1344	156	8.6	3687	3	AK079247	Mus muscu	
1272	157.5	8.7	4118	3	AK031391			1345	155.5	8.6	409	2	BE226893	U874A09.Y	
1273	157	8.7	578	5	BF368062	BP368062		1346	155.5	8.6	581	5	BP193219	BP193219	
1274	157	8.7	608	5	BX917921	BX917921		1347	155.5	8.6	581	5	BP195771	BP195771	
1275	157	8.7	612	4	BM795050	K-BST0076		1348	155.5	8.6	605	7	CF368297	852930 MA	
1276	157	8.7	641	2	BB664453	BB664453		1349	155.5	8.6	617	5	BM305475	BM305475	
1277	157	8.7	690	6	CD636219	56031467J		1350	155.5	8.6	638	5	CD629100	56059934H	
1278	157	8.7	695	7	CK949734			1351	155.5	8.6	649	1	AL864304	AL864304	
1279	157	8.7	722	6	CD805128	CD805128	UI-M-GWO-	1352	155.5	8.6	702	9	CNS02PTU	Tetraodon	
1280	157	8.7	727	7	CK961924	4076329 B		1353	155.5	8.6	718	6	CD636336	56048995J	
1281	157	8.7	737	4	BI915307	603184382		1354	155.5	8.6	727	4	BM290618	EST577152	
1282	157	8.7	757	6	CB519019	UI-M-GHO-		1355	155.5	8.6	769	7	CN505057	AGENCOURT	
1283	157	8.7	781	6	CD348686			1356	155.5	8.6	786	7	CN302526	170006001	
1284	157	8.7	805	1	AU131165	AU131165	UI-M-FYO-	1357	155.5	8.6	796	5	BX923150	BX923150	
1285	157	8.7	826	6	CB165550	BEQ603160		1358	155.5	8.6	796	5	BX926278	BX926278	
1286	157	8.7	848	7	CN020324	AGENCOURT		1359	155.5	8.6	797	6	CD642524	AGENCOURT	
1287	157	8.7	850	5	BX739790	BX739790		1360	155.5	8.6	850	5	BP264898	BP264898	
1288	157	8.7	876	5	CK948326	4073246 B		1361	155.5	8.6	850	7	CO557070	AGENCOURT	
1289	157	8.7	886	5	BQ945091			1362	155.5	8.6	861	6	CD636209	56031050J	
1290	157	8.7	896	5	BX379273	BX379273		1363	155.5	8.6	880	5	BU542115	AGENCOURT	
1291	157	8.7	910	5	BU192138	AGENCOURT		1364	155.5	8.6	979	7	CN642097	ILLUMIGEN	
1292	157	8.7	930	7	CN315936	AGENCOURT		1365	155.5	8.6	1039	5	BQ057979	AGENCOURT	
1293	157	8.7	933	9	AY417086	Mus muscu		1366	155.5	8.6	1091	7	CK232190	ILLUMIGEN	
1294	157	8.7	1020	4	BM548873	AGENCOURT		1367	155.5	8.6	1376	3	CR635265	Tetraodon	
1295	157	8.7	1034	1	AL553289	AL553289		1368	155.5	8.6	4017	3	AK028983	Mus muscu	
1296	157	8.7	1071	5	BU503048	AGENCOURT		1369	155.5	8.6	5635	9	AY412619	Mus muscu	
1297	157	8.7	1127	1	AL549623	AL549623		1370	155	8.6	427	7	CO436236	ddPCR2_17	
1298	157	8.7	1514	3	CK617300	full-leng		1371	155	8.6	545	4	BM440456	pgrin.pk0	
1299	157	8.7	1867	3	AK087272			1372	155	8.6	571	4	BU124803	BJ124803	
1300	157	8.7	1892	3	CK622259	full-leng		1373	155	8.6	602	6	CA317092	UI-M-FWO-	
1301	157	8.7	2791	3	BC013698	Hom0 sapi		1374	155	8.6	617	6	CD636187	56020455J	
1302	156.5	8.7	568	1	AI629069	fc09b12.y		1375	155	8.6	669	5	BU696122	LL21n1269	
1303	156.5	8.7	618	4	BI065290	pgrin.pk0		1376	155	8.6	694	6	CD345249	UI-M-FYO-	
1304	156.5	8.7	627	4	BU112590	BU112590		1377	155	8.6	705	7	CR753907	CR753907	
1305	156.5	8.7	630	1	AI295266	LP08849.5		1378	155	8.6	710	7	CN053418	Salamande	
1306	156.5	8.7	630	5	BQ390372	NISC mc12		1379	155	8.6	726	7	CN302510	170005318	
1307	156.5	8.7	684	6	CA354756	626528 NC		1380	155	8.6	739	7	CN302524	170004710	
1308	156.5	8.7	725	4	BI736575	603361039		1381	155	8.6	755	7	CN302501	170005322	
1309	156.5	8.7	740	5	BU058190	UI-M-F00-		1382	155	8.6	778	7	CK634628	UI-M-HNO-	
1310	156.5	8.7	751	5	BP673676	BP673676		1383	155	8.6	781	5	BU378211	603581533	
1311	156.5	8.7	768	7	CN172200	AGENCOURT		1384	155	8.6	792	4	BI772811	603054461	
1312	156.5	8.7	776	5	BQ442214	UI-M-EXO-		1385	155	8.6	793	3	CF288820	AGENCOURT	
1313	156.5	8.7	858	5	BU470108	603365843		1386	155	8.6	833	1	AA941031	LD23480.5	
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1316	156.5	8.7	937	7	CO248697			1389	155	8.6	907	5	BQ928239	AGENCOURT	
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1318	156.5	8.7	1014	6	CB206098			1391	155	8.6	922	5	BU518914	AGENCOURT	
1319	156.5	8.7	1028	7	CN642108	ILLUMIGEN		1392	155	8.6	933	9	AY417084	Homo sapi	
1320	156.5	8.7	1319	7	CV182470			1393	155	8.6	941	5	BQ928243	AGENCOURT	
1321	156.5	8.7	3465	9	AY418996	Pan trogl		1394	155	8.6	993	1	AL560725	AL560725	
1322	156.5	8.7	3689	3	AK004723	Mus muscu		1395	155	8.6	1047	7	CK230378	ILLUMIGEN	
1323	156.5	8.7	3865	3	AK087355	Mus muscu		1396	155	8.6	1971	3	AK076123	Mus muscu	



1397	155	8.6	1992	3	AK034125	AK034125	Mus muscu	1470	152.5	8.4	430	5	BU947992	BU947992	io56ell.y
1398	155	8.6	3133	3	AK085723	AK085723	Mus muscu	1471	152.5	8.4	548	5	BW271825	BW271825	BW271825
1399	154.5	8.6	247	7	CR474371	CR474371		1472	152.5	8.4	594	5	BW221728	BW221728	BW221728
1400	154.5	8.6	450	1	AA168307	AA168307	ms43b12.i	1473	152.5	8.4	668	4	BI394312	BI394312	pplin.pk0
1401	154.5	8.6	498	6	CB070225	CB070225	ig27f12.y	1474	152.5	8.4	709	5	BU316030	BU316030	603488360
1402	154.5	8.6	506	7	CO328919	CO328919	EK391651.i	1475	152.5	8.4	710	9	AG286398	AG286398	Mus muscu
1403	154.5	8.6	598	1	AL856990	AL856990		1476	152.5	8.4	723	6	CB526860	CB526860	UI-M-FY0-
1404	154.5	8.6	670	5	AX379719	AX379719	IM0135X02	1477	152.5	8.4	745	4	BI080347	BI080347	602876784
1405	154.5	8.6	670	5	BK622375	BK622375		1478	152.5	8.4	768	5	EX918182	EX918182	EX918182
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1407	154.5	8.6	689	7	CF533968	CF533968	UI-M-GH0-	1480	152.5	8.4	822	6	CB245137	CB245137	UI-M-FY0-
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1414	154.5	8.6	811	7	CF5339481	CF5339481	UI-M-GH0-	1487	152.5	8.4	2338	3	AK032604	AK032604	Mus muscu
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1423	154	8.5	588	2	AW977089	AW977089	EST389198	1496	152	8.4	878	7	CN643444	CN643444	ILLUMIGEN
1424	154	8.5	595	4	BJ071900	BJ071900		1497	152	8.4	888	5	BQ945830	BQ945830	AGENCOURT
1425	154	8.5	620	1	AL876779	AL876779		1498	152	8.4	919	7	CN646263	CN646263	ILLUMIGEN
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1467	153	8.5	866	7	CN978018	CN978018	28737.125								
1468	153	8.5	941	5	BQ917338	BQ917338	AGENCOURT								
1469	153	8.5	2802	9	AY416713	AY416713	Pan trogl								

## ALIGNMENTS

RESULT 1	AK045973	1808 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK045973		Mus musculus adult male corpora quadrigemina cDNA, RIKEN		
DEFINITION			full-length enriched library, clone:B203328N06 product:NEUROTRIMIN		
ACCESSION	AK045973.1	GI:26337738	PRECUSOR (GP65), homolog [Rattus norvegicus], full insert sequence.		
VERSION	AK045973.1	GI:26337738	HTC; CAP trapper.		
KEYWORDS			Mus musculus (house mouse)		
SOURCE			Mus musculus		
ORGANISM			Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			1		
AUTHORS			Carninci,P. and Hayashizaki,Y.		
TITLE			High-efficiency full-length cDNA cloning		
JOURNAL			Math. Enzymol. 303, 19-44 (1999)		
MEDLINE			99279253		
PUBMED			10349636		
REFERENCE			2		
AUTHORS			Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE			Normalization and subtraction of cap-trapper-selected cDNAs to		
JOURNAL			Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE			20499374		
PUBMED			11042159		
REFERENCE			3		
AUTHORS			Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
TITLE			RIKEN integrated sequence analysis (RISA) system--384-format		
JOURNAL			sequencing pipeline with 384 multicapillary sequencer		
			Genome Res. 10 (11), 1757-1771 (2000)		

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Nature 409, 685-690 (2001)  
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The FANTOM Consortium and the RIKEN Genome Exploration Research  
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Nature 420, 563-573 (2002)  
6 (bases 1 to 1808)  
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
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Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
FEATURES  
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CDs  
Alignment Scores:  
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Db 1104 CTGGGTACACCAACGCCAGCATCATGCTATTGGTCCCGGTGCTGTCAGTGAGTCAAC 1163  
Qy 1044 ACCTTTTTCACCGTCTCTGAACATGACTATGCGGAACATACACATGCTGTGTGCGCTCCCAACAG 1103  
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Qy 984 AGACTGGTCGAGGAAAGAGGGAGTCAAAGTGGAAAACAGACCTTTCTTTTCAAACTC 1043  
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US-10-017-084A-523 (1-344) x AK045973 (1-1808)

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LOCUS Mus musculus adult male corpora quadrigemina cDNA, RIKEN  
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PRCURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.  
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VERSION AK046377.1  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
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2  
Carninci, P., Shibata, K., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
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3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
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Yoneda, Y., Iehikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
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The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
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Nature 409, 685-690 (2001)  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1808)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.

## COMMENT

## FEATURES

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## CDS

## ORIGIN

## Alignment Scores:

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Query Match:	98.56%	Indels:	0
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US-10-017-084A-523 (1-344) x AK046377 (1-1808)

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Qy	41	AlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThrIleAsp	60
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RESULT 3
AY406347 874 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406347
VERSION AY406347.1 GI:39762321
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Score: 1506.00 Matches: 288
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 83.39% Indels: 2
DB: 9 Gaps: 1

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Qy 77 AlaGlyAenAspLysTyrCysLeuAspProArgValValLeuLeuSerAenThrGlnThr 96
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RESULT 3
AY406347 874 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406347
VERSION AY406347.1 GI:39762321
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Pred No.: 4,01e-166 Length: 874
Score: 1506.00 Matches: 288
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 83.39% Indels: 2
DB: 9 Gaps: 1

US-10-017-084A-523 (1-344) x AY406347 (1-874)
Qy 57 CysThrIleAspAenArgValThrArgValAlaTrpLeuAenArgSerThrIleLeuTyr 76
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Qy 77 AlaGlyAenAspLysTyrCysLeuAspProArgValValLeuLeuSerAenThrGlnThr 96
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RESULT 4
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LOCUS Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406349
VERSION AY406349.1 GI:39762323
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL gene trios
PUBMED Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
COMMENT Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source Location/Qualifiers
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Pred. No.: 5 29e-164 Length: 874
Score: 1488.00 Matches: 282
Percent Similarity: 98.97% Conservative: 5
Best Local Similarity: 97.24% Mismatches: 1
Query Match: 82.39% Indels: 2
DB: 9 Gaps: 1

US-10-017-084A-523 (1-344) x AY406349 (1-874)

Qy 57 CysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr 76
Db 2 TGCACAATTGACACCGAGTCACCGGGTGGCTGGCTTAACCGCAGTACCATCCTCTAT 61

Qy 77 AlaGlyAsnAspLysTyrTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
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VERSION AY406348.1 GI:39762322
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 773)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL gene trios
Science 302 (5652), 1960-1963 (2003)

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AUTHORS  
Clark,A.G., Glatowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE  
JOURNAL  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
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ACCESSION CO635648  
VERSION CO635648.1 GI:50538871  
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ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 1450)  
AUTHORS Fitzsimmons,C.J., Savolainen,P., Amini,B., Hjalms,G., Lundeberg,J.  
and Andersson,L.  
TITLE Detection of sequence polymorphisms in red junglefowl and White  
Leghorn ESTs  
JOURNAL Unpublished (2004)  
COMMENT Contact: Carolyn Fitzsimmons  
Leif Andersson IMBIM/Dept. Animal Breeding and Genetics  
Uppsala University/Swedish University of Agricultural Sciences  
Box 597, SE-751 24 Uppsala, SWEDEN  
Tel: 00 46 (0)18 471 4593  
Fax: 00 46 (0)18 471 4833  
Email: Carolyn.fitzsimmons@bmc.uu.se  
This EST is a consensus sequence obtained from a Phrap assembly of  
4 cDNA libraries. The consensus sequence is submitted because SNP  
data in the publication 'Detection of sequence polymorphisms in red  
junglefowl and White Leghorn ESTs', is reported with reference to  
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Seq primer: (5'-end) M13 reverse.  
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Alignment Scores:  
Pred. No.: 5,27e-144 Length: 1450  
Score: 1321.00 Matches: 255  
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ACCESSION
CD354474
VERSION
CD354474.1 GI:31146975
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 765)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@email.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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Seq primer: pYX-5.
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Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was size
selected according to mRNA size fraction, ligated with Ecor
I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTCAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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## ORIGIN

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Best Local Similarity: 96.85% Mismatches: 6
Query Match: 69.44% Indels: 2
DB: 6 Gaps: 1

US-10-017-084A-523 (1-344) x CD354474 (1-765)

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## RESULT 8

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LOCUS AGENCOURT\_7973225 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6166839  
DEFINITION 5', mRNA sequence.

ACCESSION BU155617

VERSION BU155617.1 GI:22669149

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 856)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13527 row: m column: 16

High quality sequence stop: 593.

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## ORIGIN

## Alignment Scores:

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Score: 1199.50 Matches: 243  
Percent Similarity: 92.99% Conservative: 9  
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Db 464 AACAAATTTAGCCTTCACCTGCATAGCAACTGGTAGACAGAGCCTCGGTACTTCTGGAGA 523  
Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190  
Db 524 CACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 583  
Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210  
Db 584 ATCACCGGGAGCAGTCAAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGCGCGCGCC 643  
Qy 211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230  
Db 644 GTGTACGGAGAGTAAAGGTCAACGTGAACCTATCCACATACATTTCAAGAGCCAGGGT 703  
Qy 231 ThrGlyVal-ProValGlyGlnLysGlyThrLeuGln-CysGluAlaSerAlaValProS 250  
Db 704 ACAGGTGTCCCGCTGGGACAAAAGGGGACACTCAGTTGTGAAACCTCAGCAGTCCCT 763  
Qy 250 erAlaGlu-PheGlnTrpTyrLysAspAsp---LysArgLeuIleGluGlyLysGly 268  
Db 764 CAGCAGAAATTCAGTGTACAGGGATGAACCAAGACTGTATTTGAAGGGAAAAAAGGG 823  
Qy 269 Val---LysValGluAsnArgProPhe 276  
Db 824 GTGAAAGGGGAAAAAAGAACCTTTTC 850  
RESULT 9  
BE798585 1039 bp mRNA linear EST 20-SEP-2000  
LOCUS 601581610F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3935955 5',  
DEFINITION mRNA sequence.  
ACCESSION BE798585  
VERSION BE798585.1 GI:10219783  
KEYWORDS EST.





CD327172 890 bp mRNA linear EST 28-MAY-2003  
 AGENCOURT\_14148239 NICHED\_XGC\_Eyel Xenopus laevis cDNA clone  
 IMAGE:6949575 5', mRNA sequence.  
 CD327172  
 CD327172.1 GI:31091503  
 EST.  
 Xenopus laevis (African clawed frog)

Db 429 AAAACCTCTCGTGTACATCTCATTTGTGAAGTTCCCTCGAATTTGTTGATATTTCTTCA 488  
Qy 144 AspileSerileAsnGluGlyAsnAsnileSerLeuThrCysIleAlaThrGlyArgPro 163  
Db 489 AATATTGCTGTTAATGAAGGAGTAAATGACGCTGATTTGATTCGATTCGACCGGAGACCT 548  
Qy 164 GluProThrValThrTrpArgHisIleSerProlyValAlaValGlyPheValSerGluAsp 183  
Db 549 GAACCCGTAGTGAACCTGAGATACCTGTCTCCCTAAAGCACGGGGTTTGTAAAGTGAAGAT 608  
Qy 184 GluThrLeuGluIleGlnGlyIleThrArgGlnGlnSerGlyAspThrGluCysSerAla 203  
Db 609 GAGTACCTCGGAATACACAGGAATCACTAGGAGCAGTCTGGAATATATGAATGCAAGTCG 668  
Qy 204 SerAsnAspValAlaAlaProValValArgArgValLysValThrValAsnThrProPro 223  
Db 669 TCCATGATGTCCTCGGACCCAGATGTCGGAAGGGTTAATTAACATTAATTAACCCACCA 728  
Qy 224 TyrlleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys 243  
Db 729 TACATCTGGATGCACAGAACATCGGGCTCCCTTGGCCATCGAGGTATTTTGCAGGT 788  
Qy 244 GluAlaSerAlaValProSerAla-GluPheGlnTrpTrpLysAspAspLysArgLeuI 263  
Db 789 GAAGCCTCTGCTGTACCTGCAGCCGACCTTCTCTGTTACAGGAAGAACAAAGGCTGAG 848  
Qy 263 eGluGlyLysLys-GlyValLysValGlu 272  
Db 849 TGATTCATGGAGGGGGGTCAAGTAGAG 877

RESULT 12  
CF737474  
LOCUS  
DEFINITION UI-M-HD0-cks-o-09-0-UI.r1 NIH\_BMAP\_HD0 Mus musculus cDNA clone  
IMAGE:30614264 5', mRNA sequence.

ACCESSION CF737474  
VERSION CF737474.1 GI:37633810  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 759)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.utoowa.edu/distribution/mouseefi.html>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

FEATURES  
Seq primer: pYX-5.  
Location/Qualifiers  
1..759  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strains="CS7BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30614264"  
/tissue\_type="whole eye"  
/dev\_stages="embryo 12.5,13.5,14.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP\_HD0"  
/note="Organ: Eye; Vector: pYX- Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose

gel.First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site .Double strand cDNA was  
size selected according to mRNA size fraction .ligated  
with EcoR I adaptor , digested with NotI and then cloned  
directionally into pYX-Asc vector . The library tag  
sequence located between the Not I site and the polyA tail  
is TTATGAGT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH) ."

## ORIGIN

Alignment Scores:  
Pred. No.: 9.25e-118 Length: 759  
Score: 1094.50 Matches: 216  
Percent Similarity: 92.83% Conservative: 4  
Best Local Similarity: 91.14% Mismatches: 14  
Query Match: 60.60% Indels: 4  
DB: 7 Gaps: 1  
US-10-017-084A-523 (1-344) x CF737474 (1-759)  
Qy 12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe-----GlnGly 28  
Db 45 CTGCCCTGGAAGTCCTCGTGTCTCTCAGGCTGCTATTCCTTGTATCCACACAGA 104  
Qy 29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48  
Db 105 GTGCCGTGCTAGCGGAGATGCCACCTTTCCAAAGCTATGGACACGTGACGGTCAGG 164  
Qy 49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68  
Db 165 CAGGGGAGAGCGCACCTCAGGTGCACAAATTCACCAACCGAGTCACCGGCTGGCTGG 224  
Qy 69 LeuAsnArgSerThrIleLeuThrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88  
Db 225 CTAAACCGCAGTACCATCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTG 284  
Qy 89 ValLeuLeuSerAsnThrGlnThrGlnTy-SerIleGluIleGlnAsnValAspValTyr 108  
Db 285 GTCTCTCTGAGTACACCCAGCCAGTACAGCATTCAGATCCAGATGCGATGTGTAC 344  
Qy 109 AspGluGlyProThrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128  
Db 345 GATGAGGGCCCTTATACCTGCTCGGTACAGACACCAACCCCTTAAGACCTCCAGGCTC 404  
Qy 129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148  
Db 405 CACCTCATTTGTACAAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCATTAA 464  
Qy 149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168  
Db 465 GAAGGGAACAACATCAGCCTCCTTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACC 524  
Qy 169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluThrLeuGluIle 188  
Db 525 TGGAGACATATTTCTCCCAAGCGCTTGGCTTGTGAGTGAAGTACGTACCTCGAGATC 584  
Qy 189 GlnGlyIleThrArgGluGlnSerGlyAspTrpCysSerAlaSerAsnAspValAla 208  
Db 585 CAGGGCATCACTCGGGAAACAGTCAGGCGAGTACAGGTGCAGCGCTCCAAAGACGCTGGCG 644  
Qy 209 AlaProValValArgArgValLysValThrValAsnThrProThrIleSerGluAla 228  
Db 645 GCACCATGTTGACGAAGTGAAGTCAACCGTGNACTATCCACCATACATCTCAAGAGCT 704  
Qy 229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAla 245  
Db 705 AAGGGCACAGGTGTCCCGTGGGCAAGANGGACT-CTGCAGTGTGAAGCT 754  
RESULT 13  
AL533026  
LOCUS AU533026 1027 bp mRNA linear EST 24-MAR-2004

DEFINITION AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone  
CSODN005YD20 5-PRIME, mRNA sequence.

ACCESSION AL533026

VERSION AL533026.3 GI:45707932

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1027)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:31070858.  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 6387.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?e=CSODN005YD20&e=6387.f.

FEATURES  
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/mol\_type="mRNA"  
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/clone="CSODN005YD20"  
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/dev\_stage="adult"  
/clone\_lib="Homo sapiens ADULT BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

ORIGIN  
Alignment Scores:  
Pred. No.: 8.59e-114 Length: 1027  
Score: 1062.50 Matches: 211  
Percent Similarity: 84.19% Conservative: 2  
Best Local Similarity: 83.40% Mismatches: 0  
Query Match: 58.83% Indels: 40  
DB: 1 Gaps: 1

US-10-017-084A-523 (1-344) x AL533026 (1-1027)

QY 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151  
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Db 98 ATTAAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 157  
QY 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171  
: : : : :  
Db 158 AATATTAGCCTCACCCTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGACAC 217  
QY 172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191  
: : : : :  
Db 218 ATCTCTCCCAAGCGGTTGGCTTGTGAGTAGAGACGAATACTTGGAAATTCAGGGCATC 277  
QY 192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaProVal 211  
: : : : :  
Db 278 ACCCGGAGCAGCTACGGGAGCTACGAGTGCAGTCTCCAAATGACGTGGCCGCCCGCTG 337  
QY 212 ValArgArgValLysValThrValAsnTyrProTyrIleSerGluAlaLysGlyThr 231  
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Db 338 GTACCGAGAGTAAAGGTCAACCGTGAACATTCACCATACATTTTCAGAACCCAGGGTACA 397  
QY 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251

Db 398 GGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 457  
: : : : :  
QY 252 GluPheGlnTrpTyrLysAspAsp-Lys----- 260  
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Db 458 GAATTCCAGTGGTACAAGGATGACAAAAGAGAGCTGAAATCTCAATTCACAGTTTGGTTATGA 517  
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QY 260 ----- 260  
: : : : :  
Db 518 TGGGAAGACTTCTCTCCCATGGTGGAGCAATGGTGTCAAAACGGCAGTGGGATCAATCA 577  
: : : : :  
QY 261 -----ArgLeuIleGluGlyLysGlyValGlyValGlyValGlyValGlyValGly 272  
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Db 578 GCCTGACTTGTCTCGCAGAATCTCCCGACTGATTGAAGGAAGAAAGGGGTGAAGTGGGA 637  
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QY 272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292  
: : : : :  
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QY 292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheG1 312  
: : : : :  
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QY 312 YProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLe 332  
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Db 758 TCCAGGCGCGTCAAGCAGGTGAGCAACGGCACGTCGAGGAGGCGAGGCTCGTCTGGCT 817  
: : : : :  
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Db 818 GCTGCCTCTTCTGTGGTCTTGCACCTGCTTCTCAAAATTT 854  
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RESULT 14  
LOCUS CR602526 2512 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CSODN005YD20 of Adult brain of Homo sapiens  
(human).  
ACCESSION CR602526  
VERSION CR602526.1 GI:50483333  
KEYWORDS HTC; CNSLT cDNA  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2512)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paraday Avenue  
2 (bases 1 to 2512)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source  
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/clone="CSODN005YD20"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 3.34e-113 Length: 2512

Score: 1062.50 Matches: 211  
Percent Similarity: 84.19% Conservative: 2  
Best Local Similarity: 83.40% Mismatches: 0  
Query Match: 58.83% Indels: 40  
DB: 3 Gaps: 1

US-10-017-084A-523 (1-344) x CR602526 (1-2512)

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Db : : : : :  
Qy 97 ATTAAGTATCTCCAAATTTGTAGAGATTCTTCAGATATCTCCATTAATGAAGGAAC 156  
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Db AATATTAGCCTCAGCTGCATAGCAACTGGTAGACAGAGCCAGCTACGGTTACTTGGAGACAC 216  
Qy 172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191  
Db ATCTCTCCAAAGCGTTGGCTTTGTAGTGAAGACGAACTTGGAAATTCAGGGCATC 276  
Qy 192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211  
Db ACCAGGAGCAGTCAGGGAGTACAGTGCAGTGCCTCCATGAGTGGCGCGCCGGTG 336  
Qy 212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231  
Db GTACGGAGAGTAAAGGTCCCGTGAACCTATCCACATACATTTTCAGAAAGCCAGGGTACA 396  
Qy 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251  
Db GGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCCAGCA 456  
Qy 252 GluPheGlnTrpTyrLysAspAsp-Lys- 260  
Db GAATTCAGTGTACAGGATGACAAAGAGCTGAATCTCATTCACAGTTTGGTTATGA 516  
Qy 260 ----- 260  
Db TGGGAAAGCTTCTCTCCCATCGTGGACGAATGTGTCAAAACGGCCAGTGGGATCAATCA 576  
Qy 261 -----ArgLeuIleGluGlyLysGlyValLysValG1 272  
Db GCCTGACTTGTGCGAGATCCTCCCGACTGATTGAAGGAAGAGGGGTGAAGTGA 636  
Qy 272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292  
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Qy 292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheG1 312  
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Qy 312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgAlaGlyCysValTrpLe 332  
Db TCCAGGCGCCGTACAGCGGTGAGACAGCGACGTGCGAGGAGGGCGAGCTCGCTGGCT 816  
Qy 332 uLeuProLeuLeuValLeuHisLeuLeuLysPhe 344  
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RESULT 15  
BU368328  
LOCUS  
DEFINITION 740 bp mRNA linear EST 28-NOV-2002  
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sequence.  
ACCESSION  
VERSION BU368328.1 GI:25876329  
KEYWORDS  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 740)  
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
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1..740  
/organism="Gallus gallus"  
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/db\_xref="taxon:9031"  
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/lab\_host="DH10B"  
/clone\_lib="CSEQCHN72"  
/notes="Organ: brain; Vector: pBluescript II KS(+); Site: 1:  
ECORI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
ECORI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Alignment Scores:  
Pred. No.: 3,49e-112 Length: 740  
Score: 1047.00 Matches: 192  
Percent Similarity: 91.85% Conservative: 22  
Best Local Similarity: 82.40% Mismatches: 19  
Query Match: 57.97% Indels: 0  
DB: 5 Gaps: 0

US-10-017-084A-523 (1-344) x BU368328 (1-740)

Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
Db 3 CAGATCCACGACGCTGGACGCTGATGAGAGGGCCCTACACCTGCTCCGTCGACAGAC 62  
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
Db AATCACCACCAAGACATCTCGGTGCACCTCATTTGTGCAAGTGTCCGAAATTTACCGAG 122  
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
Db ATCTCTTTCAGATCTCCATCAATGAAGTGGCAACGTCAGCCTCAGCTGCATGCCACG 182  
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
Db GGCAGGCGCAGACCCCAATCACCTCGGAGACACATCTCGCCAAAGCTGTGGGCTTCATC 242  
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGlu 200  
Db ACCGAGGACGAGTACCTTGGAGATCACAGGCATTCAGAGGGAGGAGCTCGGGCGAGTACGAG 302

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Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db |||||
Qy 303 TGCAGTGGCTCCNACGAGCTGGCCGGCTGTCTGTCAGCGAGTCNAAAGTCACCGTCAAC 362
Db |||||
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db |||||
Qy 363 TACCCACCGGTACATCTCGGATGCGAAGAGACCGCGTGTCCGGTGGGGCAGAGGGCATC 422
Db |||||
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260
Db |||||
Qy 423 CTGATGTGTGAAGCCTCCGCTGTGCCCTCCGCTGACTTCCAGTGGTACAAAGACGACAAG 482
Db |||||
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db |||||
Qy 483 CGGCTGGCTGAAGNACAGAAAGGCTGAAGGTGGNAAACAAGCCTTCTTCCCGACTG 542
Db |||||
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db |||||
Qy 543 ACTTTCTTCAACGTCTCCGAGCAGGACTACGGCAACTACACTGCGTGGCTCCCAACCCAG 602
Db |||||
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy 603 CTAGGAAACACCAACGCCAGCATGATCCTTTATGGCCCCCGTGCAGTGCACGATGGCAAC 662
Db |||||
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeu 333
Db |||||
Qy 663 AGCGGTGCGTGGCGCGGAGGAGCTGTGCTGGCTGCTG 701
Db |||||
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Search completed: October 30, 2005, 12:35:13  
Job time : 4031 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 30, 2005, 09:21:27 ; Search time 216 Seconds  
(without alignments)  
2605.922 Million cell updates/sec

Title: US-10-017-084A-523  
Perfect score: 1806  
Sequence: 1 MKTIQPKHNSISWAIFTGL.....RRAGCVWLLPLVLVLLLLK 344

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO.spool/US10017084/runat\_28102005\_112603\_9189/app.query.fasta\_1.519  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0  
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-LIST=1500 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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Database : Issued Patents NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	1032	4	US-09-700-397-1
2	1806	100.0	1693	4	US-09-700-397-2
3	1642	90.9	939	4	US-09-700-397-5
4	931.5	51.6	1195	4	US-09-976-594-403
5	926.5	51.3	1014	2	US-08-414-657D-5
6	926.5	51.3	1014	3	US-09-135-080-7
7	926.5	51.3	1238	3	US-08-414-657D-3
8	926.5	51.1	977	2	US-08-414-657D-1
9	923.5	51.1	977	3	US-09-135-080-1
10	923.5	51.1	977	3	US-09-135-080-1
11	908	50.3	924	2	US-08-414-657D-7
12	907	50.2	945	2	US-08-414-657D-8

13	902	49.9	912	2	US-08-414-657D-6	Sequence 6, Appli
14	886.5	49.1	861	2	US-08-414-657D-9	Sequence 9, Appli
15	885.5	49.0	861	2	US-08-414-657D-10	Sequence 10, Appli
16	796.5	44.1	756	2	US-08-414-657D-17	Sequence 17, Appli
17	795.5	44.0	756	2	US-08-414-657D-18	Sequence 18, Appli
18	742.5	41.1	1030	4	US-09-949-016-4587	Sequence 4587, Ap
19	545	30.2	333	4	US-09-513-999C-23289	Sequence 23289, A
20	344	19.0	352	4	US-09-513-999C-27755	Sequence 27755, Ap
21	339	18.8	113538	4	US-09-949-016-16329	Sequence 16329, A
22	302.5	16.7	913	4	US-09-774-528-410	Sequence 410, App
23	276	15.3	2599	4	US-09-949-016-4676	Sequence 4676, Ap
24	275	15.2	2633	4	US-09-023-655-950	Sequence 950, App
25	274	15.2	5807	4	US-09-976-594-245	Sequence 245, App
26	273.5	15.1	2118	4	US-09-270-767-11659	Sequence 11659, A
27	263.5	14.6	6814	3	US-09-484-370B-66	Sequence 66, Appli
28	256	14.2	1266	2	US-08-659-984A-2	Sequence 2, Appli
29	256	14.2	1266	3	US-08-660-531-2	Sequence 2, Appli
30	256	14.2	1335	2	US-08-659-984A-4	Sequence 4, Appli
31	256	14.2	1335	3	US-08-660-531-4	Sequence 4, Appli
32	249.5	13.8	4548	4	US-09-571-479C-5	Sequence 5, Appli
33	246.5	13.6	3318	4	US-09-949-016-4450	Sequence 4450, Ap
34	246.5	13.6	3360	1	US-08-408-093-5	Sequence 5, Appli
35	246.5	13.6	3360	1	US-08-408-420A-5	Sequence 5, Appli
36	246.5	13.6	3360	1	US-08-714-901-5	Sequence 5, Appli
37	246.5	13.6	3360	3	US-08-040-741-5	Sequence 5, Appli
38	241.5	13.4	4723	4	US-09-949-016-644	Sequence 644, App
39	241	13.3	6599	4	US-09-799-451-350	Sequence 350, App
40	237.5	13.2	4597	4	US-09-949-016-5173	Sequence 5173, Ap
41	237	13.1	219	2	US-08-414-657D-11	Sequence 11, Appli
42	237	13.1	219	2	US-08-414-657D-12	Sequence 12, Appli
43	230.5	12.8	2869	1	US-08-374-834-2	Sequence 2, Appli
44	230.5	12.8	2869	1	US-08-644-271-2	Sequence 2, Appli
45	230.5	12.8	2869	3	US-09-077-955-2	Sequence 2, Appli
46	230	12.7	2610	1	US-08-374-834-17	Sequence 17, Appli
47	230	12.7	2610	1	US-08-644-271-28	Sequence 28, Appli
48	230	12.7	2610	3	US-09-077-955-32	Sequence 32, Appli
49	225.5	12.5	1581	5	PCT-US95-08493-14	Sequence 14, Appli
50	225.5	12.5	2580	5	PCT-US95-08493-18	Sequence 18, Appli
51	225.5	12.5	2604	5	PCT-US95-08493-20	Sequence 20, Appli
52	225	12.4	2607	4	US-09-715-249-7	Sequence 7, Appli
53	224.5	12.4	7647	4	US-09-566-921-75	Sequence 75, Appli
54	224	12.4	3662	4	US-09-907-794A-289	Sequence 289, App
55	224	12.4	3662	4	US-09-905-125A-289	Sequence 289, App
56	224	12.4	3662	4	US-09-902-775A-289	Sequence 289, App
57	224	12.4	3662	4	US-09-906-700-289	Sequence 289, App
58	224	12.4	3662	4	US-09-903-603A-289	Sequence 289, App
59	224	12.4	3662	4	US-09-904-920A-289	Sequence 289, App
60	224	12.4	3662	4	US-09-909-064-289	Sequence 289, App
61	224	12.4	3662	4	US-09-905-381A-289	Sequence 289, App
62	224	12.4	3662	4	US-09-906-618-289	Sequence 289, App
63	224	12.4	4053	4	US-09-907-794A-293	Sequence 293, App
64	224	12.4	4053	4	US-09-905-125A-293	Sequence 293, App
65	224	12.4	4053	4	US-09-902-775A-293	Sequence 293, App
66	224	12.4	4053	4	US-09-906-700-293	Sequence 293, App
67	224	12.4	4053	4	US-09-903-603A-293	Sequence 293, App
68	224	12.4	4053	4	US-09-904-920A-293	Sequence 293, App
69	224	12.4	4053	4	US-09-909-064-293	Sequence 293, App
70	224	12.4	4053	4	US-09-905-381A-293	Sequence 293, App
71	224	12.4	4053	4	US-09-906-618-293	Sequence 293, App
72	220.5	12.2	1413	4	US-09-866-028-60	Sequence 60, Appli
73	220.5	12.2	1413	4	US-09-944-457-60	Sequence 60, Appli
74	220.5	12.2	1598	4	US-09-778-510-19	Sequence 19, Appli
75	220.5	12.2	1935	4	US-09-778-510-21	Sequence 21, Appli
76	219	12.1	4843	3	US-08-986-485-1	Sequence 1, Appli
77	213.5	11.8	1685	4	US-09-907-794A-83	Sequence 83, Appli
78	213.5	11.8	1685	4	US-09-905-125A-83	Sequence 83, Appli
79	213.5	11.8	1685	4	US-09-902-775A-83	Sequence 83, Appli
80	213.5	11.8	1685	4	US-09-906-700-83	Sequence 83, Appli
81	213.5	11.8	1685	4	US-09-903-603A-83	Sequence 83, Appli
82	213.5	11.8	1685	4	US-09-904-920A-83	Sequence 83, Appli
83	213.5	11.8	1685	4	US-09-909-064-83	Sequence 83, Appli
84	213.5	11.8	1685	4	US-09-905-381A-83	Sequence 83, Appli
85	213.5	11.8	1685	4	US-09-906-618-83	Sequence 83, Appli

86	213.5	11.8	1718	4	US-09-778-510-5	Sequence 5, Appli	159	173.5	9.6	2550	1	US-08-481-130-10	Sequence 10, Appl
87	213	11.8	177	2	US-08-414-657D-13	Sequence 13, Appl	160	173.5	9.6	2550	1	US-08-656-984A-10	Sequence 10, Appl
88	212	11.7	177	2	US-08-414-657D-14	Sequence 14, Appl	161	173.5	9.6	2550	1	US-08-485-604-10	Sequence 10, Appl
89	211.5	11.7	5506	4	US-09-976-594-530	Sequence 530, App	162	173.5	9.6	2550	2	US-08-487-595-10	Sequence 10, Appl
90	211	11.7	1273	4	US-09-778-510-3	Sequence 3, Appli	163	173.5	9.6	2988	1	US-08-245-295-1	Sequence 1, Appli
c 91	210	11.6	577	4	US-09-270-767-1011	Sequence 1011, Ap	164	173.5	9.6	2988	1	US-08-481-130-1	Sequence 1, Appli
c 92	210	11.6	577	4	US-09-270-767-16293	Sequence 16293, A	165	173.5	9.6	2988	1	US-08-656-984A-1	Sequence 1, Appli
93	210	11.6	577	4	US-09-016-434-1120	Sequence 1120, Ap	166	173.5	9.6	2988	1	US-08-485-604-1	Sequence 1, Appli
94	210	11.6	5926	4	US-09-917-254-41	Sequence 41, Appl	167	173.5	9.6	2988	2	US-08-487-595-1	Sequence 1, Appli
95	209	11.6	3093	4	US-09-949-016-4183	Sequence 4183, Ap	168	173	9.6	3189	2	US-08-427-497E-3	Sequence 3, Appli
96	209	11.6	3145	4	US-09-949-016-1149	Sequence 1149, Ap	169	173	9.6	3774	2	US-08-341-843B-1	Sequence 1, Appli
97	205.5	11.4	1542	4	US-09-205-258-123	Sequence 123, App	170	173	9.6	3774	2	US-08-427-497E-1	Sequence 1, Appli
98	205	11.4	1820	4	US-09-778-510-1	Sequence 1, Appli	171	173	9.6	3774	2	US-08-427-497E-2	Sequence 2, Appli
99	203.5	11.3	5824	4	US-09-620-312D-72	Sequence 72, Appl	172	173	9.6	3888	3	US-08-506-296B-13	Sequence 13, Appl
100	202	11.2	4059	4	US-08-799-451-560	Sequence 560, App	173	172	9.5	1630	3	US-08-468-856B-2	Sequence 2, Appli
101	201	11.1	3398	5	PCT-US95-08493-12	Sequence 12, Appl	174	172	9.5	1630	3	US-08-468-856A-2	Sequence 2, Appli
102	200	11.1	1967	3	US-09-383-586-22	Sequence 22, Appl	175	172	9.5	2116	4	US-09-023-655-1256	Sequence 1256, Ap
103	200	11.1	1967	4	US-09-823-038A-22	Sequence 22, Appl	176	172	9.5	3461	3	US-08-468-856B-6	Sequence 6, Appli
104	199	11.0	4285	3	US-09-040-774-1	Sequence 1, Appli	177	172	9.5	3461	3	US-08-468-856A-6	Sequence 6, Appli
105	198	11.0	6718	4	US-09-949-016-4632	Sequence 4632, Ap	178	171.5	9.5	2352	1	US-08-232-538-17	Sequence 17, Appl
106	197.5	10.9	4608	3	US-09-041-886-24	Sequence 24, Appl	179	171.5	9.5	2352	2	US-08-786-164-17	Sequence 17, Appl
107	197.5	10.9	4608	5	PCT-US94-05277-1	Sequence 1, Appli	180	171.5	9.5	4014	4	US-09-119-014D-5	Sequence 5, Appli
108	196.5	10.9	5905	4	US-09-949-016-5625	Sequence 5625, Ap	181	171.5	9.5	7680	4	US-09-953-318-3	Sequence 3, Appli
109	196.5	10.9	6218	4	US-09-949-016-706	Sequence 706, App	182	171	9.5	1473	2	US-08-602-725-31	Sequence 31, Appl
110	196.5	10.9	6384	4	US-09-976-594-724	Sequence 724, App	183	171	9.5	1473	4	US-09-949-016-245	Sequence 245, App
c 111	196.5	10.9	6384	4	US-09-919-039-279	Sequence 279, App	184	171	9.5	1475	4	US-09-949-016-1654	Sequence 1654, Ap
112	194	10.7	3783	3	US-08-506-296B-20	Sequence 20, Appl	185	170	9.4	862	3	US-08-468-856B-4	Sequence 4, Appli
113	192.5	10.7	2481	3	US-08-877-730-15	Sequence 15, Appl	186	170	9.4	862	3	US-08-468-856A-4	Sequence 4, Appli
114	192.5	10.7	2715	3	US-09-877-730-5	Sequence 5, Appli	187	169	9.4	1339	3	US-08-468-856B-3	Sequence 3, Appli
115	192.5	10.7	2724	3	US-09-877-730-19	Sequence 19, Appl	188	169	9.4	1339	3	US-08-468-856A-3	Sequence 3, Appli
116	192.5	10.7	2958	3	US-09-877-730-9	Sequence 9, Appli	189	168	9.3	2383	3	US-08-232-538-18	Sequence 18, Appl
117	192.5	10.7	2976	3	US-09-877-730-11	Sequence 11, Appl	190	168	9.3	2383	2	US-08-786-164-18	Sequence 18, Appl
118	192.5	10.7	3192	3	US-09-412-554A-1	Sequence 1, Appli	c 191	167.5	9.3	842	4	US-09-270-767-11483	Sequence 11483, A
119	192.5	10.7	3210	3	US-09-877-730-1	Sequence 1, Appli	192	167	9.2	2264	1	US-08-232-538-16	Sequence 16, Appl
120	192.5	10.7	3219	3	US-09-877-730-17	Sequence 17, Appl	193	167	9.2	2264	2	US-08-786-164-16	Sequence 16, Appl
121	192.5	10.7	3453	3	US-09-877-730-7	Sequence 7, Appli	194	167	9.2	2292	2	US-09-142-956B-1	Sequence 1, Appli
122	192.5	10.7	3874	3	US-09-877-730-31	Sequence 31, Appl	195	167	9.2	4071	3	US-09-098-707A-1	Sequence 1, Appli
123	192.5	10.7	3943	3	US-08-506-296B-27	Sequence 27, Appl	196	167	9.2	4071	3	US-09-483-539-1	Sequence 1, Appli
124	192	10.6	2094	4	US-09-270-767-13304	Sequence 13304, A	197	167	9.2	4236	1	US-08-810-116-7	Sequence 7, Appli
c 125	191	10.6	601	4	US-09-949-016-163724	Sequence 163724, A	198	167	9.2	4236	2	US-07-930-548A-7	Sequence 7, Appli
126	190	10.6	6055	4	US-09-953-318-10	Sequence 10, Appl	199	167	9.2	5830	4	US-09-967-655-3	Sequence 3, Appli
127	187.5	10.4	3991	3	US-08-506-296B-3	Sequence 3, Appli	200	167	9.2	5830	4	US-09-949-016-327	Sequence 327, App
128	186	10.3	3551	4	US-09-602-312D-760	Sequence 760, App	201	167	9.2	5831	4	US-09-949-016-3982	Sequence 3982, Ap
129	185.5	10.3	957	2	US-08-633-148-3	Sequence 3, Appli	202	166.5	9.2	909	3	US-09-877-730-13	Sequence 13, Appl
130	185.5	10.3	1023	2	US-08-633-148-1	Sequence 1, Appli	203	166.5	9.2	1143	3	US-09-877-730-3	Sequence 3, Appli
131	185.5	10.3	1215	4	US-09-949-016-5154	Sequence 5154, Ap	204	166.5	9.2	1405	4	US-08-755-235-3	Sequence 3, Appli
132	185.5	10.3	2031	1	US-08-217-299-2	Sequence 2, Appli	205	166	9.2	2523	3	US-09-051-363-1	Sequence 1, Appli
133	185.5	10.3	2097	2	US-08-602-725-35	Sequence 35, Appl	206	165.5	9.2	1962	4	US-09-653-961-3	Sequence 3, Appli
134	185.5	10.3	2220	1	US-08-389-459A-16	Sequence 16, Appl	207	165.5	9.2	1962	4	US-09-653-961-5	Sequence 5, Appli
135	185.5	10.3	2220	3	US-08-987-867A-16	Sequence 16, Appl	208	165.5	9.2	2487	1	US-08-261-304-1	Sequence 1, Appli
136	185.5	10.3	2349	2	US-08-184-009-145	Sequence 145, App	209	165.5	9.2	2539	2	US-08-432-016-1	Sequence 1, Appli
137	185.5	10.3	2349	2	US-08-458-356-145	Sequence 145, App	210	165.5	9.2	2539	2	US-08-684-594-1	Sequence 1, Appli
138	185.5	10.3	2349	3	US-08-460-736-145	Sequence 145, App	211	165.5	9.2	2580	4	US-09-774-528-327	Sequence 327, App
139	185.5	10.3	2349	4	US-08-460-736-145	Sequence 145, App	212	165.5	9.2	3306	4	US-09-023-655-1434	Sequence 1434, Ap
140	185.5	10.3	2349	4	US-09-535-370-145	Sequence 145, App	213	165.5	9.2	3583	4	US-09-949-016-857	Sequence 857, App
141	185.5	10.3	2349	4	US-09-663-667-145	Sequence 145, App	214	165.5	9.2	4854	4	US-09-784-358-15	Sequence 15, Appl
142	185.5	10.3	2434	2	US-08-184-009-144	Sequence 144, App	215	165.5	9.2	5076	4	US-09-784-358-1	Sequence 1, Appli
143	185.5	10.3	2434	2	US-08-458-356-144	Sequence 144, App	216	165.5	9.2	7718	4	US-09-576-594-244	Sequence 244, App
144	185.5	10.3	2434	3	US-08-460-736-144	Sequence 144, App	217	165.5	9.2	8578	4	US-09-784-358-17	Sequence 17, Appl
145	185.5	10.3	2434	4	US-09-535-370-144	Sequence 144, App	218	165	9.1	2166	2	US-09-784-358-17	Sequence 30, Appl
146	185.5	10.3	2974	4	US-09-663-667-144	Sequence 144, App	219	164.5	9.1	2539	4	US-08-408-095-30	Sequence 1496, Ap
147	185.5	10.3	2976	4	US-09-949-016-613	Sequence 613, App	220	164.5	9.1	2565	1	US-09-023-655-1496	Sequence 29, Appl
148	184.5	10.2	198	2	US-09-949-016-12297	Sequence 12297, Ap	221	164.5	9.1	2565	1	US-08-597-495B-29	Sequence 31, Appl
149	184.5	10.2	198	2	US-08-414-657D-15	Sequence 15, Appl	222	164.5	9.1	2793	3	US-09-068-051A-31	Sequence 68, Appl
150	184.5	10.2	1391	4	US-09-638-649-4	Sequence 16, Appl	223	164.5	9.1	2803	3	US-09-336-536-68	Sequence 33, Appli
151	184.5	10.2	1391	4	US-09-638-648-4	Sequence 4, Appli	224	164	9.1	1378	4	US-09-068-051A-33	Sequence 3, Appli
152	182	10.1	2346	4	US-09-949-016-1979	Sequence 1979, Ap	225	164	9.1	1742	3	US-09-383-586-23	Sequence 23, Appl
153	182	10.1	2350	4	US-09-949-016-342	Sequence 342, App	226	164	9.1	1742	4	US-09-823-038A-23	Sequence 23, Appl
154	179.5	9.9	2839	3	US-08-468-856B-5	Sequence 5, Appli	227	164	9.1	1983	3	US-09-057-860A-8	Sequence 8, Appli
155	179.5	9.9	2839	3	US-08-468-856B-5	Sequence 5, Appli	228	164	9.1	2418	4	US-09-949-016-1694	Sequence 1694, Ap
c 156	174	9.6	785	4	US-09-270-767-1269	Sequence 1269, Ap	229	163.5	9.1	1950	4	US-09-653-961-1	Sequence 1, Appli
c 157	174	9.6	785	4	US-09-270-767-16551	Sequence 16551, A	230	163.5	9.1	2539	4	US-09-949-016-3677	Sequence 3677, Ap
158	173.5	9.6	2550	1	US-08-245-295-10	Sequence 10, Appl	231	163.5	9.1	2697	4	US-09-949-016-5335	Sequence 5335, Ap



232	163.5	9.1	4235	4	US-09-702-705-317	Sequence 317, App	305	159	8.8	6363	4	US-09-023-655-879	Sequence 879, App
233	163.5	9.1	4235	4	US-09-736-457-317	Sequence 317, App	306	158.5	8.8	4890	4	US-09-677-046A-3	Sequence 3, Appli
234	163.5	9.1	4235	4	US-09-614-124B-317	Sequence 317, App	307	158.5	8.8	4943	4	US-09-677-046A-7	Sequence 7, Appli
235	163.5	9.1	4235	4	US-09-671-325-317	Sequence 317, App	308	158.5	8.8	5220	4	US-09-677-046A-1	Sequence 1, Appli
236	163.5	9.1	4235	4	US-09-589-184-317	Sequence 317, App	309	158	8.7	2208	5	PCT-US93-00031-14	Sequence 14, Appli
237	163.5	9.1	4235	4	US-09-688-824-317	Sequence 317, App	310	157.5	8.7	1140	3	US-09-462-270-1	Sequence 1, Appli
238	163.5	9.1	5720	4	US-08-800-729-18	Sequence 18, Appl	311	157.5	8.7	5170	4	US-09-677-046A-5	Sequence 5, Appli
239	163	9.0	2775	1	US-08-481-130-25	Sequence 25, Appl	312	157	8.7	1421	3	US-09-188-930-254	Sequence 254, App
240	163	9.0	2775	1	US-08-656-984A-25	Sequence 25, Appl	313	157	8.7	1421	3	US-09-312-283C-254	Sequence 254, App
241	163	9.0	2775	1	US-08-485-604-27	Sequence 27, Appl	314	157	8.7	1822	4	US-09-397-243D-1	Sequence 1, Appli
242	163	9.0	2775	2	US-08-487-595-25	Sequence 25, Appl	315	157	8.7	1857	4	US-09-907-794A-118	Sequence 118, App
243	163	9.0	2927	1	US-08-481-130-27	Sequence 27, Appl	316	157	8.7	1857	4	US-09-905-125A-118	Sequence 118, App
244	163	9.0	2927	1	US-08-636-984A-27	Sequence 27, Appl	317	157	8.7	1857	4	US-09-902-775A-118	Sequence 118, App
245	163	9.0	2927	1	US-08-485-604-27	Sequence 27, Appl	318	157	8.7	1857	4	US-09-906-700-118	Sequence 118, App
246	163	9.0	2927	2	US-08-487-595-27	Sequence 27, Appl	319	157	8.7	1857	4	US-09-903-603A-118	Sequence 118, App
247	162	9.0	1024	6	5169835-16	Patent No. 5169835	320	157	8.7	1857	4	US-09-904-920A-118	Sequence 118, App
248	162	9.0	1024	6	5169835-16	Patent No. 5169835	321	157	8.7	1857	4	US-09-909-064-118	Sequence 118, App
249	162	9.0	3503	1	US-07-631-717A-1	Sequence 1, Appli	322	157	8.7	1857	4	US-09-909-064-118	Sequence 118, App
250	162	9.0	3503	1	US-08-166-717D-1	Sequence 1, Appli	323	157	8.7	1857	4	US-09-905-381A-118	Sequence 118, App
251	161	8.9	1869	4	US-09-499-846-1	Sequence 1, Appli	324	156.5	8.7	1426	4	US-09-906-618-118	Sequence 118, App
252	161	8.9	3554	4	US-09-907-794A-422	Sequence 422, App	325	156.5	8.7	1426	4	US-09-638-649-2	Sequence 2, Appli
253	161	8.9	3554	4	US-09-905-125A-422	Sequence 422, App	326	156	8.6	1940	1	US-09-638-648-2	Sequence 2, Appli
254	161	8.9	3554	4	US-09-902-775A-422	Sequence 422, App	327	155.5	8.6	1940	1	US-08-429-742-3	Sequence 3, Appli
255	161	8.9	3554	4	US-09-906-700-422	Sequence 422, App	328	155.5	8.6	1421	3	US-09-188-930-70	Sequence 70, Appl
256	161	8.9	3554	4	US-09-903-603A-422	Sequence 422, App	329	155.5	8.6	2184	3	US-09-312-283C-70	Sequence 70, Appl
257	161	8.9	3554	4	US-09-904-920A-422	Sequence 422, App	330	155.5	8.6	3307	1	US-09-484-970B-161	Sequence 161, App
258	161	8.9	3554	4	US-09-909-064-422	Sequence 422, App	331	155.5	8.6	3307	1	US-08-456-647B-5	Sequence 5, Appli
259	161	8.9	3554	4	US-09-905-381A-422	Sequence 422, App	332	155.5	8.6	3785	3	US-08-237-401A-5	Sequence 5, Appli
260	161	8.9	3554	4	US-09-906-618-422	Sequence 422, App	333	155.5	8.6	3785	3	US-08-445-640-9	Sequence 9, Appli
261	161	8.9	5470	2	US-08-443-861-1	Sequence 1, Appli	334	155.5	8.6	3785	3	US-08-170-558-9	Sequence 9, Appli
262	161	8.9	5470	3	US-09-193-829B-1	Sequence 1, Appli	335	155.5	8.6	3785	3	US-08-447-314-9	Sequence 9, Appli
263	161	8.9	5470	3	US-09-967-655-10	Sequence 10, Appl	336	155.5	8.6	3785	3	US-08-445-461-9	Sequence 9, Appli
264	160.5	8.9	3159	3	US-08-986-485-3	Sequence 3, Appli	337	155	8.6	2431	3	US-09-223-490-9	Sequence 9, Appli
265	160.5	8.9	4111	4	US-09-375-248-1	Sequence 1, Appli	338	155	8.6	4006	4	US-08-985-526-35	Sequence 35, Appl
266	160.5	8.9	4195	1	US-08-340-011-1	Sequence 1, Appli	339	155	8.6	4006	4	US-09-949-016-4724	Sequence 4724, Ap
267	160.5	8.9	4195	3	US-08-901-710-1	Sequence 1, Appli	340	155	8.6	5406	1	US-09-949-016-4725	Sequence 4725, Ap
268	160.5	8.9	4195	3	US-08-169-079-1	Sequence 1, Appli	341	155	8.6	5406	1	US-07-813-593-3	Sequence 3, Appli
269	160.5	8.9	4416	3	US-08-795-430-1	Sequence 1, Appli	342	155	8.6	5406	1	US-07-977-451-5	Sequence 5, Appli
270	160.5	8.9	4416	3	US-09-355-700-1	Sequence 1, Appli	343	155	8.6	5406	1	US-07-946-507-3	Sequence 3, Appli
271	160.5	8.9	4416	3	US-08-601-132-36	Sequence 36, Appl	344	155	8.6	5406	1	US-08-252-517-5	Sequence 5, Appli
272	160.5	8.9	4416	4	US-08-671-573B-36	Sequence 36, Appl	345	155	8.6	5406	1	US-07-906-397A-5	Sequence 5, Appli
273	160.5	8.9	4416	4	US-09-631-092B-36	Sequence 36, Appl	346	155	8.6	5406	2	US-08-601-891-5	Sequence 5, Appli
274	160.5	8.9	4416	4	US-09-534-376A-1	Sequence 1, Appli	347	155	8.6	5406	4	US-09-021-324-5	Sequence 5, Appli
275	160.5	8.9	4425	1	US-08-222-616-31	Sequence 31, Appl	348	155	8.6	5406	5	US-08-872-136B-5	Sequence 5, Appli
276	160.5	8.9	4425	3	US-08-446-648-31	Sequence 31, Appl	349	155	8.6	5406	5	PCT-US92-03750-7	Sequence 7, Appli
277	160.5	8.9	4425	4	US-09-023-655-889	Sequence 889, App	350	155	8.6	5406	5	PCT-US92-05401-5	Sequence 5, Appli
278	160.5	8.9	4425	4	US-09-982-610-31	Sequence 31, Appl	351	154.5	8.6	1493	2	PCT-US92-09893-5	Sequence 5, Appli
279	160.5	8.9	4425	5	PCT-US95-04228-31	Sequence 31, Appl	352	154.5	8.6	1493	2	US-08-752-307B-6	Sequence 6, Appli
280	160.5	8.9	4795	1	US-08-340-011-3	Sequence 3, Appli	353	154.5	8.6	1493	3	US-09-707-802-6	Sequence 6, Appli
281	160.5	8.9	4795	3	US-08-901-710-3	Sequence 3, Appli	354	154.5	8.6	2600	2	US-09-991-326-6	Sequence 6, Appli
282	160.5	8.9	4795	4	US-09-169-079-3	Sequence 3, Appli	355	154.5	8.6	2685	4	US-08-427-497B-4	Sequence 4, Appli
283	160.5	8.9	9108	3	US-08-446-648-45	Sequence 45, Appl	356	154.5	8.6	7702	4	US-09-949-016-4734	Sequence 4734, Ap
284	160.5	8.9	9108	4	US-09-982-610-45	Sequence 45, Appl	357	154.5	8.6	7702	4	US-09-023-655-1336	Sequence 1336, Ap
285	160.5	8.9	9108	5	PCT-US95-04228-45	Sequence 45, Appl	358	154	8.5	1009	3	US-09-743-492A-3	Sequence 3, Appli
286	160	8.9	960	3	US-08-597-495B-23	Sequence 23, Appl	359	154	8.5	2061	3	US-09-462-270-3	Sequence 3, Appli
287	160	8.9	960	3	US-09-068-051A-23	Sequence 23, Appl	360	154	8.5	2061	3	US-09-173-151A-3	Sequence 3, Appli
288	160	8.9	2469	1	US-07-997-133-2	Sequence 2, Appli	361	153.5	8.5	1964	3	US-09-173-151A-3	Sequence 3, Appli
289	160	8.9	2469	1	US-08-459-296-1	Sequence 1, Appli	362	153.5	8.5	1964	3	US-08-468-856B-7	Sequence 7, Appli
290	160	8.9	2469	5	US-07-997-133-2	Sequence 2, Appli	363	153	8.5	571	4	US-08-468-859A-7	Sequence 7, Appli
291	160	8.9	2662	2	US-08-451-822A-14	Sequence 14, Appl	364	153	8.5	571	4	US-09-270-767-1097	Sequence 1097, Ap
292	160	8.9	2662	3	US-08-323-430-14	Sequence 14, Appl	365	153	8.5	1574	4	US-09-270-767-16379	Sequence 16379, A
293	160	8.9	2733	5	PCT-US96-00331-14	Sequence 14, Appl	366	153	8.5	6263	4	US-09-270-767-12428	Sequence 12428, A
294	160	8.9	2733	5	PCT-US96-00331-14	Sequence 14, Appl	367	152	8.4	3173	3	US-09-023-655-1473	Sequence 1473, Ap
295	160	8.9	3944	4	US-09-949-016-1876	Sequence 1876, Ap	368	152	8.4	3173	3	US-08-468-856B-1	Sequence 1, Appli
296	160	8.9	3944	4	US-09-949-016-1877	Sequence 1877, Ap	369	152	8.4	3766	4	US-09-468-859A-1	Sequence 1, Appli
297	160	8.9	3944	4	US-09-949-016-1878	Sequence 1878, Ap	370	152	8.4	3778	4	US-09-949-016-1651	Sequence 359, App
298	160	8.9	3944	4	US-09-949-016-1879	Sequence 1879, Ap	371	151.5	8.4	1190	4	US-09-949-016-359	Sequence 359, App
299	160	8.9	3944	4	US-09-949-016-1880	Sequence 1880, Ap	372	151.5	8.4	2003	1	US-09-036-555B-21	Sequence 21, Appl
300	160	8.9	3944	4	US-09-949-016-1881	Sequence 1881, Ap	373	151.5	8.4	2003	1	US-08-469-569-21	Sequence 21, Appl
301	160	8.9	3944	4	US-09-949-016-1882	Sequence 1882, Ap	374	151.5	8.4	2003	1	US-08-249-322A-21	Sequence 21, Appl
302	160	8.9	3944	4	US-09-949-016-1883	Sequence 1883, Ap	375	151.5	8.4	2003	1	US-08-469-526A-21	Sequence 21, Appl
303	159	8.8	462	4	US-09-270-767-2319	Sequence 2319, Ap	376	151.5	8.4	2003	2	US-08-459-526A-21	Sequence 21, Appl
304	159	8.8	462	4	US-09-270-767-17601	Sequence 17601, A	377	151.5	8.4	2003	2	US-08-469-560A-21	Sequence 21, Appl

378	151.5	8.4	2003	3	US-08-341-018-71	Sequence 71, Appl	451	141.5	7.8	1140	3	US-08-470-339-149	Sequence 149, App
379	151.5	8.4	2003	3	US-08-470-335-21	Sequence 21, Appl	452	141.5	7.8	1140	3	US-08-467-602-149	Sequence 149, App
380	151.5	8.4	2003	3	US-08-735-021-21	Sequence 21, Appl	453	141.5	7.8	1140	4	US-08-411-295F-48	Sequence 48, Appl
381	151.5	8.4	2003	3	US-08-734-664A-21	Sequence 21, Appl	454	141.5	7.8	1140	5	PCT-US94-05083C-145	Sequence 145, App
382	151.5	8.4	2003	3	US-08-470-339-21	Sequence 21, Appl	455	141.5	7.8	1140	5	PCT-US95-06846A-149	Sequence 149, App
383	151.5	8.4	2003	3	US-08-467-602-21	Sequence 21, Appl	456	141.5	7.8	1164	1	US-08-445-640-11	Sequence 11, Appl
384	151.5	8.4	2003	4	US-08-411-295F-64	Sequence 64, Appl	457	141.5	7.8	1164	3	US-08-170-558-11	Sequence 11, Appl
385	151.5	8.4	2003	5	PCT-US94-05083C-21	Sequence 21, Appl	458	141.5	7.8	1164	3	US-08-447-314-11	Sequence 11, Appl
386	151.5	8.4	2003	5	PCT-US95-06846A-21	Sequence 21, Appl	459	141.5	7.8	1164	3	US-08-445-461-11	Sequence 11, Appl
387	150.5	8.3	1364	4	US-09-924-103-3	Sequence 3, Appli	460	141.5	7.8	1164	4	US-09-223-490-11	Sequence 11, Appl
388	150.5	8.3	2287	4	US-09-923-655-1216	Sequence 1216, Ap	461	141.5	7.8	1193	1	US-08-036-555B-134	Sequence 134, App
389	150	8.3	1079	1	US-08-471-570-13	Sequence 13, Appl	462	141.5	7.8	1193	1	US-08-469-569-134	Sequence 134, App
390	150	8.3	1954	1	US-08-471-570-5	Sequence 5, Appli	463	141.5	7.8	1193	1	US-08-249-322A-134	Sequence 134, App
391	150	8.3	2676	1	US-08-471-570-7	Sequence 7, Appli	464	141.5	7.8	1193	2	US-08-469-660-134	Sequence 134, App
392	149.5	8.3	5690	2	US-08-447-464-2	Sequence 2, Appli	465	141.5	7.8	1193	5	PCT-US94-05083C-130	Sequence 130, App
393	149.5	8.3	5690	2	US-08-716-679-2	Sequence 2, Appli	466	141.5	7.8	1193	5	PCT-US95-06846A-134	Sequence 134, App
394	148.5	8.2	4078	4	US-09-016-434-1132	Sequence 1132, Ap	467	141.5	7.8	1194	4	US-08-411-295F-3	Sequence 3, Appli
395	148.5	8.2	6000	1	US-08-348-006B-6	Sequence 6, Appli	468	141	7.8	2079	4	US-09-949-016-3171	Sequence 3171, Ap
396	148.5	8.2	6000	2	US-08-800-825A-6	Sequence 6, Appli	469	141	7.8	2079	4	US-09-949-016-3172	Sequence 3172, Ap
397	148.5	8.2	6000	3	US-09-158-657-6	Sequence 6, Appli	470	141	7.8	2079	4	US-09-949-016-3173	Sequence 3173, Ap
398	148.5	8.2	6000	5	PCT-US94-10166-6	Sequence 6, Appli	471	141	7.8	2079	4	US-09-949-016-3174	Sequence 3174, Ap
399	148	8.2	2351	1	US-08-168-091A-1	Sequence 1, Appli	472	141	7.8	2079	4	US-09-949-016-3175	Sequence 3175, Ap
400	147.5	8.2	1347	4	US-09-638-648-6	Sequence 6, Appli	473	141	7.8	2079	4	US-09-949-016-3176	Sequence 3176, Ap
401	147.5	8.2	1348	4	US-09-638-649-6	Sequence 6, Appli	474	141	7.8	2079	4	US-09-949-016-3177	Sequence 3177, Ap
402	147	8.1	2430	4	US-09-620-312D-176	Sequence 176, App	475	141	7.8	2079	4	US-09-949-016-3178	Sequence 3178, Ap
403	145.5	8.1	1199	4	US-09-270-767-13050	Sequence 13050, A	476	141	7.8	2079	4	US-09-949-016-3179	Sequence 3179, Ap
404	145	8.0	726	3	US-09-254-465A-4	Sequence 4, Appli	477	141	7.8	2079	4	US-09-949-016-3180	Sequence 3180, Ap
405	145	8.0	726	4	US-09-953-499-4	Sequence 4, Appli	478	141	7.8	6172	4	US-09-774-528-89	Sequence 89, Appl
406	144	8.0	3992	4	US-09-944-807-9	Sequence 9, Appli	479	140.5	7.8	1659	4	US-09-969-532-7	Sequence 7, Appli
407	143.5	7.9	1103	2	US-08-602-725-33	Sequence 33, Appl	480	140.5	7.8	1692	4	US-09-969-532-5	Sequence 5, Appli
408	143.5	7.9	1896	3	US-09-412-554A-8	Sequence 8, Appli	481	140.5	7.8	1701	4	US-09-969-532-3	Sequence 3, Appli
409	143.5	7.9	3416	2	US-08-451-822A-15	Sequence 15, Appl	482	140.5	7.8	1734	4	US-09-969-532-1	Sequence 1, Appli
410	143.5	7.9	3416	3	US-08-323-430-15	Sequence 15, Appl	483	140.5	7.8	1767	4	US-09-866-510-11	Sequence 11, Appl
411	143	7.9	2313	1	US-08-232-538-5	Sequence 5, Appli	484	140.5	7.8	2661	4	US-09-969-532-15	Sequence 15, Appl
412	143	7.9	2313	3	US-09-427-353-1	Sequence 1, Appli	485	140.5	7.8	2694	4	US-09-969-532-13	Sequence 13, Appl
413	143	7.9	2651	4	US-08-786-164-5	Sequence 5, Appli	486	140.5	7.8	2703	4	US-09-969-532-11	Sequence 11, Appl
414	143	7.9	3934	4	US-09-953-318-19	Sequence 19, Appl	487	140.5	7.8	2736	4	US-09-969-532-9	Sequence 9, Appli
415	143	7.9	3394	4	US-09-953-318-100	Sequence 100, App	488	140.5	7.8	2742	1	US-08-286-305A-2	Sequence 2, Appli
416	142.5	7.9	1320	4	US-09-592-998C-8	Sequence 8, Appli	489	140.5	7.8	2742	2	US-08-441-104A-2	Sequence 2, Appli
417	142.5	7.9	1958	6	5169835-1	Patent No. 5169835	490	140.5	7.8	2742	3	US-08-440-816A-2	Sequence 2, Appli
418	142.5	7.9	1958	6	5169835-1	Patent No. 5169835	491	140.5	7.8	2742	4	US-09-417-381A-2	Sequence 2, Appli
419	142.5	7.9	2205	5	PCT-US93-00031-12	Sequence 12, Appl	492	140.5	7.8	2768	4	US-09-949-016-1697	Sequence 1697, Ap
420	142.5	7.9	2217	5	PCT-US93-00031-8	Sequence 8, Appli	493	140.5	7.8	3270	4	US-09-866-510-1	Sequence 1, Appli
421	142.5	7.9	3080	3	US-08-482-073-4	Sequence 4, Appli	494	140.5	7.8	3270	4	US-09-866-510-3	Sequence 3, Appli
422	142	7.9	992	1	US-08-481-130-24	Sequence 24, Appl	495	140.5	7.8	3270	4	US-09-866-510-5	Sequence 5, Appli
423	142	7.9	992	1	US-08-656-984A-24	Sequence 24, Appl	496	140.5	7.8	3270	4	US-09-866-510-7	Sequence 7, Appli
424	142	7.9	992	1	US-08-485-604-24	Sequence 24, Appl	497	140.5	7.8	3270	4	US-09-866-510-9	Sequence 9, Appli
425	142	7.9	992	2	US-08-487-595-24	Sequence 24, Appl	498	140.5	7.8	3411	4	US-09-969-532-33	Sequence 33, Appl
426	141.5	7.8	1108	1	US-08-036-555B-135	Sequence 135, App	499	140.5	7.8	3611	1	US-08-445-640-1	Sequence 1, Appli
427	141.5	7.8	1108	1	US-08-469-569-135	Sequence 135, App	500	140.5	7.8	3611	3	US-08-170-558-1	Sequence 1, Appli
428	141.5	7.8	1108	1	US-08-249-322A-135	Sequence 135, App	501	140.5	7.8	3611	3	US-08-447-314-1	Sequence 1, Appli
429	141.5	7.8	1108	1	US-08-469-526A-135	Sequence 135, App	502	140.5	7.8	3611	3	US-08-445-461-1	Sequence 1, Appli
430	141.5	7.8	1108	2	US-08-734-591A-135	Sequence 135, App	503	140.5	7.8	3611	4	US-09-223-490-1	Sequence 1, Appli
431	141.5	7.8	1108	2	US-08-469-660-135	Sequence 135, App	504	140.5	7.8	4054	1	US-08-180-195-35	Sequence 35, Appl
432	141.5	7.8	1108	3	US-08-341-018-5	Sequence 5, Appli	505	140.5	7.8	4054	1	US-08-477-329-35	Sequence 35, Appl
433	141.5	7.8	1108	3	US-08-470-335-135	Sequence 135, App	506	140.5	7.8	4054	2	US-08-475-458-35	Sequence 35, Appl
434	141.5	7.8	1108	3	US-08-735-021-135	Sequence 135, App	507	140.5	7.8	4054	3	US-08-980-400-35	Sequence 35, Appl
435	141.5	7.8	1108	3	US-08-734-664A-135	Sequence 135, App	508	140.5	7.8	4054	3	US-09-583-459A-35	Sequence 35, Appl
436	141.5	7.8	1108	3	US-08-470-339-135	Sequence 135, App	509	140.5	7.8	4054	3	US-09-583-210-35	Sequence 35, Appl
437	141.5	7.8	1108	3	US-08-467-602-135	Sequence 135, App	510	140.5	7.8	4054	3	US-09-583-449A-35	Sequence 35, Appl
438	141.5	7.8	1108	4	US-08-411-295F-5	Sequence 5, Appli	511	140.5	7.8	4054	3	US-09-435-059-35	Sequence 35, Appl
439	141.5	7.8	1108	5	PCT-US94-05083C-131	Sequence 131, App	512	140.5	7.8	4100	1	US-08-168-917-3	Sequence 3, Appli
440	141.5	7.8	1108	5	PCT-US95-06846A-135	Sequence 135, App	513	140.5	7.8	4100	2	US-08-460-510-3	Sequence 3, Appli
441	141.5	7.8	1140	1	US-08-036-555B-149	Sequence 149, App	514	140.5	7.8	4100	2	US-08-460-490-3	Sequence 3, Appli
442	141.5	7.8	1140	1	US-08-469-569-149	Sequence 149, App	515	140.5	7.8	4100	5	PCT-US92-00730-3	Sequence 3, Appli
443	141.5	7.8	1140	1	US-08-249-322A-149	Sequence 149, App	516	140.5	7.8	4100	5	PCT-US92-00862-3	Sequence 3, Appli
444	141.5	7.8	1140	2	US-08-469-526A-149	Sequence 149, App	517	140.5	7.8	6373	3	US-08-462-728-1	Sequence 1, Appli
445	141.5	7.8	1140	2	US-08-734-591A-149	Sequence 149, App	518	140.5	7.8	6373	3	US-08-461-917-1	Sequence 1, Appli
446	141.5	7.8	1140	2	US-08-469-660-149	Sequence 149, App	519	140.5	7.8	6373	4	US-08-464-436-1	Sequence 1, Appli
447	141.5	7.8	1140	3	US-08-341-018-55	Sequence 55, Appli	520	140.5	7.8	6375	1	US-08-168-917-5	Sequence 5, Appli
448	141.5	7.8	1140	3	US-08-470-335-149	Sequence 149, App	521	140.5	7.8	6375	1	US-08-460-510-5	Sequence 5, Appli
449	141.5	7.8	1140	3	US-08-735-021-149	Sequence 149, App	522	140.5	7.8	6375	2	US-08-460-490-5	Sequence 5, Appli
450	141.5	7.8	1140	3	US-08-734-664A-149	Sequence 149, App	523	140.5	7.8	6375	2	US-08-460-490-5	Sequence 5, Appli

524	140.5	7.8	6375	5	PCT-US92-00730-5	Sequence 5, Appli	597	134.5	7.4	1602	3	US-09-651-200-11	Sequence 11, Appl
525	140.5	7.8	6375	5	PCT-US92-00862-5	Sequence 5, Appli	598	134.5	7.4	1929	5	PCT-US93-00031-18	Sequence 18, Appl
526	140.5	7.8	6378	4	US-09-023-655-1194	Sequence 1194, Ap	599	134.5	7.4	1941	5	PCT-US93-00031-10	Sequence 10, Appl
527	140.5	7.8	6378	4	US-09-919-497-40	Sequence 40, Appl	600	134.5	7.4	1941	5	PCT-US93-00031-22	Sequence 22, Appl
528	140.5	7.8	6378	4	US-09-949-016-832	Sequence 832, App	601	134.5	7.4	2220	5	PCT-US93-00031-16	Sequence 16, Appl
529	140.5	7.8	6412	4	US-09-769-987-1	Sequence 1, Appli	602	134.5	7.4	2229	3	US-09-651-200-5	Sequence 5, Appli
530	140	7.8	610	4	US-09-270-767-39243	Sequence 29243, A	603	134.5	7.4	2811	3	US-08-482-073-3	Sequence 3, Appli
531	140	7.8	753	4	US-09-270-767-11521	Sequence 11521, A	604	134.5	7.4	2813	2	US-08-344-155C-99	Sequence 99, Appl
532	140	7.8	5084	1	US-08-306-691B-21	Sequence 21, Appl	605	134.5	7.4	2813	3	US-09-009-490A-90	Sequence 90, Appl
533	140	7.8	5084	1	US-09-023-655-1335	Sequence 1335, Ap	606	134.5	7.4	3063	3	US-09-620-312D-844	Sequence 844, App
534	140	7.8	5084	5	PCT-US93-06251-25	Sequence 25, Appl	607	134	7.4	1573	6	5169835-5	Patent No. 5169835
535	140	7.8	8083	3	US-09-383-630-4	Sequence 4, Appli	608	134	7.4	1573	6	5169835-5	Patent No. 5169835
536	140	7.8	8083	3	US-09-383-630-5	Sequence 5, Appli	609	133.5	7.4	1467	4	US-09-499-846-11	Sequence 11, Appl
537	139.5	7.7	2110	4	US-09-907-794A-319	Sequence 319, App	610	133	7.4	952	4	US-09-684-708A-22	Sequence 22, Appl
538	139.5	7.7	2110	4	US-09-905-125A-319	Sequence 319, App	611	133	7.4	1004	4	US-09-684-708A-24	Sequence 24, Appl
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548	139	7.7	2477	1	US-08-429-742-1	Sequence 1, Appli	621	133	7.4	2715	3	US-08-444-622A-5	Sequence 5, Appli
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551	138.5	7.7	1193	1	US-08-469-526A-134	Sequence 134, App	624	133	7.4	2903	4	US-09-949-016-5033	Sequence 5033, Ap
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553	138.5	7.7	1193	3	US-08-341-018-3	Sequence 3, Appli	626	133	7.4	2940	2	US-08-441-104A-8	Sequence 8, Appli
554	138.5	7.7	1193	3	US-08-470-335-134	Sequence 134, App	627	133	7.4	2940	2	US-08-440-816A-8	Sequence 8, Appli
555	138.5	7.7	1193	3	US-08-735-021-134	Sequence 134, App	628	133	7.4	2940	2	US-09-417-381A-8	Sequence 8, Appli
556	138.5	7.7	1193	3	US-08-734-664A-134	Sequence 134, App	629	133	7.4	7476	4	US-09-949-016-17005	Sequence 17005, A
557	138.5	7.7	1193	3	US-08-470-339-134	Sequence 134, App	630	132.5	7.3	2009	3	US-08-468-856B-8	Sequence 8, Appli
558	138.5	7.7	1193	3	US-08-467-602-134	Sequence 134, App	631	132.5	7.3	2009	3	US-08-468-859A-8	Sequence 8, Appli
559	138.5	7.7	1545	4	US-09-949-016-5509	Sequence 5509, Ap	632	132	7.3	2166	3	US-09-175-928-1	Sequence 1, Appli
560	138.5	7.7	1710	4	US-09-723-368-3	Sequence 3, Appli	633	132	7.3	2434	3	US-09-272-496-1	Sequence 1, Appli
561	138.5	7.7	3199	4	US-09-628-188A-2	Sequence 2, Appli	634	132	7.3	2434	3	US-09-949-016-193	Sequence 193, App
562	137	7.6	1164	1	US-08-445-640-5	Sequence 5, Appli	635	132	7.3	2866	3	US-09-724-864-30	Sequence 30, Appl
563	137	7.6	1164	3	US-08-170-558-5	Sequence 5, Appli	636	131.5	7.3	1182	3	US-09-336-536-38	Sequence 38, Appl
564	137	7.6	1164	3	US-08-447-314-5	Sequence 5, Appli	637	131.5	7.3	1295	3	US-09-254-465A-8	Sequence 8, Appli
565	137	7.6	1164	3	US-08-445-461-5	Sequence 5, Appli	638	131.5	7.3	1295	4	US-09-907-794A-63	Sequence 63, Appl
566	137	7.6	1164	3	US-09-223-490-5	Sequence 5, Appli	639	131.5	7.3	1295	4	US-09-905-125A-63	Sequence 63, Appl
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568	137	7.6	1591	3	US-08-468-859A-9	Sequence 9, Appli	641	131.5	7.3	1295	4	US-09-906-700-63	Sequence 63, Appl
569	137	7.6	2598	4	US-09-949-016-3414	Sequence 3414, Ap	642	131.5	7.3	1295	4	US-09-903-603A-63	Sequence 63, Appl
570	137	7.6	3111	3	US-08-891-845-1	Sequence 1, Appli	643	131.5	7.3	1295	4	US-09-904-920A-63	Sequence 63, Appl
571	137	7.6	3111	4	US-09-514-573-1	Sequence 1, Appli	644	131.5	7.3	1295	4	US-09-909-064-63	Sequence 63, Appl
572	136.5	7.6	1004	3	US-09-383-586-24	Sequence 24, Appl	645	131.5	7.3	1295	4	US-09-905-381A-63	Sequence 63, Appl
573	136.5	7.6	1004	3	US-09-823-038A-24	Sequence 24, Appl	646	131.5	7.3	1295	4	US-09-906-618-63	Sequence 63, Appl
574	136.5	7.6	2244	3	US-09-354-151-1	Sequence 1, Appli	647	131.5	7.3	1295	4	US-09-953-499-8	Sequence 8, Appli
575	136.5	7.6	2426	4	US-09-023-655-1156	Sequence 1156, Ap	648	131.5	7.3	1846	3	US-09-336-536-37	Sequence 37, Appl
576	136.5	7.6	2557	2	US-09-044-506A-1	Sequence 1, Appli	649	131	7.3	734	1	US-08-471-570-11	Sequence 11, Appl
577	136.5	7.6	2557	3	US-08-478-208-31	Sequence 31, Appl	650	131	7.3	1027	4	US-09-684-708A-26	Sequence 26, Appl
578	136.5	7.6	2557	3	US-09-336-536-72	Sequence 72, Appl	651	131	7.3	1423	4	US-09-823-038A-46	Sequence 46, Appl
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580	136.5	7.6	2557	6	5264554-1	Sequence 5264554	653	131	7.3	1604	4	US-09-419-788-18	Sequence 18, Appl
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582	136	7.5	1377	3	US-09-435-956A-2	Sequence 2, Appli	655	131	7.3	3086	4	US-09-684-708A-20	Sequence 20, Appl
583	136	7.5	1603	1	US-08-471-570-3	Sequence 3, Appli	656	131	7.3	3321	4	US-09-866-510-13	Sequence 13, Appl
584	136	7.5	1932	5	PCT-US93-00031-20	Sequence 20, Appl	657	131	7.3	3321	4	US-09-866-510-15	Sequence 15, Appl
585	136	7.5	2310	1	US-08-471-570-9	Sequence 9, Appli	658	131	7.3	3321	4	US-09-866-510-17	Sequence 17, Appl
586	135	7.5	1042	2	US-08-427-497E-6	Sequence 6, Appli	659	131	7.3	3321	4	US-09-866-510-19	Sequence 19, Appl
587	135	7.5	1494	4	US-09-499-846-5	Sequence 5, Appli	660	131	7.3	3321	4	US-09-866-510-21	Sequence 21, Appl
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589	135	7.5	1578	4	US-09-499-846-3	Sequence 3, Appli	662	131	7.3	4465	1	US-08-477-329-1	Sequence 1, Appli
590	135	7.5	1578	4	US-09-499-846-7	Sequence 7, Appli	663	131	7.3	4465	2	US-08-475-458-1	Sequence 1, Appli
591	135	7.5	2214	1	US-08-245-295-7	Sequence 7, Appli	664	131	7.3	4465	3	US-08-980-400-1	Sequence 1, Appli
592	135	7.5	2214	1	US-08-481-130-7	Sequence 7, Appli	665	131	7.3	4465	3	US-09-583-459A-1	Sequence 1, Appli
593	135	7.5	2214	1	US-08-651-984A-7	Sequence 7, Appli	666	131	7.3	4465	3	US-09-583-210-1	Sequence 1, Appli
594	135	7.5	2214	1	US-08-485-604-7	Sequence 7, Appli	667	131	7.3	4465	3	US-09-583-449A-1	Sequence 1, Appli
595	135	7.5	2214	1	US-08-487-595-7	Sequence 7, Appli	668	131	7.3	4465	3	US-09-435-059-1	Sequence 1, Appli
596	135	7.5	2768	4	US-09-774-528-426	Sequence 426, App	669	131	7.3	5427	1	US-08-168-917-1	Sequence 1, Appli

670	131	7.3	5427	2	US-08-460-510-1	Sequence 1, Appli	743	127.5	7.1	1554	4	US-09-949-016-3333	Sequence 3333, Ap
671	131	7.3	5427	2	US-08-460-490-3	Sequence 1, Appli	744	127.5	7.1	1554	4	US-09-949-016-3334	Sequence 3334, Ap
672	131	7.3	5427	3	US-08-462-728-1	Sequence 3, Appli	745	127.5	7.1	1554	4	US-09-949-016-3335	Sequence 3335, Ap
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674	131	7.3	5427	4	US-08-464-436-3	Sequence 3, Appli	747	127.5	7.1	1652	1	US-08-469-569-148	Sequence 148, App
675	131	7.3	5427	4	US-08-464-436-3	Sequence 3, Appli	748	127.5	7.1	1652	1	US-08-249-322A-148	Sequence 148, App
676	131	7.3	5427	5	PCT-US92-00730-1	Sequence 1, Appli	749	127.5	7.1	1652	1	US-08-469-526A-148	Sequence 148, App
677	131	7.3	5427	5	PCT-US92-00862-1	Sequence 1, Appli	750	127.5	7.1	1652	1	US-08-734-591A-148	Sequence 148, App
678	131	7.3	5570	4	US-09-023-655-1193	Sequence 1193, Ap	751	127.5	7.1	1652	2	US-08-469-660-148	Sequence 148, App
679	130.5	7.2	1022	3	US-09-152-060-35	Sequence 35, Appli	752	127.5	7.1	1652	3	US-08-341-018-53	Sequence 53, Appli
680	130.5	7.2	1401	4	US-09-604-107A-7	Sequence 7, Appli	753	127.5	7.1	1652	3	US-08-470-335-148	Sequence 148, App
681	130.5	7.2	1452	4	US-09-949-016-5250	Sequence 5250, Ap	754	127.5	7.1	1652	3	US-08-735-021-148	Sequence 148, App
682	130.5	7.2	1452	4	US-09-949-016-5251	Sequence 5251, Ap	755	127.5	7.1	1652	3	US-08-734-664A-148	Sequence 148, App
683	130	7.2	743	4	US-08-411-295F-1	Sequence 1, Appli	756	127.5	7.1	1652	3	US-08-470-339-148	Sequence 148, App
684	130	7.2	744	1	US-08-036-555B-133	Sequence 133, App	757	127.5	7.1	1652	3	US-08-467-602-148	Sequence 148, App
685	130	7.2	744	1	US-08-469-569-133	Sequence 133, App	758	127.5	7.1	1652	4	US-08-411-295F-46	Sequence 46, Appli
686	130	7.2	744	1	US-08-249-322A-133	Sequence 133, App	759	127.5	7.1	1652	5	PCT-US94-05083C-144	Sequence 144, App
687	130	7.2	744	1	US-08-469-526A-133	Sequence 133, App	760	127.5	7.1	1652	5	PCT-US95-06846A-148	Sequence 148, App
688	130	7.2	744	2	US-08-734-591A-133	Sequence 133, App	761	127.5	7.1	1831	3	US-09-484-970B-84	Sequence 84, Appli
689	130	7.2	744	2	US-08-469-660-133	Sequence 133, App	762	127.5	7.1	32207	2	US-08-770-379-20	Sequence 20, Appli
690	130	7.2	744	3	US-08-341-018-1	Sequence 1, Appli	763	127.5	7.1	32207	3	US-08-757-669A-20	Sequence 20, Appli
691	130	7.2	744	3	US-08-470-335-133	Sequence 133, App	764	127.5	7.1	32207	3	US-09-230-371A-20	Sequence 20, Appli
692	130	7.2	744	3	US-08-735-021-133	Sequence 133, App	765	127	7.0	1046	4	US-09-419-788-163	Sequence 163, App
693	130	7.2	744	3	US-08-734-664A-133	Sequence 133, App	766	127	7.0	1730	4	US-09-919-172-19	Sequence 19, Appli
694	130	7.2	744	3	US-08-470-339-133	Sequence 133, App	767	127	7.0	2430	4	US-09-949-016-5179	Sequence 5179, Ap
695	130	7.2	744	3	US-08-467-602-133	Sequence 133, App	768	127	7.0	2885	4	US-09-949-016-5773	Sequence 5773, Ap
696	130	7.2	744	5	PCT-US94-05083C-129	Sequence 129, App	769	127	7.0	2901	4	US-09-949-016-251	Sequence 251, App
697	130	7.2	744	5	PCT-US95-06846A-133	Sequence 133, App	770	127	7.0	2949	3	US-09-412-554A-3	Sequence 3, Appli
698	129.5	7.2	2534	2	US-09-569-611C-4	Sequence 30, Appli	771	126.5	7.0	377	4	US-09-270-767-6506	Sequence 6506, Ap
699	129.5	7.2	1459	4	US-09-569-611C-4	Sequence 4, Appli	772	126.5	7.0	377	4	US-09-270-767-21788	Sequence 21788, A
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701	129.5	7.2	1884	3	US-09-398-496-5	Sequence 5, Appli	774	126	7.0	1870	2	US-08-286-846A-3	Sequence 3, Appli
702	129.5	7.2	2376	1	US-07-913-952-3	Sequence 3, Appli	775	126	7.0	1870	2	US-08-457-880A-3	Sequence 3, Appli
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706	129.5	7.2	3453	1	US-08-252-517-1	Sequence 1, Appli	779	126	7.0	3060	1	US-08-286-305A-6	Sequence 6, Appli
707	129.5	7.2	3453	1	US-07-906-397A-1	Sequence 1, Appli	780	126	7.0	3060	2	US-08-441-104A-6	Sequence 6, Appli
708	129.5	7.2	3453	1	US-08-601-891-1	Sequence 1, Appli	781	126	7.0	3060	2	US-08-440-816A-6	Sequence 6, Appli
709	129.5	7.2	3453	2	US-09-021-324-1	Sequence 1, Appli	782	126	7.0	3060	3	US-09-417-381A-6	Sequence 6, Appli
710	129.5	7.2	3453	4	US-09-872-136B-1	Sequence 1, Appli	783	126	7.0	3194	2	US-08-359-705B-1	Sequence 1, Appli
711	129.5	7.2	3453	5	PCT-US92-02750-1	Sequence 1, Appli	784	126	7.0	3194	2	US-08-286-846A-1	Sequence 1, Appli
712	129.5	7.2	3453	5	PCT-US92-05401-1	Sequence 1, Appli	785	126	7.0	3194	2	US-08-457-880A-1	Sequence 1, Appli
713	129.5	7.2	3453	5	PCT-US92-09893-1	Sequence 1, Appli	786	126	7.0	3194	3	US-08-444-622A-1	Sequence 1, Appli
714	129	7.1	1370	4	US-09-949-016-1693	Sequence 1693, Ap	787	126	7.0	3194	3	US-08-942-562-1	Sequence 1, Appli
715	129	7.1	1459	4	US-09-949-016-658	Sequence 858, App	788	126	7.0	3194	3	US-09-156-923-1	Sequence 1, Appli
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717	129	7.1	2449	4	US-09-949-016-1248	Sequence 1248, Ap	790	125	6.9	1176	5	PCT-US95-15696-1	Sequence 1, Appli
718	129	7.1	2866	4	US-09-949-016-2340	Sequence 2340, Ap	791	125	6.9	1472	1	US-08-245-295-9	Sequence 9, Appli
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720	129	7.1	3008	3	US-09-188-930-65	Sequence 65, Appli	793	125	6.9	1472	1	US-08-656-984A-9	Sequence 9, Appli
721	129	7.1	3008	4	US-09-312-283C-65	Sequence 65, Appli	794	125	6.9	1472	1	US-08-485-604-9	Sequence 9, Appli
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723	128.5	7.1	3521	2	US-08-434-878-1	Sequence 1, Appli	796	125	6.9	1715	1	US-07-847-743B-24	Sequence 24, Appli
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725	128	7.1	1110	3	US-09-336-536-27	Sequence 27, Appli	798	125	6.9	1715	2	US-08-456-241-24	Sequence 24, Appli
726	128	7.1	1460	2	US-08-392-338A-18	Sequence 18, Appli	799	125	6.9	1715	5	PCT-US92-04295A-24	Sequence 24, Appli
727	128	7.1	1460	3	US-09-166-750-18	Sequence 18, Appli	800	125	6.9	2199	1	US-07-847-743B-7	Sequence 7, Appli
728	128	7.1	1460	3	US-09-166-093-18	Sequence 18, Appli	801	125	6.9	2199	1	US-08-086-277-7	Sequence 7, Appli
729	128	7.1	1460	3	US-09-172-019-18	Sequence 18, Appli	802	125	6.9	2199	2	US-08-456-201-7	Sequence 7, Appli
730	128	7.1	1460	3	US-09-166-094-18	Sequence 18, Appli	803	125	6.9	2199	2	US-08-456-241-7	Sequence 7, Appli
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733	128	7.1	2378	4	US-09-949-016-2703	Sequence 2703, Ap	806	125	6.9	2199	5	PCT-US92-04295A-7	Sequence 7, Appli
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735	128	7.1	3707	4	US-09-949-016-827	Sequence 827, App	808	125	6.9	2431	1	US-08-456-201-25	Sequence 25, Appli
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737	128	7.1	5993	3	US-09-383-630-1	Sequence 1, Appli	810	125	6.9	2431	5	PCT-US92-04295A-25	Sequence 25, Appli
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739	127.5	7.1	1554	4	US-09-949-016-3329	Sequence 3329, Ap	812	125	6.9	2490	1	US-08-456-201-23	Sequence 23, Appli
740	127.5	7.1	1554	4	US-09-949-016-3330	Sequence 3330, Ap	813	125	6.9	2490	2	US-08-456-241-23	Sequence 23, Appli
741	127.5	7.1	1554	4	US-09-949-016-3331	Sequence 3331, Ap	814	125	6.9	2490	5	PCT-US92-04295A-23	Sequence 23, Appli
742	127.5	7.1	1554	4	US-09-949-016-3332	Sequence 3332, Ap	815	124.5	6.9	2049	3	US-09-099-749-10	Sequence 10, Appli

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817	124.5	6.9	2681	2	US-08-885-418-9	Sequence 9, Appli	890	121.5	6.7	390	3	US-09-953-499-3	Sequence 3, Appli
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c 819	124	6.9	439	4	US-09-270-767-16840	Sequence 16840, A	892	121.5	6.7	948	4	US-09-910-174B-27	Sequence 27, Appl
820	124	6.9	1561	4	US-09-419-788-24	Sequence 24, Appl	893	121.5	6.7	948	4	US-09-620-461-27	Sequence 27, Appl
821	124	6.9	2010	1	US-07-847-743B-12	Sequence 12, Appl	894	121.5	6.7	5207	4	US-09-558-664A-1	Sequence 1, Appli
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825	124	6.9	2010	2	US-08-440-401-10	Sequence 10, Appl	898	121.5	6.7	5207	4	US-10-697-263-3	Sequence 3, Appli
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827	124	6.9	2010	3	US-09-173-480-10	Sequence 10, Appl	900	120.5	6.7	591	3	US-08-833-488B-6	Sequence 6, Appli
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830	124	6.9	2164	1	US-08-096-277-6	Sequence 6, Appli	c 903	120.5	6.7	591	3	US-08-833-488B-12	Sequence 12, Appl
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832	124	6.9	2164	3	US-08-703-089-6	Sequence 6, Appli	c 905	120.5	6.7	609	3	US-08-833-488B-5	Sequence 5, Appli
833	124	6.9	2387	3	US-08-891-845-11	Sequence 11, Appl	906	120.5	6.7	609	3	US-08-833-488B-8	Sequence 8, Appli
834	124	6.9	2387	4	US-08-544-573-11	Sequence 11, Appl	c 907	120.5	6.7	609	3	US-08-833-488B-10	Sequence 10, Appl
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838	124	6.9	3501	1	US-07-977-451-3	Sequence 3, Appli	911	120	6.6	721	4	US-09-357-243D-2	Sequence 2, Appli
839	124	6.9	3501	1	US-08-252-517-3	Sequence 3, Appli	912	120	6.6	3173	3	US-09-149-476-174	Sequence 174, App
840	124	6.9	3501	1	US-07-906-397A-3	Sequence 3, Appli	913	120	6.6	3296	4	US-09-949-016-1456	Sequence 1456, Ap
841	124	6.9	3501	1	US-08-601-891-3	Sequence 3, Appli	914	120	6.6	3299	4	US-09-949-016-557	Sequence 557, App
842	124	6.9	3501	2	US-09-021-324-3	Sequence 3, Appli	915	120	6.6	4286	4	US-09-899-634C-1	Sequence 1, Appli
843	124	6.9	3501	4	US-09-872-136B-3	Sequence 3, Appli	916	119.5	6.6	591	3	US-08-833-488B-27	Sequence 27, Appl
844	124	6.9	3501	5	PCT-US92-05401-3	Sequence 3, Appli	c 917	119.5	6.6	591	3	US-08-833-488B-29	Sequence 29, Appl
845	124	6.9	3501	5	PCT-US92-09893-3	Sequence 3, Appli	918	119.5	6.6	759	3	US-08-833-488B-22	Sequence 22, Appl
846	124	6.9	3608	4	US-09-016-434-1408	Sequence 1408, Ap	c 919	119.5	6.6	759	3	US-08-833-488B-23	Sequence 23, Appl
847	124	6.9	3608	4	US-09-949-016-847	Sequence 847, App	920	119.5	6.6	915	4	US-09-419-788-14	Sequence 14, Appl
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849	123	6.8	1693	6	5169835-3	Patent No. 5169835	922	119.5	6.6	1295	1	US-08-481-130-6	Sequence 6, Appli
850	123	6.8	1693	6	5169835-3	Patent No. 5169835	923	119.5	6.6	1295	1	US-08-656-984A-6	Sequence 6, Appli
851	123	6.8	1744	3	US-09-484-970B-83	Sequence 83, Appl	924	119.5	6.6	1295	1	US-08-485-604-6	Sequence 6, Appli
852	123	6.8	2165	2	US-08-263-911-8	Sequence 8, Appli	925	119.5	6.6	1295	2	US-08-487-595-6	Sequence 6, Appli
853	123	6.8	2181	3	US-09-254-465A-7	Sequence 7, Appli	926	119.5	6.6	1295	3	US-08-863-790-25	Sequence 25, Appl
854	123	6.8	2181	3	US-09-254-465A-11	Sequence 11, Appl	927	119.5	6.6	1295	3	US-08-296-749-25	Sequence 25, Appl
855	123	6.8	2181	4	US-09-953-499-7	Sequence 7, Appli	928	119.5	6.6	1518	3	US-09-240-915-2	Sequence 2, Appli
856	123	6.8	2181	4	US-09-953-499-11	Sequence 11, Appl	929	119.5	6.6	1518	3	US-09-591-435-2	Sequence 2, Appli
857	123	6.8	2463	1	US-08-339-578-1	Sequence 1, Appli	930	119.5	6.6	1582	4	US-09-419-788-25	Sequence 25, Appl
858	123	6.8	2537	3	US-09-173-151A-34	Sequence 34, Appl	931	119.5	6.6	1654	4	US-09-419-788-28	Sequence 28, Appl
859	123	6.8	5727	4	US-09-628-188A-1	Sequence 1, Appli	932	119.5	6.6	2360	4	US-09-023-655-1288	Sequence 1288, Ap
860	122.5	6.8	483	1	US-08-096-277-17	Sequence 17, Appl	933	119.5	6.6	2587	4	US-09-949-016-3321	Sequence 3321, Ap
861	122.5	6.8	483	2	US-08-550-815-17	Sequence 17, Appl	934	119.5	6.6	2587	4	US-09-949-016-3322	Sequence 3322, Ap
862	122.5	6.8	483	3	US-08-703-089-17	Sequence 17, Appl	935	119.5	6.6	2587	4	US-09-949-016-3323	Sequence 3323, Ap
863	122.5	6.8	1387	2	US-08-979-424-2	Sequence 2, Appli	936	119.5	6.6	2587	4	US-09-949-016-3324	Sequence 3324, Ap
864	122.5	6.8	1813	4	US-09-907-794A-38	Sequence 38, Appl	937	119.5	6.6	2587	4	US-09-949-016-3325	Sequence 3325, Ap
865	122.5	6.8	1813	4	US-09-905-125A-38	Sequence 38, Appl	938	119.5	6.6	2587	4	US-09-949-016-3326	Sequence 3326, Ap
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869	122.5	6.8	1813	4	US-09-904-920A-38	Sequence 38, Appl	942	119	6.6	2387	4	US-09-949-016-2268	Sequence 2268, Ap
870	122.5	6.8	1813	4	US-09-909-064-38	Sequence 38, Appl	943	119	6.6	2733	4	US-09-313-942-27	Sequence 27, Appl
871	122.5	6.8	1813	4	US-09-905-361A-38	Sequence 38, Appl	944	119	6.6	3397	4	US-09-949-016-2188	Sequence 2188, Ap
872	122.5	6.8	1813	4	US-09-906-618-38	Sequence 38, Appl	945	118.5	6.6	1077	4	US-09-419-788-27	Sequence 27, Appl
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875	122	6.8	991	3	US-08-833-488B-19	Sequence 19, Appl	948	118.5	6.6	8906	2	US-08-826-267-1	Sequence 2, Appl
c 876	122	6.8	991	3	US-08-833-488B-21	Sequence 21, Appl	949	117.5	6.5	576	4	US-09-270-767-2049	Sequence 2049, Ap
877	122	6.8	1476	3	US-08-753-007A-7	Sequence 7, Appli	950	117.5	6.5	576	4	US-09-270-767-17331	Sequence 17331, A
878	122	6.8	1476	3	US-09-398-496-7	Sequence 7, Appli	951	117.5	6.5	617	3	US-08-833-488B-13	Sequence 13, Appl
879	122	6.8	2081	4	US-09-949-016-3203	Sequence 3203, Ap	c 952	117.5	6.5	617	3	US-08-833-488B-15	Sequence 15, Appl
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881	122	6.8	2105	4	US-09-949-016-3204	Sequence 3204, Ap	954	117.5	6.5	1008	1	US-07-904-071-1	Sequence 1, Appli
882	122	6.8	2123	4	US-09-949-016-3202	Sequence 3202, Ap	955	117.5	6.5	1770	2	US-08-381-603-1	Sequence 1, Appli
883	122	6.8	2268	3	US-08-753-007A-31	Sequence 31, Appl	956	117.5	6.5	1770	3	US-08-924-376-1	Sequence 1, Appli
884	122	6.8	2268	3	US-09-398-496-31	Sequence 31, Appl	957	117.5	6.5	1770	3	US-08-685-212-1	Sequence 1, Appli
885	122	6.8	2390	4	US-09-774-528-334	Sequence 334, App	958	117.5	6.5	1770	3	US-08-466-932A-1	Sequence 1, Appli
886	122	6.8	3575	4	US-09-023-655-1395	Sequence 1395, Ap	959	117.5	6.5	1770	5	PCT-US94-02414-1	Sequence 1, Appli
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888	122	6.8	18478	4	US-09-949-016-15925	Sequence 15925, A	961	117.5	6.5	3011	1	US-07-821-716-1	Sequence 1, Appli

962	117.5	6.5	3011	4	US-08-406-824A-5	Sequence 5, Appli	1035	115	6.4	820	4	US-09-270-767-1214	Sequence 1214, Ap
963	117.5	6.5	4079	4	US-09-016-434-1219	Sequence 1219, Ap	1036	115	6.4	820	4	US-09-270-767-16456	Sequence 16456, A
964	117.5	6.5	4907	4	US-09-943-016-2701	Sequence 2701, Ap	1037	115	6.4	1078	6	5223394-10	Patent No. 5223394
965	117.5	6.5	4910	4	US-09-943-655-1125	Sequence 1125, Ap	1038	115	6.4	1078	6	5223394-10	Patent No. 5223394
966	117.5	6.5	4910	4	US-09-814-915A-75	Sequence 75, Appl	1039	115	6.4	1346	3	US-08-463-903-9	Sequence 9, Appli
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968	117	6.5	551	4	US-09-023-655-786	Sequence 786, App	1041	115	6.4	1796	3	US-08-477-460B-1	Sequence 1, Appli
969	117	6.5	793	4	US-09-270-767-1486	Sequence 1486, Ap	1042	115	6.4	1796	3	US-08-379-516-1	Sequence 1, Appli
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972	117	6.5	1607	3	US-09-398-496-3	Sequence 3, Appli	1045	115	6.4	1796	3	US-09-409-006A-1	Sequence 1, Appli
973	117	6.5	2290	4	US-09-131-648-4	Sequence 4, Appli	1046	115	6.4	1796	3	US-08-484-681-1	Sequence 1, Appli
974	117	6.5	2290	4	US-09-949-016-1143	Sequence 1143, Ap	1047	115	6.4	1796	3	US-09-766-995-1	Sequence 1, Appli
975	117	6.5	2461	4	US-09-620-312D-350	Sequence 350, App	1048	115	6.4	1796	5	PCT-US93-07422-1	Sequence 1, Appli
976	117	6.5	2461	4	US-08-753-007A-1	Sequence 1, Appli	1049	115	6.4	2027	4	US-08-896-537A-1	Sequence 1, Appli
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979	117	6.5	2639	4	US-09-907-794A-68	Sequence 68, Appl	1052	114.5	6.3	1781	1	US-08-314-615-2	Sequence 2, Appli
980	117	6.5	2639	4	US-09-905-125A-68	Sequence 68, Appl	1053	114.5	6.3	1781	1	US-08-314-615-2	Sequence 2, Appli
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982	117	6.5	2639	4	US-09-906-700-68	Sequence 68, Appl	1055	114.5	6.3	1781	1	US-08-245-295-4	Sequence 4, Appli
983	117	6.5	2639	4	US-09-903-603A-68	Sequence 68, Appl	1056	114.5	6.3	1781	1	US-08-481-130-4	Sequence 4, Appli
984	117	6.5	2639	4	US-09-904-920A-68	Sequence 68, Appl	1057	114.5	6.3	1781	1	US-08-656-984A-4	Sequence 4, Appli
985	117	6.5	2639	4	US-09-909-064-68	Sequence 68, Appl	1058	114.5	6.3	1781	1	US-08-482-882-2	Sequence 2, Appli
986	117	6.5	2639	4	US-09-905-381A-68	Sequence 68, Appl	1059	114.5	6.3	1781	1	US-08-485-604-4	Sequence 4, Appli
987	117	6.5	2639	4	US-09-906-618-68	Sequence 68, Appl	1060	114.5	6.3	1781	1	US-08-483-389-2	Sequence 2, Appli
988	117	6.5	3227	1	US-08-372-852-3	Sequence 3, Appli	1061	114.5	6.3	1781	2	US-08-487-113D-2	Sequence 2, Appli
989	117	6.5	3227	1	US-09-919-497-2	Sequence 2, Appli	1062	114.5	6.3	1781	2	US-08-487-595-4	Sequence 4, Appli
990	117	6.5	3254	1	US-08-372-892-1	Sequence 1, Appli	1063	114.5	6.3	1781	2	US-08-473-503-2	Sequence 2, Appli
991	117	6.5	4987	4	US-09-949-016-1724	Sequence 1724, Ap	1064	114.5	6.3	1781	2	US-08-483-932-2	Sequence 2, Appli
992	117	6.5	98708	4	US-09-949-016-16392	Sequence 16392, A	1065	114.5	6.3	1781	2	US-08-720-420A-2	Sequence 2, Appli
993	116.5	6.5	900	4	US-09-419-788-12	Sequence 12, Appl	1066	114.5	6.3	1781	3	US-08-714-017-2	Sequence 2, Appli
994	116.5	6.5	900	4	US-09-419-788-15	Sequence 15, Appl	1067	114.5	6.3	1781	3	US-08-863-790-2	Sequence 2, Appli
995	116.5	6.5	918	4	US-09-419-788-13	Sequence 13, Appl	1068	114.5	6.3	1781	3	US-08-475-680-2	Sequence 2, Appli
996	116.5	6.5	924	2	US-08-332-562A-82	Sequence 82, Appl	1069	114.5	6.3	1781	3	US-08-296-749-2	Sequence 2, Appli
997	116.5	6.5	1368	4	US-09-949-016-1078	Sequence 1078, Ap	1070	114.5	6.3	1781	4	US-08-314-369-2	Sequence 2, Appli
998	116.5	6.5	2043	3	US-08-227-496C-14	Sequence 14, Appl	1071	114.5	6.3	25321	4	US-09-949-016-12355	Sequence 12355, A
999	116.5	6.5	2372	4	US-09-023-655-1076	Sequence 1076, Ap	1072	114.5	6.3	25321	4	US-09-949-016-14039	Sequence 14039, A
1000	116	6.4	597	3	US-08-833-488B-16	Sequence 16, Appl	1073	113.5	6.3	711	6	5455030-8	Patent No. 5455030
c1001	116	6.4	597	3	US-08-833-488B-17	Sequence 17, Appl	1074	113.5	6.3	711	6	5455030-8	Patent No. 5455030
1002	116	6.4	1323	3	US-08-651-200-9	Sequence 9, Appli	1075	113.5	6.3	797	1	US-08-323-445A-3	Sequence 3, Appli
1003	116	6.4	2636	1	US-08-554-612C-12	Sequence 12, Appl	1076	113.5	6.3	797	1	US-08-515-903A-3	Sequence 3, Appli
1004	116	6.4	2885	3	US-09-651-200-3	Sequence 3, Appli	1077	113.5	6.3	797	5	PCT-US95-12840-3	Sequence 3, Appli
1005	116	6.4	2898	1	US-08-554-612C-51	Sequence 51, Appl	1078	113.5	6.3	921	3	US-08-996-338-4	Sequence 4, Appli
1006	116	6.4	2909	1	US-08-554-612C-10	Sequence 10, Appl	1079	113.5	6.3	921	3	US-09-556-972-4	Sequence 4, Appli
1007	116	6.4	2909	1	US-08-554-612C-11	Sequence 11, Appl	1080	113.5	6.3	921	3	US-08-996-338-11	Sequence 11, Appl
1008	116	6.4	3476	1	US-08-183-211-1	Sequence 1, Appli	1081	113.5	6.3	975	4	US-09-556-972-11	Sequence 11, Appl
1009	116	6.4	3476	5	PCT-US95-00176A-1	Sequence 2, Appli	1082	113.5	6.3	1453	4	US-09-773-877B-21	Sequence 21, Appl
1010	116	6.4	5843	1	US-08-554-612C-2	Sequence 2, Appli	1083	113.5	6.3	1557	3	US-08-996-338-2	Sequence 2, Appli
1011	115.5	6.4	687	3	US-08-833-488B-30	Sequence 30, Appl	1084	113.5	6.3	1557	4	US-09-556-972-2	Sequence 2, Appli
1012	115.5	6.4	755	1	US-08-323-445A-5	Sequence 5, Appli	1085	113.5	6.3	1739	4	US-09-016-434-1268	Sequence 1268, Ap
1013	115.5	6.4	755	1	US-08-515-903A-5	Sequence 5, Appli	1086	113.5	6.3	1817	1	US-08-473-981A-5	Sequence 5, Appli
1014	115.5	6.4	755	5	PCT-US95-12840-5	Sequence 5, Appli	1087	113.5	6.3	1817	2	US-08-474-087-5	Sequence 5, Appli
1015	115.5	6.4	1368	4	US-09-949-016-5155	Sequence 5155, Ap	1088	113.5	6.3	2830	1	US-08-604-333-3	Sequence 3, Appli
1016	115.5	6.4	1693	2	US-08-487-113D-118	Sequence 118, App	1089	113.5	6.3	2830	3	US-09-110-618-3	Sequence 3, Appli
1017	115.5	6.4	1693	2	US-08-720-420A-118	Sequence 118, App	1090	113.5	6.3	2830	3	US-09-578-178-3	Sequence 3, Appli
1018	115.5	6.4	2675	1	US-08-070-165F-5	Sequence 5, Appli	1091	113.5	6.3	2830	4	US-09-577-606-3	Sequence 3, Appli
1019	115.5	6.4	2675	2	US-08-885-418-5	Sequence 5, Appli	1092	113.5	6.3	2830	4	US-09-621-502-7	Sequence 7, Appli
c1020	115	6.4	344	4	US-09-702-705-964	Sequence 964, App	1093	113.5	6.3	3095	3	US-08-434-000A-7	Sequence 7, Appli
1021	115	6.4	344	4	US-09-702-705-1148	Sequence 1148, Ap	1094	113.5	6.3	3095	3	US-09-312-157-7	Sequence 7, Appli
1022	115	6.4	344	4	US-09-702-705-1321	Sequence 1321, Ap	1095	113.5	6.3	3095	4	US-09-717-888-7	Sequence 7, Appli
c1023	115	6.4	344	4	US-09-736-457-964	Sequence 964, App	1096	113.5	6.3	3556	4	US-09-270-767-10439	Sequence 10439, A
1024	115	6.4	344	4	US-09-736-457-1148	Sequence 1148, Ap	c1097	113	6.3	536	4	US-09-702-705-1461	Sequence 1461, Ap
1025	115	6.4	344	4	US-09-736-457-1321	Sequence 1321, Ap	c1098	113	6.3	536	4	US-09-736-457-1461	Sequence 1461, Ap
c1026	115	6.4	344	4	US-09-614-124B-964	Sequence 964, App	c1099	113	6.3	536	4	US-09-614-124B-1461	Sequence 1461, Ap
1027	115	6.4	344	4	US-09-614-124B-1148	Sequence 1148, Ap	c1100	113	6.3	536	4	US-09-671-325-1461	Sequence 1461, Ap
1028	115	6.4	344	4	US-09-614-124B-1321	Sequence 1321, Ap	c1101	113	6.3	536	4	US-09-658-824-1461	Sequence 1461, Ap
c1029	115	6.4	344	4	US-09-671-325-964	Sequence 964, App	1102	112.5	6.2	1106	3	US-09-361-434-16	Sequence 16, Appl
1030	115	6.4	344	4	US-09-671-325-1148	Sequence 1148, Ap	c1103	112.5	6.2	1106	3	US-09-361-434-18	Sequence 18, Appl
1031	115	6.4	344	4	US-09-671-325-1321	Sequence 1321, Ap	1104	112.5	6.2	1106	3	US-09-635-025-16	Sequence 16, Appl
c1032	115	6.4	344	4	US-09-658-824-964	Sequence 964, App	c1105	112.5	6.2	1106	3	US-09-635-025-18	Sequence 18, Appl
1033	115	6.4	344	4	US-09-658-824-1148	Sequence 1148, Ap	1106	112.5	6.2	1331	3	US-08-463-903-7	Sequence 7, Appli
1034	115	6.4	344	4	US-09-658-824-1321	Sequence 1321, Ap	1107	112.5	6.2	1331	3	US-07-935-695-7	Sequence 7, Appli

1108	112.5	6.2	1515	3	US-08-928-383B-25	Sequence 25, Appl	1181	110	6.1	1456	4	US-09-828-995B-16	Sequence 16, Appl
1109	112.5	6.2	1557	1	US-08-481-130-26	Sequence 26, Appl	c1182	110	6.1	1456	4	US-09-828-995B-18	Sequence 18, Appl
1110	112.5	6.2	1557	1	US-08-656-984A-26	Sequence 26, Appl	1183	110	6.1	1742	3	US-09-517-605-7	Sequence 7, Appl
1111	112.5	6.2	1557	1	US-08-485-604-26	Sequence 26, Appl	1184	110	6.1	1742	3	US-09-023-655-1013	Sequence 1013, Ap
1112	112.5	6.2	1557	2	US-08-487-595-26	Sequence 26, Appl	c1185	110	6.1	1742	3	US-09-453-702B-243	Sequence 243, App
1113	112.5	6.2	2433	4	US-08-999-889A-2	Sequence 2, Appl	1186	109.5	6.1	1213	1	US-08-554-612C-14	Sequence 14, Appl
1114	112.5	6.2	2433	4	US-09-944-807-3	Sequence 3, Appl	1187	109.5	6.1	1443	1	US-08-443-965B-10	Sequence 10, Appl
1115	112	6.2	1330	3	US-08-463-903-5	Sequence 5, Appl	1188	109.5	6.1	1443	2	US-08-425-989B-10	Sequence 10, Appl
1116	112	6.2	1330	3	US-07-935-695-5	Sequence 5, Appl	1189	109.5	6.1	1443	2	US-08-443-966B-10	Sequence 10, Appl
1117	112	6.2	2309	3	US-09-075-215A-16	Sequence 16, Appl	1190	109.5	6.1	1452	3	US-09-039-982A-36	Sequence 36, Appl
1118	111.5	6.2	989	3	US-09-361-434-21	Sequence 21, Appl	1191	109.5	6.1	1452	3	US-09-019-641-36	Sequence 36, Appl
1119	111.5	6.2	989	3	US-09-361-434-23	Sequence 23, Appl	1192	109.5	6.1	1452	3	US-09-039-762A-36	Sequence 36, Appl
1120	111.5	6.2	989	3	US-09-635-025-21	Sequence 21, Appl	1193	109.5	6.1	1452	3	US-09-042-492D-36	Sequence 36, Appl
1121	111.5	6.2	989	3	US-09-635-025-23	Sequence 23, Appl	1194	109.5	6.1	1452	3	US-08-913-612A-36	Sequence 36, Appl
1122	111.5	6.2	1359	4	US-08-961-309-69	Sequence 69, Appl	1195	109.5	6.1	1452	4	US-10-266-463A-36	Sequence 36, Appl
1123	111.5	6.2	1377	4	US-09-733-877B-25	Sequence 25, Appl	1196	109.5	6.1	1518	3	US-09-240-915-1	Sequence 1, Appl
1124	111.5	6.2	1704	3	US-09-032-337-38	Sequence 38, Appl	1197	109.5	6.1	1518	3	US-09-591-435-1	Sequence 1, Appl
1125	111.5	6.2	1907	4	US-09-949-016-1692	Sequence 1692, Ap	1198	109.5	6.1	1599	2	US-08-689-870-1	Sequence 1, Appl
1126	111.5	6.2	1928	4	US-09-723-368-1	Sequence 1, Appl	1199	109.5	6.1	1599	2	US-08-689-873-1	Sequence 1, Appl
1127	111.5	6.2	1928	4	US-09-949-016-407	Sequence 407, App	1200	109.5	6.1	1611	3	US-09-039-982A-35	Sequence 35, Appl
1128	111.5	6.2	3120	1	US-08-222-616-22	Sequence 22, Appl	1201	109.5	6.1	1611	3	US-09-039-641-35	Sequence 35, Appl
1129	111.5	6.2	3120	3	US-08-446-648-22	Sequence 22, Appl	1202	109.5	6.1	1611	3	US-09-039-762A-35	Sequence 35, Appl
1130	111.5	6.2	3120	4	US-09-982-610-22	Sequence 22, Appl	1203	109.5	6.1	1611	3	US-08-042-492D-35	Sequence 35, Appl
1131	111.5	6.2	3120	5	PCT-US93-64228-22	Sequence 22, Appl	1204	109.5	6.1	1611	3	US-08-913-612A-35	Sequence 35, Appl
1132	111.5	6.2	4989	3	US-09-560-639-3	Sequence 3, Appl	1205	109.5	6.1	1611	4	US-10-266-463A-35	Sequence 35, Appl
1133	111	6.1	966	3	US-09-361-434-19	Sequence 19, Appl	1206	109.5	6.1	1656	3	US-08-318-039A-2	Sequence 2, Appl
1134	111	6.1	966	3	US-09-361-434-20	Sequence 20, Appl	1207	109.5	6.1	1656	3	US-08-318-038D-16	Sequence 16, Appl
1135	111	6.1	966	3	US-09-635-025-19	Sequence 19, Appl	1208	109.5	6.1	1656	3	US-08-227-496C-20	Sequence 20, Appl
1136	111	6.1	966	3	US-09-635-025-20	Sequence 20, Appl	1209	109.5	6.1	1656	3	US-08-435-568A-2	Sequence 2, Appl
1137	111	6.1	1264	4	US-09-579-845-5	Sequence 5, Appl	1210	109.5	6.1	1784	1	US-08-554-612C-13	Sequence 13, Appl
1138	111	6.1	1286	4	US-09-949-016-3587	Sequence 3587, Ap	1211	109.5	6.1	1846	1	US-08-483-389-117	Sequence 117, App
1139	111	6.1	1357	1	US-08-091-519-1	Sequence 1, Appl	1212	109.5	6.1	2986	3	US-09-062-416-1	Sequence 1, Appl
1140	111	6.1	1357	1	US-08-442-043A-1	Sequence 1, Appl	1213	109.5	6.1	3003	4	US-09-023-655-1115	Sequence 1115, Ap
1141	111	6.1	1357	4	US-09-461-908-1	Sequence 1, Appl	1214	109.5	6.1	3016	2	US-08-344-155C-97	Sequence 97, Appl
1142	111	6.1	1357	4	US-08-441-893A-1	Sequence 1, Appl	1215	109.5	6.1	3017	3	US-09-009-490A-86	Sequence 86, Appl
1143	111	6.1	1357	4	US-08-406-824A-7	Sequence 7, Appl	1216	109.5	6.1	3024	6	5284931-1	Patent No. 5284931
1144	111	6.1	1357	4	US-09-921-667-7	Sequence 7, Appl	1217	109.5	6.1	3024	6	5284931-1	Patent No. 5284931
1145	111	6.1	1357	5	PCT-US91-03478-1	Sequence 1, Appl	1218	109	6.0	2142	4	US-09-774-528-100	Sequence 100, App
1146	111	6.1	1458	4	US-08-030-175-6	Sequence 6, Appl	1219	109	6.0	2163	4	US-09-774-528-99	Sequence 99, Appl
1147	111	6.1	1458	4	US-08-030-175-7	Sequence 7, Appl	1220	109	6.0	3734	3	US-09-579-692B-7	Sequence 7, Appl
1148	110.5	6.1	534	4	US-09-702-705-1325	Sequence 1325, Ap	1221	108.5	6.0	1255	4	US-09-412-554A-7	Sequence 7, Appl
1149	110.5	6.1	534	4	US-09-736-457-1325	Sequence 1325, Ap	1222	108.5	6.0	1320	2	US-08-125-462-3	Sequence 3, Appl
1150	110.5	6.1	534	4	US-09-614-124B-1325	Sequence 1325, Ap	1223	108.5	6.0	1320	2	US-08-891-848-3	Sequence 3, Appl
1151	110.5	6.1	534	4	US-09-671-325-1325	Sequence 1325, Ap	1224	108.5	6.0	2818	4	US-09-620-312D-92	Sequence 92, Appl
1152	110.5	6.1	534	4	US-09-658-824-1325	Sequence 1325, Ap	1225	108.5	6.0	2820	4	US-09-799-451-370	Sequence 370, App
1153	110.5	6.1	2614	2	US-08-795-868-15	Sequence 15, Appl	1226	108.5	6.0	4900	1	US-08-245-295-5	Sequence 5, Appl
1154	110.5	6.1	2614	3	US-09-303-069-15	Sequence 15, Appl	1227	108.5	6.0	4900	1	US-08-481-130-5	Sequence 5, Appl
1155	110.5	6.1	2614	3	US-09-134-250-15	Sequence 15, Appl	1228	108.5	6.0	4900	1	US-08-656-984A-5	Sequence 5, Appl
1156	110.5	6.1	2906	4	US-09-907-794A-291	Sequence 291, App	1229	108.5	6.0	4900	1	US-08-485-604-5	Sequence 5, Appl
1157	110.5	6.1	2906	4	US-09-905-125A-291	Sequence 291, App	1230	108.5	6.0	4900	2	US-08-487-595-5	Sequence 5, Appl
1158	110.5	6.1	2906	4	US-09-902-775A-291	Sequence 291, App	1231	108.5	6.0	4900	3	US-08-863-790-26	Sequence 26, Appl
1159	110.5	6.1	2906	4	US-09-906-700-291	Sequence 291, App	1232	108.5	6.0	4900	3	US-08-296-749-26	Sequence 26, Appl
1160	110.5	6.1	2906	4	US-09-903-603A-291	Sequence 291, App	1233	108.5	6.0	5077	1	US-08-245-295-8	Sequence 8, Appl
1161	110.5	6.1	2906	4	US-09-904-920A-291	Sequence 291, App	1234	108.5	6.0	5077	1	US-08-481-130-8	Sequence 8, Appl
1162	110.5	6.1	2906	4	US-09-909-064-291	Sequence 291, App	1235	108.5	6.0	5077	1	US-08-656-984A-8	Sequence 8, Appl
1163	110.5	6.1	2906	4	US-09-905-381A-291	Sequence 291, App	1236	108.5	6.0	5077	1	US-08-485-604-8	Sequence 8, Appl
1164	110.5	6.1	2906	4	US-09-906-618-291	Sequence 291, App	1237	108.5	6.0	5077	2	US-08-487-595-8	Sequence 8, Appl
1165	110.5	6.1	2926	4	US-08-724-394A-13	Sequence 13, Appl	1238	108	6.0	836	3	US-08-463-903-1	Sequence 1, Appl
1166	110.5	6.1	2970	4	US-09-566-921-105	Sequence 105, App	1239	108	6.0	836	3	US-07-935-695-1	Sequence 1, Appl
1167	110.5	6.1	7100	4	US-09-949-016-16418	Sequence 16418, A	1240	108	6.0	856	3	US-08-463-903-16	Sequence 16, Appl
1168	110	6.1	738	2	US-08-224-591-13	Sequence 13, Appl	1241	108	6.0	856	3	US-07-935-695-16	Sequence 16, Appl
1169	110	6.1	738	2	US-08-392-338A-22	Sequence 22, Appl	1242	108	6.0	1642	4	US-10-000-489-77	Sequence 77, Appl
1170	110	6.1	738	2	US-08-926-789-13	Sequence 13, Appl	1243	108	6.0	1645	2	US-08-724-394A-14	Sequence 14, Appl
1171	110	6.1	738	3	US-09-166-750-22	Sequence 22, Appl	1244	108	6.0	4626	4	US-09-566-921-4	Sequence 4, Appl
1172	110	6.1	738	3	US-09-166-093-22	Sequence 22, Appl	1245	108	6.0	24154	4	US-09-949-016-16374	Sequence 16374, A
1173	110	6.1	738	3	US-09-172-019-22	Sequence 22, Appl	1246	107.5	6.0	597	2	US-08-768-964-11	Sequence 11, Appl
1174	110	6.1	738	3	US-09-166-094-22	Sequence 22, Appl	c1247	107.5	6.0	597	2	US-08-768-964-16	Sequence 16, Appl
1175	110	6.1	738	4	US-09-443-213-22	Sequence 22, Appl	1248	107.5	6.0	597	3	US-09-005-299-11	Sequence 11, Appl
1176	110	6.1	738	5	PCT-US93-11138-13	Sequence 13, Appl	c1249	107.5	6.0	597	3	US-09-005-299-16	Sequence 16, Appl
1177	110	6.1	1213	6	5223418-1	Patent No. 5223418	1250	107.5	6.0	597	3	US-09-515-431-11	Sequence 11, Appl
1178	110	6.1	1213	6	5223418-1	Patent No. 5223418	c1251	107.5	6.0	597	3	US-09-515-431-16	Sequence 16, Appl
1179	110	6.1	1352	3	US-08-463-903-11	Sequence 11, Appl	1252	107.5	6.0	789	2	US-08-768-964-4	Sequence 4, Appl
1180	110	6.1	1352	3	US-07-935-695-11	Sequence 11, Appl	c1253	107.5	6.0	789	2	US-08-768-964-5	Sequence 5, Appl



c1254	107.5	6.0	789	3	US-09-005-299-4	Sequence 4, Appli	1327	103.5	5.7	409	4	US-09-702-705-1328	Sequence 1328, Ap
c1255	107.5	6.0	789	3	US-09-005-299-5	Sequence 5, Appli	1328	103.5	5.7	409	4	US-09-736-457-1328	Sequence 1328, Ap
c1256	107.5	6.0	789	3	US-09-515-431-4	Sequence 5, Appli	1329	103.5	5.7	409	4	US-09-614-124B-1328	Sequence 1328, Ap
c1257	107.5	6.0	789	3	US-09-515-431-5	Sequence 5, Appli	1330	103.5	5.7	409	4	US-09-671-325-1328	Sequence 1328, Ap
c1258	107.5	6.0	803	1	US-08-323-445A-7	Sequence 7, Appli	1331	103.5	5.7	409	4	US-09-688-824-1328	Sequence 1328, Ap
c1259	107.5	6.0	803	1	US-08-515-903A-7	Sequence 7, Appli	1332	103.5	5.7	522	2	US-08-768-964-14	Sequence 14, Appl
c1260	107.5	6.0	803	5	PCT-US95-12840-1	Sequence 7, Appli	c1333	103.5	5.7	522	2	US-08-768-964-15	Sequence 15, Appl
c1261	107.5	6.0	1069	2	US-08-768-964-1	Sequence 1, Appli	1334	103.5	5.7	522	3	US-09-005-299-14	Sequence 14, Appl
c1262	107.5	6.0	1069	2	US-08-768-964-3	Sequence 3, Appli	c1335	103.5	5.7	522	3	US-09-005-299-15	Sequence 15, Appl
c1263	107.5	6.0	1069	2	US-09-005-299-1	Sequence 1, Appli	1336	103.5	5.7	522	3	US-09-515-431-14	Sequence 14, Appl
c1264	107.5	6.0	1069	3	US-09-005-299-3	Sequence 3, Appli	c1337	103.5	5.7	522	3	US-09-515-431-15	Sequence 15, Appl
c1265	107.5	6.0	1069	3	US-09-515-431-1	Sequence 1, Appli	1338	103.5	5.7	714	2	US-08-768-964-6	Sequence 6, Appli
c1266	107.5	6.0	1069	3	US-09-515-431-3	Sequence 3, Appli	c1339	103.5	5.7	714	2	US-08-768-964-8	Sequence 8, Appli
c1267	107.5	6.0	63183	4	US-09-949-016-13047	Sequence 13047, A	1340	103.5	5.7	714	3	US-09-005-299-6	Sequence 6, Appli
c1268	107.5	6.0	63183	4	US-09-949-016-13048	Sequence 13048, A	c1341	103.5	5.7	714	3	US-09-005-299-8	Sequence 8, Appli
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c1270	107	5.9	752	6	5455030-12	Patent No. 5455030	c1343	103.5	5.7	714	3	US-09-515-431-8	Sequence 8, Appli
c1271	107	5.9	1149	3	US-08-477-460B-5	Sequence 5, Appli	1344	103.5	5.7	819	4	US-09-910-174B-20	Sequence 20, Appl
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ALIGNMENTS

RESULT 1  
US-09-700-397-1  
; Sequence 1, Application US/09700397  
; Patent No. 6664383  
; GENERAL INFORMATION:  
; APPLICANT: Ono Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of t  
; FILE REFERENCE: Q61459  
; CURRENT APPLICATION NUMBER: US/09/700,397  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: JP 10-131815  
; PRIOR FILING DATE: 1998-05-14  
; PRIOR APPLICATION NUMBER: PCT/JP99/02485  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1032  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-700-397-1  
Alignment Scores:  
Pred. No.: 1.43e-221 Length: 1032  
Score: 1806.00 Matches: 344  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
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Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
Db 241 AAGTGGTCCCTGGATCTCTCGGTGGTCTTCTGAGCAACACCCCAACGCAGTACAGCATC 300  
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
Db 301 GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360  
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
Db 361 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGAAGTATCTCCCAAAATTTGTAGAG 420  
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
Db 421 ATTCTTCAGATATCTCATTTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT 480  
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
Db 481 GGTAGACCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540  
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
Db 541 AGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600  
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220  
Db 601 TGCAGTGCTCTCAATGAGCTGGCCGCCCGGTGGTACGGAGAGTAAGGTCAACGTGAGAC 660  
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
Db 661 TATCCACCATACATTTACAGAGCCAAAGGTACAGGTGTCCCGCTGGGACAAAGGGGACA 720  
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260  
Db 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCTCAGCAGAAATTCACAGTGATACAAAGGATGACAAA 780  
Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
Db 781 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAATCTC 840  
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
Db 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACATACCTTGGCTGGCCTCCCAACAG 900  
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
Db 901 CTGGGCCACACCAATGCGCAGCATCATGTATTTGGTCCAGCGCGCGTCCAGCGAGTGAGC 960  
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340  
Db 961 AACGGCAGCTGAGAGGGGAGGCTGCGTCTGGCTGCTGCTTCTTCTGCTTTCGCTTTCGACCTG 1020  
Qy 341 LeuLeuLysPhe 344  
Db 1021 CTCTCAAAATTT 1032

RESULT 2  
US-09-700-397-2  
; Sequence 2, Application US/09700397  
; Patent No. 6664383  
; GENERAL INFORMATION:  
; APPLICANT: Ono Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of  
; FILE REFERENCE: Q61459  
; CURRENT APPLICATION NUMBER: US/09/700,397  
; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: JP 10-131815  
; PRIOR FILING DATE: 1998-05-14  
; PRIOR APPLICATION NUMBER: PCT/JP99/02485  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1693  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Clone OC001 derived from human brain  
; NAME/KEY: CDS  
; LOCATION: (130)..(1161)  
; NAME/KEY: sig\_peptide  
; LOCATION: (130)..(213)  
; NAME/KEY: mat\_peptide  
; LOCATION: (214)..()  
US-09-700-397-2  
Alignment Scores:  
Pred. No.: 3,35e-221 Length: 1693  
Score: 1806.00 Matches: 344  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-10-017-084A-523 (1-344) x US-09-700-397-2 (1-1693)  
Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20  
Db 130 ATGAAACCATTCAGCCCAAAATGCACAATTTCTCTTTGGGCAATCTTCACGGGGCTG 189  
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
Db 190 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCGAGGAGATGCCACCTTCCCAAAA 249  
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
Db 250 GCTATGACAAACGTGACGGTCCGGCAGGGGAGAGCCACCTTCAGGTGCATATTGAC 309  
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
Db 310 AACCGGTTCACCCGGGTGGCTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 369  
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
Db 370 AAGTGGTCCCTGGATCTCTCGGTGGTCTTCTGAGCAACACCCCAACGCAGTACAGCATC 429  
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
Db 430 GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 489  
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
Db 490 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCNAATTTGTAGAG 549  
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
Db 550 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCAACT 609  
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
Db 610 GGTAGACCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTCGGCTTTGTG 669  
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
Db 670 AGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 729  
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220

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Db 730 TGCAGTCCCTCAATGAGTGGCGCGCCGTGTGTACGGAGGTAAAGGTACCGTGAAC 789
Qy 221 TyrProPtyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 790 TATCCACCATACATTTTCAAGAGCAAGGGGTACAGGTGTCCCGGTGGACAAAAGGGGACA 849
Qy 241 LeuGlnCysGluAlaSerAlaValProSerIleGluPheGlnTyrLysAspAspLys 260
Db 850 CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGCAATTTCCAGTGTGTACAAAGGATGACAAA 909
Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 910 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAATC 969
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 970 ATCTTCTCAATGCTCTGAAATGACTATATGGAACTATACCTTCGGTGGCTCCAAACAG 1029
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1030 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGTCAGCGAGGTGAGC 1089
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLysLeu 340
Db 1090 AACGGCAGTCGAGAGGGCGAGGCTGGCTGTGGCTGTGCTCTCTCTGCTTTCACCTG 1149
Qy 341 LeuLeuLysPhe 344
Db 1150 CTTCTCAAAATTT 1161

RESULT 3
US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-5

Alignment Scores:
Pred. No.: 1,41e-200 Length: 939
Score: 1642.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.92% Indels: 0
DB: 4 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-700-397-5 (1-939)

Qy 32 ArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGlu 51
Db 1 CGCAGCGAGATGCCACCTTCCCAAGATATGACAACTGACGGTCCGGCAGGGGAG 60
Qy 52 SerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArg 71
Db 61 AGCGCACCTTCAGGTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGC 120
Qy 72 SerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeu 91
Db 121 AGCACCATCTCTATGTCTGGGAATGACAAAGTGGTGGCTGGATCTCGCGTGGCTCTTCTG 180
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Qy 92 SerAsnThrGlnThrGlnTyrSerIleGluIleAsnValAspValTyrAspGluGly 111
Db 181 AGCAACACCCAAACCGCAGTACAGCATCCAGATCCAGAACCGTGGATGTGTATGACAGGGC 240
Qy 112 ProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIle 131
Db 241 CTTTACACCTGCTCGGTGGTGACAGACAGAACCCAAAGACCTCTAGGGTCCACCTCAT 300
Qy 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
Db 301 GTGCAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAC 360
Qy 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
Db 361 AATATTAGCCTCACCTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACAC 420
Qy 172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrIleGlnGlyIle 191
Db 421 ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAATACTTTGGAATTTACAGGGCATC 480
Qy 192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
Db 481 ACCGGGAGCAGTCAGGGGACTACGAGTCAGTGCCTTCCAATGACGTGGCGCGCCGGTG 540
Qy 212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
Db 541 GTACGGAGAGTAAAGGTACCGTGAACCTATCCACCACATACATTTTCAGAAAGCAAGGGTACA 600
Qy 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
Db 601 GGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 660
Qy 252 GluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLysVal 271
Db 661 GAATTCAGTGTGTACAGGATGACAAAGACTGATTAAGGAAGAAAGGGGTGAAGGTG 720
Qy 272 GluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGly 291
Db 721 GAAACACAGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGG 780
Qy 292 AsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe 311
Db 781 AACTACACTTGGCGTGGCTCCAAACAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 840
Qy 312 GlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrp 331
Db 841 GGTCCAGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCTCTGG 900
Qy 332 LeuLeuProLeuLeuValLeuHisLeuLeuLysPhe 344
Db 901 CTGCTGCTCTTCTGTGCTTTGCACCTGCTTCTCAAAATTT 939

RESULT 4
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 403
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CB1
US-09-976-594-403

Alignment Scores:
Pred. No.:      3.83e-109      Length:      1195
Score:          931.50        Matches:      180
Percent Similarity: 73.85%      Conservative: 60
Best Local Similarity: 55.38%    Mismatches:  80
Query Match:     51.58%        Indels:       5
DB:              4            Gaps:          4

US-10-017-084A-523 (1-344) x US-09-976-594-403 (1-1195)

Qy 20 LeuAlaLeuLeuLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 49 CTGAGATTGCTCTGCTCTCTCCACAGAGTCTGCTGTTCGCGCGTGGAT-----TTT 102

Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 103 AACCGAGGCACGGACAACATCACCGTGAGCGAGGGGACACAGCCATCCTCAGGTGGTT 162

Qy 59 IleAspAsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyAlaGly 78
Db 163 CTAGAAGACAAGAACTCAAGGTGGCTGTGTGAACCGTTCTGGCATCATTTTGTGGA 222

Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnTyr 98
Db 223 CATGACAAGTGGTCTCTGGACCCAGGGTGTGAGTGGAGAAACGCCATTTCTCGAATAC 282

Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
Db 283 AGCCTCCGAATCCAGAAAGTGGATGCTATGATGAGGGTCTCTACACTTGTCTGATTCAG 342

Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 343 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAAGTCCCAACCAAGATC 402

Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
Db 403 TCCAAATATCTCTCGATGTCTGATGTGAATGAGGCGACAACGTGACTCTGGTCTGGATG 462

Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 463 GCCAATGCGCGTCTCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGAA 522

Qy 179 PheValSerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
Db 523 TTTGAAGGAGAAGAATAATCTGGAGATCTCTGGCATCCTCACCAGGAGCAGTCAGGCAAA 582

Qy 199 TyrGluCysSerAlaSerAsnAspValAlaProValValArgArgValLysValThr 218
Db 583 TATGAGTCAAAGCTGCCAAGAGGTCTCTCGGGGGATGTCAAACAAGTCAAGTCACT 642

Qy 219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 643 GTGAACATATCTCCCATCTATCACAGAACTCAAGAGCAATGAAGCCACCACAGGACGAA 702

Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAsp 258
Db 703 GCTTCACATAAATGTGAGGCGCTCGGCAGTGTGTCACCTGAGTGTGAGTGTACCGGAT 762

Qy 259 AspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 763 GACACTAGG---ATAAATAGTGCCCAATGGCTTGAATTAAGACGACGAGGGCGGAGTCT 819

Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
Db 820 TCCCTGAGCGGTGACCAACGTCTACTGAGGAGCAGTACGGCACTACACCTGTGTGCTGCC 879

Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 880 AACAAAGCTGGGGGTCAACCAATGCCAGCCTAGTCTCTTTTTCAGACCTGGGTGGTGAGGGA 939
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Qy 319 ValSerAsnGlyThrSerArgAlaGlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
Db 940 ATA---AATGGATCCATCAGTCTGGCGGTACCACCTGTGGCTGTGGCAGCATCTCTGCTC 996

Qy 339 HisLeuLeuLeuLys 343
Db 997 TGCCTTCTCAGCAA 1011

RESULT 5
US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1014
; OTHER INFORMATION:
US-08-414-657D-5

Alignment Scores:
Pred. No.:      1.27e-108      Length:      1014
Score:          926.50        Matches:      179
Percent Similarity: 73.54%      Conservative: 60
Best Local Similarity: 55.08%    Mismatches:  81
Query Match:     51.30%        Indels:       5
DB:              2            Gaps:          4

US-10-017-084A-523 (1-344) x US-08-414-657D-5 (1-1014)

Qy 20 LeuAlaLeuLeuLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 49 CTGAGACTGCTCTGCTCTCTCCACAGGAGTGGCCGTTCGACGCTGGAT-----TTT 102
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Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58  
Db 103 AACCGAGGACCGACCAATCACCGTGGAGGAGGAGGACCGGCATCTCAGGTGTG 162  
Qy 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78  
Db 163 GTAGAAGACAAAGATCGAAAGTGGCTGTGTGAACCGCTCTGCATCATCTTCGCTGA 222  
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98  
Db 223 CACGACAGTGTCTCTGGACCTCGGTTGAGTGGAGAACGCCATGCTCTCGAATAC 282  
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118  
Db 283 AGCTCTCGAATCCAGAAGTGGATGTCTATGATGAAGATCCTACATGCTCAGTTTCAG 342  
Qy 119 ThrAspAsnHisProLysThrSerArgValHisIleLeuValGlnValSerProLysIle 138  
Db 343 ACACAGATGAGCCCAAGACCTCTCAAGTTTACTTGTATGATTGATCAAGTTCCACCAAGATC 402  
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158  
Db 403 TCCAACTCTCTGGATGTCTGATGTGATGAGGAGCAGCATGTAAACCTGTCTGATG 462  
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178  
Db 463 GCCAATGGCGCCCTGAACCTGTATCACTACCTGGAGACACCTTACACCACTTGGGAAGAA 522  
Qy 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyLeuThrArgGluGlnSerGlyAsp 198  
Db 523 TTTGAAGGAGGAAGAATATCTCGAGATCTCGAGATCTAGGCATCACCGGGAACAGTCAGGCAA 582  
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218  
Db 583 TATGATGTCAGGTGTCACAGAGTCTCTCCGCGGATGTCAACAAAGTCAAGTCAAGTCACT 642  
Qy 219 ValAsnTyrProTyrTrpIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238  
Db 643 GTGAACATATCCACCACCATCACAGAGTCTAAGAGCAATGAAGCCACACAGGACGAA 702  
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258  
Db 703 GCTTCCCTCAATGGAAGCCTCAGCGTGCCTGCACCTGACTTTGAGTGTGTACCGGAT 762  
Qy 259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278  
Db 763 GACACCAAG---ATAACAGTGCACACCGCCTTGAGATTAGAGCAGTACGAGGCCAGTCC 819  
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298  
Db 820 TCCCTGACGGTGACCAACGTCCTACCTGAGGAACACTACGCGCACTATACCTGTGTGCTGCC 879  
Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318  
Db 880 AACAAAGTCTGGCGTCACCAATGTCAGCGCTAGTCTCTTTTCAGACCGGGTCCGTGAGAGA 939  
Qy 319 ValSerAsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeu 338  
Db 940 ATC---AACGGATCATCATGCTGCGGTACACTGTGGCTGCTGGCAGCGCTCCTGTC 996  
Qy 339 HisLeuLeuLeuLys 343  
Db 997 TGCCTTCTCAGCAAA 1011

## RESULT 6

US-09-135-080-7  
; Sequence 7, Application US/09135080  
; Patent No. 6423827

## GENERAL INFORMATION:

; APPLICANT: Levitt, Pat R.  
; APPLICANT: Pimenta, Aurea  
; APPLICANT: Fischer, Itzhak

; APPLICANT: Zhukareva, Victoria  
; TITLE OF INVENTION: Limbic System-Associated Membrane  
; TITLE OF INVENTION: Protein and DNA  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/135,080  
; FILING DATE: 17-AUG-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/414,657  
; FILING DATE: 31-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 317743-102A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-620-3214  
; TELEFAX: 609-620-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1014 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1..1014  
; OTHER INFORMATION:  
; US-09-135-080-7

## Alignment Scores:

Pred. No.: 1,27e-108 Length: 1014  
Score: 926.50 Matches: 179  
Percent Similarity: 73.54% Conservative: 60  
Best Local Similarity: 55.08% Mismatches: 81  
Query Match: 51.30% Indels: 5  
DB: 3 Gaps: 4

US-10-017-084A-523 (1-344) x US-09-135-080-7 (1-1014)

Qy 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38  
Db 49 CTGAGACTGTCTTCCTCTTCTCCACAGGACTGCGCGTTCGACGCTGGAT-----TTT 102  
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58  
Db 103 AACCGAGGACCGACCAATCACCGTGGAGGAGGAGGACCGGCATCTCAGGTGTG 162  
Qy 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78  
Db 163 GTAGAAGACAAAGATCTCGAAAGTGGCTGTGTGAACCGCTCTGCATCATCTTCGCTGA 222  
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98  
Db 223 CACGACAGTGTCTCTGGACCTCTCGGACCTTCGAGTGGAGAAACGCCATGCTCTCGAATAC 282  
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118  
Db 283 AGCTCTCGAATCCAGAAGTGGATGTCTATGATGAAGATCCTACATGCTCAGTTTCAG 342

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Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 343 ACACAGATGATGCGCCCAAGACCTCTCAAGTTTACTTGTGTACAAAGTTCCACCAAGATC 402
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
Db 403 TCCAAACATCTCTCGGATGTCACTGTGAATGAGGCGAGCAATGTAACCCCTGTCTGCATG 462
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 463 GCCAATGGCCGCCCTGAACTGTTATCACCTGGAGACACCTTACACACTTGGAGAGAA 522
Qy 179 PheValSerGluAspGluTyLeuGluIleGlnGlyLeuThrArgGluGlnSerGlyAsp 198
Db 523 TTTGAAGGAGAAGAATAATCTGGAGATCTCGAGATCTAGGCATCACAGGAAACAGTCAGGCAA 582
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValIleValThr 218
Db 583 TATGAGTCAAGGCTGCGCAACGAGGTCTCTCCGCGGATGTCAAAACAAGTCAAGGTCACT 642
Qy 219 ValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 643 GTGAACACTACCCACCATCACAGAGTCTAAGACAAATGAAGCCACACAGGACGAA 702
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
Db 703 GCTTCCCTCAAAATGTGAAGCTCAGCGGTGCTGCACCTGACTTTGAGTGTGTACCGGAT 762
Qy 259 AspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 763 GACACACAGG---ATAAACAGATGCAACCGCCCTTGAGATTAAAGAGCAGCTGAGGGCCAGTCC 819
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
Db 820 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGCAACTATACCTGTGTGGCTGCC 879
Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 880 AACAGCTCGCGGTCAACCAATGCCAGCTAGTCTCTTTTCAGACCCGGGTGCGTGAGAGGA 939
Qy 319 ValSerAsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
Db 940 ATC---AACGGATCCATCAGTCTGCGCCGTACCACTGTGGCTGTGGCAGCGTCCCTGTTC 996
Qy 339 HisLeuLeuLys 343
Db 997 TGCCTTCTCAGCAA 1011
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## RESULT 7

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US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:
; US-08-414-657D-3
Alignment Scores:
Pred. No.: 1-78e-108 Length: 1238
Score: 926.50 Matches: 179
Percent Similarity: 73.54% Conservative: 60
Best Local Similarity: 55.08% Mismatches: 81
Query Match: 51.30% Indels: 5
DB: 2 Gaps: 4
US-10-017-084a-523 (1-344) x US-08-414-657D-3 (1-1238)
Qy 20 LeuAlaAlaLeuCysLeuPhe--GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 104 CTGAGACTGCTTGCCTTCTCCACAGGACTGCCGTTCGACGCTGGAT-----TTT 157
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 158 AACCGAGCGCAGCAACATCACCGTGAGCGAGGCGGACACGGCCATCTCTCAGGTGTGTG 217
Qy 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
Db 218 GTAGAACACAGAACTCGAAAGTGGCTGTGTGAACCGCTCTGCATCATCTTCGCTGGA 277
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
Db 278 CACGACAAGTGGTCTCTGGACCCCTCGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 337
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
Db 338 AGCCTCCGAATCCAGAAGGTGGATGCTATGATGAAGGATCCTACACATGCTCAGTTCAG 397
Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGTGTGTACAAAGTTCCACCAAGATC 457
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
Db 458 TCCAAACATCTCTCGGATGTCACTGTGAATGAGGCGAGCAATGTAACCCCTGTCTGCATG 517
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 518 GCCAATGGCGCCCTGAACTGTTATCACCTGGAGACACCTTACACCACTTGGAGAGAA 577
Qy 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
Db 578 TTTGAAGGAGAAGAATAATCTGGAGATCTCGAGATCTACAGGAAACAGTCAGGCAA 637
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
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Db 638 TATGAGTGAAGGCTGCAACGAGGTCTCTCCCGGATGTCACAAAGTCAAGGTCACT 697
Qy 219 ValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 698 GTGAACATATCCACCACCATCACAGAGTCTAAGAGCAATGAAGCCACACAGGACGACAA 757
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAsp 258
Db 758 GCTTCCCTCAAAATGTGAAGCCTCAGCGGTGCTGCACCTGACTTTGAGTGTGACGGGAT 817
Qy 259 AspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 818 GACACCAAGG---ATAAACAGTGCACGCGCTTGAAGTTAAGAGCAGCTGAGGCGCAGTCC 874
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
Db 875 TCCCTGAGCGGTGACCAAGTCTACTGAGGAACACTACGCGCACTATACCTGTGTGCTGCC 934
Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 935 AACAAAGTCCGCGTCACCAATGCCAGCTAGTCTCTTTTCAGACCGCGGTGAGAGGA 994
Qy 319 ValSerAsnGlyThrSerArgAlaGlyCysValTyrPheLeuProLeuValLeu 338
Db 995 ATC---AACGGATCCATCAGTCTGCGCGGTACCACTGCTGTGCTGCTGCGCAGCGTCCCTGTTCC 1051
Qy 339 HisLeuLeuLys 343
Db 1052 TGCCTTCTCAGCAAA 1066

RESULT 8
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56..1069
; OTHER INFORMATION:
; US-09-135-080-3
Alignment Scores:
Pred. No.: 1.78e-108 Length: 1238
Score: 926.50 Matches: 179
Percent Similarity: 73.54% Conservative: 60
Best Local Similarity: 55.08% Mismatches: 81
Query Match: 51.30% Indels: 5
DB: 3 Gaps: 4
US-10-017-084a-523 (1-344) x US-09-135-080-3 (1-1238)
Qy 20 LeuAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 104 CTGAGACTGTCTGCTTCTTCCACAGGACTGCCCGTTGCGACGTGGAT-----TTT 157
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyLeuSerAlaThrLeuArgCysThr 58
Db 158 AACCGAGCGCAGGCAACATCACCGTGAGCGAGGGGACACGGCCATCTCTCAGGTGTGTG 217
Qy 59 IleAspAsnArgValThrArgValAlaTyrPheAsnArgSerThrIleLeuTyrAlaGly 78
Db 218 GTAGAGACAGAACTCGAAAGTGGCTGTGTGACCGCTCTGGCATCATCTTCTGCTGGA 277
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
Db 278 CACGACAAGTGGTCTCTGACCCCTCGCGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 337
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
Db 338 AGCCTCCGAATCCAGAAAGTGGATGCTATGATGAAGGATCCTACACATGCTCTGATTCAG 397
Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 398 ACACAGCATGAGCCCAAGACTCTCAAGTTTACTTTGATTGTACAGTTCCACCAAGATC 457
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIle 158
Db 458 TCCAAATCTCTCTCGGATGTCACTGTGAATGAGGCGAGCAATGTAACCTGCTCTGCATG 517
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 518 GCCAATGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACCTTGGAGAGAA 577
Qy 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAsp 198
Db 578 TTTGAAGAGAAAGAAATATCTGGAGATCTTAGGCATCACCAGGAAACAGTCAAGGCAAA 637
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
Db 638 TATGAGTGAAGGCTGCCAAGAGTCTCTCTCCCGGATGTCTCAAAACAGTCAAGTCACT 697
Qy 219 ValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlnLys 238
Db 698 GTGAACATATCCACCACCATCACAGAGTCTAAGAGCAATGAAGCCACACAGGACGACAA 757
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAsp 258
Db 758 GCTTCCCTCAAAATGTGAAGCCTCAGCGGTGCTGCACCTGACTTTGAGTGTGACGGGAT 817
Qy 259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 818 GACACCAAGG---ATAAACAGTGCACGCGCTTGAAGTTAAGAGCAGCTGAGGCGCAGTCC 874
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
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Db 875 TCCCTGACGGTGACCAACGTCACCTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 934  
Qy 299 AenlyseLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318  
Db 935 AACAGCTCGGGCGTCACCAATGCCAGCGCTAGTCCTTTTCAGACCCGGGTCCGTGAGAGGA 994  
Qy 319 ValSerAenGlyThrSerArgAlaGlyCysValTrpLeuProLeuLeuValLeu 338  
Db 995 ATC---AACGGATCCATCAGTCTGGCGCTACCACTGTGTGGCTGCTGGCAGCGCTCCCTGTTC 1051  
Qy 339 HisLeuLeuLeuLys 343  
Db 1052 TGCCTTCTCAGCAAA 1066

## RESULT 9

US-08-414-657D-1  
; Sequence 1, Application US/08414657D  
; Patent No. 5861283  
; GENERAL INFORMATION:  
; APPLICANT: Levitt, Pat  
; APPLICANT: Pimenta, Aurea  
; APPLICANT: Fischer, Itzhak  
; APPLICANT: Zhukareva, Victoria  
; TITLE OF INVENTION: Lmbic System-Associated Membrane  
; TITLE OF INVENTION: Protein and DNA  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,657D  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 317743-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 977 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 2...976  
; OTHER INFORMATION:  
US-08-414-657D-1

Alignment Scores:  
Pred. No.: 2,89e-108 Length: 977  
Score: 923.50 Matches: 177  
Percent Similarity: 74.06% Conservative: 60  
Best Local Similarity: 55.31% Mismatches: 78  
Query Match: 51.14% Indels: 5  
DB: 2 Gaps: 4

US-10-017-084A-523 (1-344) x US-08-414-657D-1 (1-977)  
Qy 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38  
Db 29 CTGAGATTGCTCTGCCCTTCTTCCACAGGACTGCTGTTCGACGGTGGAT-----TTT 82  
Qy 39 ProlyseAlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58  
Db 83 AACCGAGGCACGGACAACATCACCGTCAGGACGGGACACAGCATCTCTCAGGTGGT 142  
Qy 59 IleAspAenArgValThrArgValAlaTrpLeuAenArgSerThrIleLeuTyAlaGly 78  
Db 143 CTAGACACAAGAACTCAAAGGTGGCTGTGTGAACCGTTCTCGCATCATCTTTTGTCTGA 202  
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnTyr 98  
Db 203 CATGACAAGTGGTCTCTGGACCCACGGGTGAGCTGGAGAAACGCCATTCTCTGGAATAC 262  
Qy 99 SerIleGluIleGlnAenValAspValTyAspGluGlyProTyThrCysSerValGln 118  
Db 263 AGCTCTCCGAATCCAGAGGTGGATGCTATGATGAGGGTTCCTACACTTGTCTCAGTTCAG 322  
Qy 119 ThrAspAenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138  
Db 323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGTATCGTACAAGTCCCAACCAAGATC 382  
Qy 139 ValGluIleSerSerAspIleSerIleAenGluGlyAenAenIleSerLeuThrCysIle 158  
Db 383 TCCNATATCTCTCGGATGTCATGTGAATGAGGGCAGCAACGTGACTCTGCTGTGCAIG 442  
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178  
Db 443 GCCAATGGCGTCTCTGAACCTGTTATCACCTGGAGACACCTTACCAACCTGGAAGGAA 502  
Qy 179 PheValSerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198  
Db 503 TTTGAAGGAGAAGAATAATCTGGAGATCTCTGGCATCTCCAGGAGCAGTCAGGCAAA 562  
Qy 199 TyGluCysSerAlaSerAenAspValAlaAlaProValValArgValValValThr 218  
Db 563 TATGAGTGCAAAAGTGCACACGAGGTCTCTCTGGCGGATGTCAAAACAGTCAAGGTCACT 622  
Qy 219 ValAenTyProTyTrpIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238  
Db 623 GTGAACCTATCTCCCACTATCACAGATCCAAGAGCAATGAAGCCACCACAGGACGACAA 682  
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAsp 258  
Db 683 GCTTCACTCAATGTGAGGCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGAT 742  
Qy 259 AspLysArgLeuIleGluGlyLysLysValLysValGluAenArgProPheLeuSer 278  
Db 743 GACACTAGG---ATAAATAGTGCCTTGGCTTGAATTAAGACACGGAGGGCCAGTCT 799  
Qy 279 LysLeuIlePhePheAenValSerGluHisAspTyTrpGlyAenTyThrCysValAlaSer 298  
Db 800 TCCCTGACGGTGACCAACGTCACCTGAGGAGCAGTACGGCACTACACCTGTGTGGTCCC 859  
Qy 299 AsnLysLeuGlyHisThrAenAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318  
Db 860 AACAAAGCTGGGGGTCAACCAATGCCAGCTAGTCTCTTTTCAGACCTGGGTTCGGTGAAGA 919  
Qy 319 ValSerAenGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338  
Db 920 ATA---AATGGATCCATCAGTCTGGCGGTACCACTGTGGCTGTGGCAGCATCTCTGTCTC 976

## RESULT 10

US-09-135-080-1  
; Sequence 1, Application US/09135080  
; Patent No. 6423827  
; GENERAL INFORMATION:  
; APPLICANT: Levitt, Pat R.  
; APPLICANT: Pimenta, Aurea



APPLICANT: Fischer, Itzhak  
APPLICANT: Zhukareva, Victoria  
TITLE OF INVENTION: Limbic System-Associated Membrane  
TITLE OF INVENTION: Protein and DNA  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dechert Price & Rhoads  
STREET: 997 Lenox Drive, Building 3, Suite 210  
CITY: Lawrenceville  
STATE: NJ  
COUNTRY: USA  
ZIP: 08543

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/135,080  
FILING DATE: 17-AUG-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/414,657  
FILING DATE: 31-MAR-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Bloom, Allen  
REGISTRATION NUMBER: 29,135  
REFERENCE/DOCKET NUMBER: 317743-102A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-620-3214  
TELEFAX: 609-620-3259  
TELEX:

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 2...976  
OTHER INFORMATION:

US-09-135-080-1

Alignment Scores:

Pred. No.: 2,89e-108 Length: 977

Score: 923.50 Matches: 177

Percent Similarity: 74.06% Conservative: 60

Best Local Similarity: 55.31% Mismatches: 78

Query Match: 51.14% Indels: 5

DB: 3 Gaps: 4

US-10-017-084A-523 (1-344) x US-09-135-080-1 (1-977)

Qy 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38

Db 29 CTGAGATTGCTCTGCTTCTCCACAGACTGCTGTTGCGAGCGTGGAT-----TTT 82

Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58

Db 83 AACCGAGCCAGGACACATCACCGTGGAGGGGGGACACAGCCATCTCAGGTGGGTT 142

Qy 59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGly 78

Db 143 CTAGAAGACAAGAACTCAAGAGTGCCCTGGTGTGAACCGTTCTGGCATCATTTTGGCTGGA 202

Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrp 98

Db 203 CATGACAGTGGTCTCTGGACCCAGCGGTGAGTGGAGAACGCCATCTCTGGAATAC 262

Qy 99 SerTleGluIleGlnAsnValAspValTrpAspGluGlyProTyThrCysSerValGln 118

Db 263 AGCCTCCGAATCCAGAAGGTGGATGCTTATGATGAGGGTTCTTACACTTGTCTAGTTTCTAG 322

Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138

Db 323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGTGCTGTACAGTCCCAACCAAGATC 382

Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158

Db 383 TCCAATATCTCTCGGATGTCTGTAATGAGGGCAGCAACGTGACTCTGCTGTCATG 442

Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178

Db 443 GCCAATGGCCGTCTGAACCTGTATCACCCTGGAGACACCTTACCACTGGAAGGAA 502

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Db 860 AACAGCTGGGGTCCACCAATGCCAGCTAGTCTTTTCAGACCTGGTGGTGAGAGGA 919

Qy 319 ValSerAsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338

Db 920 ATA---AATGATCCATCAGTCTGGCGGTACCACTGTGGCTGTGGCAGCATCTCTGCTC 976

## RESULT 11

US-08-414-657D-7

; Sequence 7, Application US/08414657D

; Patent No. 5861283

; GENERAL INFORMATION:

; APPLICANT: Levitt, Pat

; APPLICANT: Pimenta, Aurea

; APPLICANT: Fischer, Itzhak

; APPLICANT: Zhukareva, Victoria

; TITLE OF INVENTION: Limbic System-Associated Membrane

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

; COUNTRY: USA

; ZIP: 08543

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/414,657D

; FILING DATE: 31-MAR-1995

; CLASSIFICATION: 435

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...924
; OTHER INFORMATION:
;
US-08-414-657D-7

Alignment Scores:
Pred. No.: 2,57e-106 Length: 924
Score: 908.00 Matches: 170
Percent Similarity: 75.50% Conservative: 58
Best Local Similarity: 56.29% Mismatches: 70
Query Match: 50.28% Indels: 4
DB: 2 Gaps: 3

US-10-017-084a-523 (1-344) x US-08-414-657D-7 (1-924)

Qy 20 LeuAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 28 CTGAGATTGCTCGCTCTTCCACAGGACTGCTGTTCGACGGTGGAT-----TTT 81
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 82 AACCGAGCGCAGGACACACATCACCGTGAGCGAGGGGACAGCATCTCCTCAGTGGT 141
Qy 59 IleAspAsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGly 78
Db 142 CTAGAAGACAGAACTCAAAGTGGCTGGTGAACCGTTCTGGCATCATTTTGTCTGGA 201
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
Db 202 CATGACAAAGTGGTCTCTGGACCCACGGGTTCAGCTGGAGAAACGCCATTCTCTGGAATAC 261
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
Db 262 AGCTCCGAATCCAGAGGTGGATGCTATGATGAGGGTTCCTACACTTGTCTCAGTTCAG 321
Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 322 ACACAGCATGAGCCCAACAGCTCCCAAGTTTACTTTGATCGTACAGTCCCAACCAAGATC 381
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAniIleSerLeuThrCysIle 158
Db 382 TCCAATATCTCTCGGATGTCACTGTGAATGAGGCGACCAACGTAAGTCTGTCTGTCATG 441
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 442 GCCAATGGCCGCTCTGAACCTGTTATCACCTGGAGACACCTTACACCACTGGAGGGAA 501
Qy 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
Db 502 TTGAAGGAGAAGAATAATCTCGAGATCTTGGCATCACCGAGGAGCAGTCAAGGCAA 561
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValIleValThr 218
Db 562 TATGAGTCAAAGCTGCCAACGAGGTCTCTCGCGGGATGTCAAAACAAAGTCAAGGTCACT
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US-08-414-657D-8		US-08-414-657D-6	
Alignment Scores:		Sequence 6, Application US/08414657D	
Pred. No.:	3-59e-106	Length:	945
Score:	907.00	Matches:	170
Percent Similarity:	75.50%	Conservative:	58
Best Local Similarity:	56.29%	Mismatches:	70
Query Match:	50.22%	Indels:	4
DB:	2	Gaps:	3
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Qy	20	LeuAlaLeuCysLeuPhe	38
Db	49	CTGAGACTGCTGCTCTTCCACAGACTGCGCGTTCGACGGTGGAT-----TTT	102
Qy	39	ProLysAlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThr	58
Db	103	AACCGAGGCGGACAAATCACCCTGAGCGGCGGACACGGCCATCCTCAGGTGTGTG	162
Qy	59	IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGly	78
Db	163	GTAGAAGCAAGAACTCGAAGTGGCTGTGACCGCTCTGGCATCATCTTCGCTGGA	222
Qy	79	AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr	98
Db	223	CACGACAAGTGGTCTCTGGACCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC	282
Qy	99	SerIleGluIleGlnAsnValAspValTyAspGluGlyProTyThrCysSerValGln	118
Db	283	AGCTCCGAATCCAGAAAGGTGGATGCTATGATGAAGGATCCTACATGCTCAGTTCAG	342
Qy	119	ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle	138
Db	343	ACACAGATGAGCCCAAGACTCTCAAGTTTACTTGATTGTACAGTTCCACCAAGATC	402
Qy	139	ValGluSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle	158
Db	403	TCCAACATCTCTCGGATGTCACTGTGAATGAGGCGCAAGTGAACCTGTGTGTCATG	462
Qy	159	AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly	178
Db	463	GCCAATGGGCGCCTGAACTGTTATCACCTGGAGACACCTTACACCCTTGGAAAGAA	522
Qy	179	PheValSerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp	198
Db	523	TTTGAAGAGAGAGAGATATCTGGAGATCTAGGATCACCAGGACAGTCAAGGAAA	582
Qy	199	TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr	218
Db	583	TATGAGTGAAGGTGCGCAACGAGGTCTCTCCCGCGATGTCAAAACAAGTCAAGGTCACT	642
Qy	219	ValAsnTyProProTyIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys	238
Db	643	GTGAACATATCCACCACCATCACAGGTCTTAAGAGCAATGAAGCCACACAGGACGAA	702
Qy	239	GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAsp	258
Db	703	GTCTCCCTCAATGTGAAGCCCTCAGCGGTGCTGCACCTGACTTGTAGTGTACGGGAT	762
Qy	259	AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer	278
Db	763	GACACACAGG---ATAAAGAGTGCAACCGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC	819
Qy	279	LysLeuIlePhePheAsnValSerGluHisAspTyArgIleAsnTyThrCysValAlaSer	298
Db	820	TCCCTGAGCGGTGACCAACGTCCTGAGGAAACACTACGCGCACTATCTGTGTGCTGCC	879
Qy	299	AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu	318
Db	880	AACAGCTCGCGGTGACCAATGCCAGCTTAGTCTCTTTTCAGACCCCGGTGCGTGAGAGGA	939
Qy	319	ValSer	320
US-08-414-657D-6		US-10-017-084A-523 (1-344) x US-08-414-657D-6 (1-912)	
RESULT 13		31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly	
Sequence 6, Application US/08414657D		1 GTTCGACGCTGGAT-----TTTACCGAGGCGGACCAACATCAGGTGAGCGAGGGG	
Patent No. 5861283		51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn	
GENERAL INFORMATION:		55 GACACACCATCTCAGTGGTCTTAGAAGACAAAGAACTCAAAGGTGGCTGTGTTGAAC	
APPLICANT: Levitt, Pat		71 ArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu	
APPLICANT: Pimenta, Aurea			
APPLICANT: Fischer, Itzhak			
APPLICANT: Zhukareva, Victoria			
TITLE OF INVENTION: Limbic System-Associated Membrane			
TITLE OF INVENTION: Protein and DNA			
NUMBER OF SEQUENCES: 60			
CORRESPONDENCE ADDRESS:			
ADDRESSER: Dechert Price & Rhoads			
STREET: 997 Lenox Drive, Building 3, Suite 210			
CITY: Lawrenceville			
STATE: NJ			
COUNTRY: USA			
ZIP: 08543			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette			
COMPUTER: IBM Compatible			
OPERATING SYSTEM: DOS			
SOFTWARE: FastSeq for Windows Version 2.0			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/414,657D			
FILING DATE: 31-MAR-1995			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:			
FILING DATE:			
ATTORNEY/AGENT INFORMATION:			
NAME: Bloom, Allen			
REGISTRATION NUMBER: 29,135			
REFERENCE/DOCKET NUMBER: 317743-102			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 609-520-3214			
TELEFAX: 609-520-3259			
TELEX:			
INFORMATION FOR SEQ ID NO: 6:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 912 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: double			
TOPOLOGY: linear			
FEATURE:			
NAME/KEY: Coding Sequence			
LOCATION: 1...912			
OTHER INFORMATION:			
US-08-414-657D-6			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			

Db 115 CGTTCTGGCATCATTTTGTGGACATGACAAGTGGTCTCTGGACCCACCGGTTGAGCTG 174  
Qy 91 LeuSerAsnThrGlnThrGlnThrSerIleGluLeuGlnAsnValAspValTyrAspGlu 110  
Db 175 GAGAAACGCCATTCTCTGGAATACAGCTCCGAATCCAGAAAGGTGGATGTCTATGATGAG 234  
Qy 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130  
Db 235 GGTTCCTACACTTGTCTAGTTCAAGACAGCATGAGGCCAAGACCTCCCAAGTTTACTTG 294  
Qy 131 IleValGlnValSerProLysIleValGluLeuSerSerAspIleSerIleAsnGluGly 150  
Db 295 ATCGTACAAGTCCCAACAGATCTCCAATATCTCTCGGATGTCACCTGTGAATGAGGCG 354  
Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170  
Db 355 AGCAACGTGACTCTGGTCTGATGGCCCAATGCGCGTCTGAACTCTTATCACCCTGGAGA 414  
Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190  
Db 415 CACCTTACACCACTGGAGGGAATTTGAGGAGAGAGAAATATCTGGAGATCCTTGGC 474  
Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210  
Db 475 ATCACCAGGAGCAGTCAGGCAAAATATGAGTGCAAGCTGCCAAGAGGTCTCTCGCGC 534  
Qy 211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230  
Db 535 GATGTCAAACAAAGTCAAGGTCACTGTGAACATATCTCCCACTATCAGAGAATCCAAAGC 594  
Qy 231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250  
Db 595 AATGAAGCCACACAGGACGACAGCTTCACTCAATGTGAGGCTCGGCAGTCCCTGCA 654  
Qy 251 AlaGluPheGlnTyrLysAspAspLysArgLeuIleGluGlyLysGlyValLys 270  
Db 655 CTGACTTTGAGTGGTACCGGATGACACTAGG--ATAAATAGTGCAATGGCCTTGAG 711  
Qy 271 ValGluAsnArgProPheLeuSerLysIlePhePheAsnValSerGluHisAspTyr 290  
Db 712 ATTAAGACACGAGGCGGACACTCTTCCCTGACGGTGACCAACGTCACCTGAGGAGCACTAC 771  
Qy 291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310  
Db 772 GGCACCTACACTGTGTGGCTGCCAACAGCTGGGGTCCCAATGCCAGCTAGTCTCT 831  
Qy 311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330  
Db 832 TTCAGACCTGGTGGTGAGAGGAATA--AATGGATCCATCACTCTGGCGGTACCACCTG 888  
Qy 331 TrpLeuLeuProLeuLeuValLeu 338  
Db 889 TGGCTGCTGGCAGCATCTCTGCTC 912

RESULT 14

US-08-414-657D-9  
; Sequence 9, Application US/08414657D  
; Patent No. 5861283  
; GENERAL INFORMATION:  
; APPLICANT: Levitt, Pat  
; APPLICANT: Pimenta, Aurea  
; APPLICANT: Fischer, Itzhak  
; APPLICANT: Zhukareva, Victoria  
; TITLE OF INVENTION: Limbic System-Associated Membrane  
; NUMBER OF INVENTION: Protein and DNA  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA

; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,657D  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 317743-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 861 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1..861  
; OTHER INFORMATION:  
; US-08-414-657D-9  
Alignment Scores:  
Pred. No.: 1,31e-103 Length: 861  
Score: 886.50 Matches: 164  
Percent Similarity: 76.21% Conservative: 57  
Best Local Similarity: 56.55% Mismatches: 66  
Query Match: 49.09% Indels: 3  
DB: 2 Gaps: 2  
US-10-017-084A-523 (1-344) x US-08-414-657D-9 (1-861)  
Qy 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50  
Db 1 GTTCCGACGCTGGAT-----TTTACCAGGACGACGACCAATCACCCTGAGGACGAGG 54  
Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70  
Db 55 GACACAGCCATCTCAGGTGCGTTCTAGAAAGACAAGAACTCAAAGGTGGCTGGTTCGAAC 114  
Qy 71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90  
Db 115 CGTTCTGGCATCATTTTGTGGACATGACAAGTGGTCTCTGGACCCACCGGTTGAGCTG 174  
Qy 91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110  
Db 175 GAGAAACGCCATTCTCTGGAATACAGCTCCGAATCCAGAGGTGGATGTCTATGATGAG 234  
Qy 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130  
Db 235 GGTTCCTACACTTGTCTCAGTTTCAGACACAGCATGAGGCCAAGACCTCCCAAGTTTACTTG 294  
Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150  
Db 295 ATCGTACAAGTCCCAACAGATCTCCAATATCTCTCGGATGTCACCTGTGAATGAGGCG 354  
Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170  
Db 355 AGCAACGTGACTCTGGTCTGATGGCCCAATGCGCGTCTGAACTCTTATCACCCTGGAGA 414  
Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190

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Db 415 CACCTTACCACTGGAAGGAATTTGAAGGAGAAGAAATATCTGGAGATCCTTGGC 474
Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
Db 475 ATCCACGGGAGCAGTCAGGCAATATAGTGCAAGGTGCCACGAGGTCTCTCGCGC 534
Qy 211 ValValArgValLysValThrValAsnTyrProTyrIleSerGluAlaLysGly 230
Db 535 GATGTCAACAAAGTCAAGGTCACTGTGAATCTATCTCCCACTATCACAGAAATCCAAGAGC 594
Qy 231 ThrGlyValProValGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
Db 595 AATGAGCCACACAGGAGCAAGCTTCACTCAAAATGTGAGGCTCGGAGTGCCTGCA 654
Qy 251 AlaGluPheGlnTyrTyrLysAspLysArgLeuIleGluGlyLysLysGlyValLys 270
Db 655 CTGACTTTGAGTGTACCGGATGACACTAGG---ATAAATAGTGCCCAATGGCCTTGAG 711
Qy 271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
Db 712 ATTAAGAGCAAGGAGGCGAGTCTTCCCTGACGGGTGACCAACGTCACCTGAGGAGCACTAC 771
Qy 291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
Db 772 GGCACACTACCTGTGTGGCTGCCAACAAAGCTGGGGGTGCACCAATGCCAGCCTAGTCCTT 831
Qy 311 PheGlyProGlyAlaValSerGluValSer 320
Db 832 TTCAGACCTGGGTGGTGAGGAGTAATAAT 861

RESULT 15
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastsEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...861
; OTHER INFORMATION:
US-08-414-657D-10
Alignment Scores:
Pred. No.: 1.77e-103 Length: 861
Score: 885.50 Matches: 164
Percent Similarity: 76.21% Conservative: 57
Best Local Similarity: 56.55% Mismatches: 66
Query Match: 49.03% Indels: 3
DB: 2 Gaps: 2
US-10-017-084A-523 (1-344) x US-08-414-657D-10 (1-861)
Qy 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
Db 1 GTTCGCGAGCGTGGAT-----TTTAAACCGAGGCGACGCAACATCATCCGTGAGGCGGGG 54
Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaThrLeuAsn 70
Db 55 GACACGGCCATCTCTCAGGTGTGTGAGAGACAAAGAACTCGAAAGTGGCCCTGTTGAAC 114
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Db 115 CGCTCTGGCATCATCTTCGCTGGACACGACAAAGTGTCTCTGGACCCCTCGGTTGAGCTG 174
Qy 91 LeuSerAsnThrGlnThrGlnTyrSerIleGlnLeuIleGlnAsnValAspValTyrAspGlu 110
Db 175 GAGAAACGCCATCTCTCGGAATACAGCCTCGGAATCCAGAAGGTGGATGTCTATGATGAA 234
Qy 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
Db 235 GGATCTTACATCATCTCAGTTCAGACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTG 294
Qy 131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
Db 295 ATTGTACAGTTCCACCAAGATCTCCAAATCTCTCGGATGTCATCTGTGAAATGAGGCG 354
Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
Db 355 AGCAATGTAAACCTCTGTCATGGCCCAATGGGGCCCTCGAACCTGTATCACCTGGAGA 414
Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
Db 415 CACCTTACACCACTTGGAGAGAAATTTTGAAGGAGAAGAAATATCTGGAGATCCTTAGGC 474
Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
Db 475 ATCCACGGGAGCAAGTCAGGCAATATAGTGCAAGGTGCCACGAGGTCTCTCGCGC 534
Qy 211 ValValArgValLysValThrValAsnTyrProTyrIleSerGluAlaLysGly 230
Db 535 GATGTCAACAAAGTCAAGGTCACTGTGAATCTATCTCCACCCCACTCACAGAGTCTAAGAGC 594
Qy 231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
Db 595 AATGAGCCACACAGGAGCAAGCTTCCCTCAAAATGTGAGGCTCGGAGTGCCTGCA 654
Qy 251 AlaGluPheGlnTyrTyrLysAspLysArgLeuIleGluGlyLysLysGlyValLys 270
Db 655 CTGACTTTGAGTGTACCGGATGACCAAGG---ATAAAGTGCACCAAGCGCTTGAG 711
Qy 271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
Db 712 ATTAAGAGCACTGAGGCGCAGTCTCTCTGACGGGTGACCAACGTCACCTGAGGAAACACTAC 771
Qy 291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
Db 772 GGCACACTATACCTGTGTGGCTGCCAACAAAGCTGGGGGTGCACCAATGCCAGCCTAGTCCTT 831
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 30, 2005, 11:29:37 ; Search time 936 Seconds  
(without alignments)  
3035.355 Million cell updates/sec

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Sequence: 1 MKTIQPMHNSISWAIFTGL.....RRACCVWLLPLLVHLHLKPF 344

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9784742 seqs, 4129495052 residues

Total number of hits satisfying chosen parameters: 19569484

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO.spool/US10017084/runat\_28102005\_112719\_9558/app\_query.fasta\_1.519  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=1500 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1806	100.0	1032	19	US-10-657-103-1	Sequence 1, Appl
53	1806	100.0	1679	15	US-10-066-269-103	Sequence 103, App
65	1806	100.0	1679	15	US-10-167-749-522	Sequence 522, App
227	1806	100.0	1679	16	US-10-223-085-55	Sequence 55, Appl
233	1806	100.0	1679	16	US-10-219-065-125	Sequence 125, App
263	1806	100.0	1679	16	US-10-223-084-55	Sequence 55, Appl
264	1806	100.0	1679	16	US-10-223-088-55	Sequence 55, Appl
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270	1806	100.0	1679	16	US-10-223-087-55	Sequence 55, Appl
272	1806	100.0	1679	16	US-10-223-083-55	Sequence 55, Appl
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663	1806	100.0	1679	22	US-10-805-667-522	Sequence 522, App
664	1806	100.0	1679	22	US-10-897-359-522	Sequence 522, App
666	1806	100.0	1679	22	US-10-893-800-522	Sequence 522, App
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684	1665.5	92.2	1678	14	US-10-098-841-72	Sequence 72, Appl
685	1665.5	92.2	1839	15	US-10-161-572-16	Sequence 16, Appl
686	1665.5	92.2	1839	18	US-10-295-027-455	Sequence 455, App
687	1665.5	92.2	3987	21	US-10-723-860-5804	Sequence 5804, Ap
688	1665.5	92.2	3987	21	US-10-723-860-7421	Sequence 7421, Ap
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693	1268	70.2	1071	15	US-10-161-572-34	Sequence 34, Appl
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695	1268	70.2	1478	15	US-10-161-572-35	Sequence 35, Appl
696	1268	70.2	3092	22	US-10-696-639-8	Sequence 8, Appli
697	1268	70.2	3110	15	US-10-161-572-32	Sequence 32, Appl
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855	823	45.6	4834	16	US-10-042-865-13	Sequence 13, Appl	1127	246.5	13.6	3360	9	US-09-954-531-985	Sequence 985, App
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1143	240	13.3	12667	22	US-10-852-335A-44	Sequence 44, Appl	1216	228	12.6	4452	24	US-10-450-763-28598	Sequence 28598, A
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1147	237.5	13.2	8180	9	US-09-905-129-8	Sequence 8, Appl	1220	225	12.5	2607	9	US-09-817-487A-1	Sequence 1, Appl
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1156	235.5	13.0	7872	19	US-10-454-351-31	Sequence 31, Appl	1229	224.5	12.4	7491	19	US-10-435-751-151	Sequence 151, App
1157	234	13.0	2420	18	US-10-104-047-333	Sequence 333, App	1230	224.5	12.4	7491	19	US-10-435-751-153	Sequence 153, App
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1195	229.5	12.7	7329	19	US-10-435-751-165	Sequence 165, App							
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